

GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: January 14, 2004, 10:28:18 ; Search time 32.5171 Seconds
(without alignments)
165.965 Million cell updates/sec

Title: US-09-843-221A-163
Perfect score: 34
Sequence: 1 SVSEIQLMHNKGKHLNSMERVEWLRKKLQDVHNF 34

Scoring table: OLIGO
Gapop 60.0 , Gapext 60.0

Searched: 1107863 seqs, 158726573 residues

Word size : 0

Total number of hits satisfying chosen parameters: 75810

Minimum DB seq length: 28

Maximum DB seq length: 40

Post-processing: Listing first 1000 summaries

Database : A_Geneseq_19Jun03:*

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- 23: /SIDS1/gcgdata/geneseq/geneseqp-embl/AA2002.DAT:*
- 24: /SIDS1/gcgdata/geneseq/geneseqp-embl/AA2003.DAT:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed,

and is derived by analysis of the total score distribution.

SUMMARIES

| Result No. | Score | % Query Match | Length | DB | ID | Description |
|------------|-------|------------------|--------|----|----------|--------------------|
| 1 | 34 | 100.0 | 34 | 13 | AAR22296 | Human parathyroid |
| 2 | 34 | 100.0 | 34 | 23 | AAU73030 | Parathyroid hormon |
| 3 | 30 | 88.2 | 30 | 23 | AAU73053 | Parathyroid hormon |
| 4 | 30 | 88.2 | 35 | 23 | AAU73174 | Parathyroid hormon |
| 5 | 24 | 70.6 | 34 | 18 | AAW08108 | Human parathyroid |
| 6 | 23 | 67.6 | 28 | 13 | AAR22064 | Modified hPTH(7-34 |
| 7 | 23 | 67.6 | 28 | 21 | ABJ10776 | Human parathyroid |
| 8 | 23 | 67.6 | 28 | 23 | AAE23734 | Human parathyroid |
| 9 | 23 | 67.6 | 28 | 23 | AAU73044 | Parathyroid hormon |
| 10 | 23 | 67.6 | 30 | 23 | AAE23752 | Human parathyroid |
| 11 | 23 | 67.6 | 32 | 21 | AAB07468 | Antigenic peptide |
| 12 | 23 | 67.6 | 32 | 23 | AAE23735 | Human parathyroid |
| 13 | 23 | 67.6 | 34 | 4 | AAP30022 | Human parathyroid- |
| 14 | 23 | 67.6 | 34 | 6 | AAP50377 | [Met(O)8,18]hPTH-(|
| 15 | 23 | 67.6 | 34 | 7 | AAP60031 | Sequence of the fi |
| 16 | 23 | 67.6 | 34 | 11 | AAR07919 | Human parathyroid |
| 17 | 23 | 67.6 | 34 | 13 | AAR22283 | Parathyroid hormon |
| 18 | 23 | 67.6 | 34 | 13 | AAR22292 | Human parathyroid |
| 19 | 23 | 67.6 | 34 | 13 | AAR22293 | Human parathyroid |
| 20 | 23 | 67.6 | 34 | 13 | AAR22294 | Human parathyroid |
| 21 | 23 | 67.6 | 34 | 14 | AAR41549 | [D-Ser3]hPTH (1-34 |
| 22 | 23 | 67.6 | 34 | 14 | AAR41550 | [D-Ala3]hPTH (1-34 |
| 23 | 23 | 67.6 | 34 | 14 | AAR41570 | [Gln25]hPTH (1-34) |
| 24 | 23 | 67.6 | 34 | 15 | AAR49697 | Sequence of varian |
| 25 | 23 | 67.6 | 34 | 15 | AAR49698 | Sequence of varian |
| 26 | 23 | 67.6 | 34 | 15 | AAR58291 | [Lys(For)26, Lys(F |
| 27 | 23 | 67.6 | 34 | 15 | AAR58228 | [D-Asp30]-hPTH(1-3 |
| 28 | 23 | 67.6 | 34 | 15 | AAR58016 | N-alpha-Isopropyl- |
| 29 | 23 | 67.6 | 34 | 15 | AAR58017 | [Lys(N-epsilon-Iso |
| 30 | 23 | 67.6 | 34 | 15 | AAR55724 | Parathormone N-ter |
| 31 | 23 | 67.6 | 34 | 16 | AAR74521 | Human parathyroid |
| 32 | 23 | 67.6 | 34 | 17 | AAW99449 | Human parathyroid |
| 33 | 23 | 67.6 | 34 | 17 | AAW15812 | [Trp(10)]-hPTH(1-3 |
| 34 | 23 | 67.6 | 34 | 17 | AAR99978 | Human parathyroid |
| 35 | 23 | 67.6 | 34 | 17 | AAR98951 | Target peptide (PT |
| 36 | 23 | 67.6 | 34 | 17 | AAR98966 | PTH(1-34). Not sp |
| 37 | 23 | 67.6 | 34 | 17 | AAR88835 | Human parathyroid |
| 38 | 23 | 67.6 | 34 | 18 | AAW24273 | Wild type parathyr |
| 39 | 23 | 67.6 | 34 | 18 | AAW08120 | Human PTH derivati |
| 40 | 23 | 67.6 | 34 | 18 | AAW08109 | Human parathyroid |
| 41 | 23 | 67.6 | 34 | 18 | AAW08113 | Human PTH derivati |
| 42 | 23 | 67.6 | 34 | 18 | AAW08114 | Human PTH derivati |
| 43 | 23 | 67.6 | 34 | 18 | AAW08117 | Human PTH derivati |
| 44 | 23 | 67.6 | 34 | 18 | AAW08118 | Human PTH derivati |
| 45 | 23 | 67.6 | 34 | 18 | AAW08119 | Human PTH derivati |
| 46 | 23 | 67.6 | 34 | 18 | AAW19994 | Cyclised human par |
| 47 | 23 | 67.6 | 34 | 18 | AAW20000 | Cyclised human par |
| 48 | 23 | 67.6 | 34 | 18 | AAW20006 | Cyclised human par |
| 49 | 23 | 67.6 | 34 | 18 | AAW17941 | Human parathyroid |
| 50 | 23 | 67.6 | 34 | 18 | AAW17943 | Human parathyroid |

| | | | | | | |
|-----|----|------|----|----|----------|--------------------|
| 51 | 23 | 67.6 | 34 | 18 | AAW17939 | Human parathyroid |
| 52 | 23 | 67.6 | 34 | 18 | AAW17957 | Human parathyroid |
| 53 | 23 | 67.6 | 34 | 18 | AAW01609 | Parathyroid hormon |
| 54 | 23 | 67.6 | 34 | 19 | AAW67274 | Parathyroid hormon |
| 55 | 23 | 67.6 | 34 | 19 | AAW67276 | Parathyroid hormon |
| 56 | 23 | 67.6 | 34 | 19 | AAW67278 | Parathyroid hormon |
| 57 | 23 | 67.6 | 34 | 19 | AAW67290 | Parathyroid hormon |
| 58 | 23 | 67.6 | 34 | 19 | AAW67291 | Parathyroid hormon |
| 59 | 23 | 67.6 | 34 | 19 | AAW67299 | Parathyroid hormon |
| 60 | 23 | 67.6 | 34 | 19 | AAW61658 | Parathyroid hormon |
| 61 | 23 | 67.6 | 34 | 19 | AAW65975 | Human parathyroid |
| 62 | 23 | 67.6 | 34 | 20 | AAV50593 | Resin bound cyclic |
| 63 | 23 | 67.6 | 34 | 20 | AAV17752 | Human parathyroid |
| 64 | 23 | 67.6 | 34 | 20 | AAV14151 | Human parathyroid |
| 65 | 23 | 67.6 | 34 | 20 | AAV02579 | N-terminal 34 resi |
| 66 | 23 | 67.6 | 34 | 20 | AAW81871 | Human PTH N-termin |
| 67 | 23 | 67.6 | 34 | 21 | ABJ10706 | Human parathyroid |
| 68 | 23 | 67.6 | 34 | 21 | ABJ10712 | Human parathyroid |
| 69 | 23 | 67.6 | 34 | 21 | ABJ10713 | Human parathyroid |
| 70 | 23 | 67.6 | 34 | 21 | ABJ10714 | Human parathyroid |
| 71 | 23 | 67.6 | 34 | 21 | ABJ10717 | Human parathyroid |
| 72 | 23 | 67.6 | 34 | 21 | ABJ10719 | Human parathyroid |
| 73 | 23 | 67.6 | 34 | 21 | ABJ10722 | Human parathyroid |
| 74 | 23 | 67.6 | 34 | 21 | ABJ10724 | Human parathyroid |
| 75 | 23 | 67.6 | 34 | 21 | ABJ10727 | Human parathyroid |
| 76 | 23 | 67.6 | 34 | 21 | ABJ10729 | Human parathyroid |
| 77 | 23 | 67.6 | 34 | 21 | ABJ10730 | Human parathyroid |
| 78 | 23 | 67.6 | 34 | 21 | ABJ10733 | Human parathyroid |
| 79 | 23 | 67.6 | 34 | 21 | ABJ10736 | Human parathyroid |
| 80 | 23 | 67.6 | 34 | 21 | ABJ10737 | Human parathyroid |
| 81 | 23 | 67.6 | 34 | 21 | ABJ10769 | Human parathyroid |
| 82 | 23 | 67.6 | 34 | 21 | AAB07454 | Amino acids 1-34 o |
| 83 | 23 | 67.6 | 34 | 21 | AAV98010 | Human amino-termin |
| 84 | 23 | 67.6 | 34 | 21 | AAV98011 | Human amino-termin |
| 85 | 23 | 67.6 | 34 | 21 | AAV98014 | Human amino-termin |
| 86 | 23 | 67.6 | 34 | 21 | AAV98017 | Human amino-termin |
| 87 | 23 | 67.6 | 34 | 21 | AAV82631 | Human parathyroid |
| 88 | 23 | 67.6 | 34 | 21 | AAV68763 | Amino acids 1-34 o |
| 89 | 23 | 67.6 | 34 | 22 | AAB84778 | Native rat parathy |
| 90 | 23 | 67.6 | 34 | 22 | AAB96898 | Human parathyroid |
| 91 | 23 | 67.6 | 34 | 22 | AAB81079 | Human parathyroid |
| 92 | 23 | 67.6 | 34 | 22 | AAB91098 | Parathyroid hormon |
| 93 | 23 | 67.6 | 34 | 22 | AAB91113 | Parathyroid hormon |
| 94 | 23 | 67.6 | 34 | 22 | AAB61638 | Peptide #1 that ca |
| 95 | 23 | 67.6 | 34 | 23 | ABJ05328 | Human PTH(1-34) pe |
| 96 | 23 | 67.6 | 34 | 23 | AAE23727 | Human parathyroid |
| 97 | 23 | 67.6 | 34 | 23 | AAE23728 | Human parathyroid |
| 98 | 23 | 67.6 | 34 | 23 | ABB06329 | Human parathyroid |
| 99 | 23 | 67.6 | 34 | 23 | ABB08595 | C-terminal truncat |
| 100 | 23 | 67.6 | 34 | 23 | AAE18395 | Human PTH peptide |
| 101 | 23 | 67.6 | 34 | 23 | AAE18399 | Human PTH peptide |
| 102 | 23 | 67.6 | 34 | 23 | ABB07147 | Parathyroid hormon |
| 103 | 23 | 67.6 | 34 | 23 | AAU73028 | Parathyroid hormon |
| 104 | 23 | 67.6 | 34 | 23 | AAU73029 | Parathyroid hormon |
| 105 | 23 | 67.6 | 34 | 23 | AAU73032 | Parathyroid hormon |
| 106 | 23 | 67.6 | 34 | 24 | ABP71500 | Human parathyroid |
| 107 | 23 | 67.6 | 34 | 24 | ABG74235 | Human parathyroid |

| | | | | | | |
|-----|----|------|----|----|----------|---------------------|
| 165 | 23 | 67.6 | 36 | 15 | AAR58197 | [Ala3]-hPTH(1-36)- |
| 166 | 23 | 67.6 | 36 | 15 | AAR58198 | [D-Ser3]-hPTH(1-36 |
| 167 | 23 | 67.6 | 36 | 15 | AAR58199 | [D-Glu4]-hPTH(1-36 |
| 168 | 23 | 67.6 | 36 | 15 | AAR58200 | [D-His9]-hPTH(1-36 |
| 169 | 23 | 67.6 | 36 | 15 | AAR58201 | [Ala10]-hPTH(1-36) |
| 170 | 23 | 67.6 | 36 | 15 | AAR58202 | [D-Asn10]-hPTH(1-3 |
| 171 | 23 | 67.6 | 36 | 15 | AAR58210 | [D-His14]-hPTH(1-3 |
| 172 | 23 | 67.6 | 36 | 15 | AAR58211 | [D-Asn16]-hPTH(1-3 |
| 173 | 23 | 67.6 | 36 | 15 | AAR58213 | [D-Ser17]-hPTH(1-3 |
| 174 | 23 | 67.6 | 36 | 15 | AAR58215 | [D-Glu19]-hPTH(1-3 |
| 175 | 23 | 67.6 | 36 | 15 | AAR58220 | [D-Lys26]-hPTH(1-3 |
| 176 | 23 | 67.6 | 36 | 15 | AAR58169 | [D-Pro1]-hPTH(1-36 |
| 177 | 23 | 67.6 | 36 | 15 | AAR58170 | [Nva1]-hPTH(1-36)- |
| 178 | 23 | 67.6 | 36 | 15 | AAR58171 | [N-Me-Ser1]-hPTH(1 |
| 179 | 23 | 67.6 | 36 | 15 | AAR58172 | [Indole-2-carboxyl |
| 180 | 23 | 67.6 | 36 | 15 | AAR58173 | [Indole-3-carboxyl |
| 181 | 23 | 67.6 | 36 | 15 | AAR58174 | [Pyridine-3-carbox |
| 182 | 23 | 67.6 | 36 | 15 | AAR58175 | [Pyridine-2-carbox |
| 183 | 23 | 67.6 | 36 | 15 | AAR58176 | [Hexahydropyridazi |
| 184 | 23 | 67.6 | 36 | 15 | AAR58177 | [Morpholine-2-carb |
| 185 | 23 | 67.6 | 36 | 15 | AAR58178 | [Pro1]-hPTH(1-36)- |
| 186 | 23 | 67.6 | 36 | 15 | AAR58179 | [Leu1]-hPTH(1-36)- |
| 187 | 23 | 67.6 | 36 | 15 | AAR58180 | [Ile1]-hPTH(1-36)- |
| 188 | 23 | 67.6 | 36 | 15 | AAR58182 | [Nva8]-hPTH(1-36)- |
| 189 | 23 | 67.6 | 36 | 15 | AAR58026 | N-alpha-methyl [Ala |
| 190 | 23 | 67.6 | 36 | 15 | AAR58168 | [1-amino-cyclopent |
| 191 | 23 | 67.6 | 37 | 12 | AAR11882 | Parathyroid hormon |
| 192 | 23 | 67.6 | 37 | 13 | AAR24778 | hPTH(1-37)-amide/e |
| 193 | 23 | 67.6 | 37 | 15 | AAR58244 | [Ala0]-hPTH(1-36)- |
| 194 | 23 | 67.6 | 37 | 15 | AAR58245 | [Pro0]-hPTH(1-36)- |
| 195 | 23 | 67.6 | 37 | 22 | AAB86226 | Human parathyroid |
| 196 | 23 | 67.6 | 37 | 22 | AAB86229 | Human parathyroid |
| 197 | 23 | 67.6 | 37 | 23 | ABB82203 | Human parathyroid |
| 198 | 23 | 67.6 | 37 | 23 | AAU73027 | Parathyroid hormon |
| 199 | 23 | 67.6 | 38 | 15 | AAR58269 | [Leu8]-hPTH(1-38)- |
| 200 | 23 | 67.6 | 38 | 15 | AAR58282 | [Trp(SO2Pmc)23]-hP |
| 201 | 23 | 67.6 | 38 | 15 | AAR58283 | [Trp(Pmc)23]-hPTH(|
| 202 | 23 | 67.6 | 38 | 15 | AAR58018 | Isopropyl-[Lys(Iso |
| 203 | 23 | 67.6 | 38 | 15 | AAR58019 | N-alpha-methyl [Ala |
| 204 | 23 | 67.6 | 38 | 15 | AAR58022 | [Ile1]-hPTH(1-38)- |
| 205 | 23 | 67.6 | 38 | 15 | AAR58023 | [Ala1, Abu2 or Nva2 |
| 206 | 23 | 67.6 | 38 | 15 | AAR58024 | [Ala1, Ile2]-hPTH(1 |
| 207 | 23 | 67.6 | 38 | 15 | AAR58028 | [Thr1]-hPTH(1-38)- |
| 208 | 23 | 67.6 | 38 | 15 | AAR58029 | [Leu1]-hPTH(1-38)- |
| 209 | 23 | 67.6 | 38 | 15 | AAR58030 | [Abu1 or Gabal]-hP |
| 210 | 23 | 67.6 | 38 | 15 | AAR54234 | PTH N-terminal. S |
| 211 | 23 | 67.6 | 38 | 17 | AAR98958 | Target peptide (PT |
| 212 | 23 | 67.6 | 38 | 20 | AAV02580 | N-terminal 38 resi |
| 213 | 23 | 67.6 | 38 | 22 | AAB91101 | Parathyroid hormon |
| 214 | 23 | 67.6 | 38 | 23 | AAE23729 | Human parathyroid |
| 215 | 23 | 67.6 | 38 | 23 | AAE18400 | Human PTH peptide |
| 216 | 23 | 67.6 | 38 | 23 | AAU73026 | Parathyroid hormon |
| 217 | 22 | 64.7 | 28 | 13 | AAR22065 | Modified [Tyr_34]h |
| 218 | 22 | 64.7 | 31 | 5 | AAP40760 | Human parathyroid |
| 219 | 22 | 64.7 | 32 | 5 | AAP40427 | Parathyroid antago |
| 220 | 22 | 64.7 | 33 | 17 | AAR88841 | Human parathyroid |
| 221 | 22 | 64.7 | 33 | 21 | AAV98012 | Human amino-termin |

| | | | | | | |
|-----|----|------|----|----|----------|---------------------|
| 108 | 23 | 67.6 | 35 | 22 | AAB91112 | Parathyroid hormon |
| 109 | 23 | 67.6 | 35 | 23 | AAU73172 | Parathyroid hormon |
| 110 | 23 | 67.6 | 35 | 23 | AAU73173 | Parathyroid hormon |
| 111 | 23 | 67.6 | 36 | 12 | AAR15842 | Human parathyroid |
| 112 | 23 | 67.6 | 36 | 13 | AAR23995 | Human paprthyroid |
| 113 | 23 | 67.6 | 36 | 14 | AAR39450 | Ser-Val-(hPTH 3-35 |
| 114 | 23 | 67.6 | 36 | 15 | AAR58286 | [D-Leu24]-hPTH(1-3 |
| 115 | 23 | 67.6 | 36 | 15 | AAR58292 | [D-Lys27]-hPTH(1-3 |
| 116 | 23 | 67.6 | 36 | 15 | AAR58293 | [D-Leu28]-hPTH(1-3 |
| 117 | 23 | 67.6 | 36 | 15 | AAR58294 | [D-Phe34]-hPTH(1-3 |
| 118 | 23 | 67.6 | 36 | 15 | AAR58295 | [D-Val35]-hPTH(1-3 |
| 119 | 23 | 67.6 | 36 | 15 | AAR58296 | [Ala35]-hPTH(1-36) |
| 120 | 23 | 67.6 | 36 | 15 | AAR58297 | [Pro35]-hPTH(1-36) |
| 121 | 23 | 67.6 | 36 | 15 | AAR58298 | [NMeVal35]-hPTH(1- |
| 122 | 23 | 67.6 | 36 | 15 | AAR58299 | [Thr35,Ala36]-hPTH |
| 123 | 23 | 67.6 | 36 | 15 | AAR58300 | [D-Ala36]-hPTH(1-3 |
| 124 | 23 | 67.6 | 36 | 15 | AAR58301 | [NMeAla36]-hPTH(1- |
| 125 | 23 | 67.6 | 36 | 15 | AAR58254 | [4-aminosalicylic |
| 126 | 23 | 67.6 | 36 | 15 | AAR58255 | [TMSA1]-hPTH(1-36) |
| 127 | 23 | 67.6 | 36 | 15 | AAR58256 | [Phe1]-hPTH(1-36)- |
| 128 | 23 | 67.6 | 36 | 15 | AAR58257 | [Propargylglycin1] |
| 129 | 23 | 67.6 | 36 | 15 | AAR58259 | [aBU2]-hPTH(1-36)- |
| 130 | 23 | 67.6 | 36 | 15 | AAR58260 | [D-Val2]-hPTH(1-36 |
| 131 | 23 | 67.6 | 36 | 15 | AAR58261 | [Tert. Leu]-hPTH(1- |
| 132 | 23 | 67.6 | 36 | 15 | AAR58262 | [Ala1]-hPTH(1-36)- |
| 133 | 23 | 67.6 | 36 | 15 | AAR58263 | [D-Ile5]-hPTH(1-36 |
| 134 | 23 | 67.6 | 36 | 15 | AAR58264 | [D-Gln6]-hPTH(1-36 |
| 135 | 23 | 67.6 | 36 | 15 | AAR58265 | [D-Leu7]-hPTH(1-36 |
| 136 | 23 | 67.6 | 36 | 15 | AAR58266 | [Nle8]-hPTH(1-36)- |
| 137 | 23 | 67.6 | 36 | 15 | AAR58267 | [Phe8]-hPTH(1-36)- |
| 138 | 23 | 67.6 | 36 | 15 | AAR58268 | [Cha8]-hPTH(1-36)- |
| 139 | 23 | 67.6 | 36 | 15 | AAR58270 | [D-Leu11]-hPTH(1-3 |
| 140 | 23 | 67.6 | 36 | 15 | AAR58271 | [Ala11]-hPTH(1-36) |
| 141 | 23 | 67.6 | 36 | 15 | AAR58272 | [D-Lys13]-hPTH(1-3 |
| 142 | 23 | 67.6 | 36 | 15 | AAR58273 | [D-Leu15]-hPTH(1-3 |
| 143 | 23 | 67.6 | 36 | 15 | AAR58276 | [Met(O2)18]-hPTH(1 |
| 144 | 23 | 67.6 | 36 | 15 | AAR58278 | [D-Met18]-hPTH(1-3 |
| 145 | 23 | 67.6 | 36 | 15 | AAR58280 | [D-Arg20]-hPTH(1-3 |
| 146 | 23 | 67.6 | 36 | 15 | AAR58281 | [D-Val21]-hPTH(1-3 |
| 147 | 23 | 67.6 | 36 | 15 | AAR58284 | [D-Trp23]-hPTH(1-3 |
| 148 | 23 | 67.6 | 36 | 15 | AAR58227 | [D-Gln29]-hPTH(1-3 |
| 149 | 23 | 67.6 | 36 | 15 | AAR58230 | [D-Val31]-hPTH(1-3 |
| 150 | 23 | 67.6 | 36 | 15 | AAR58233 | [D-His32]-hPTH(1-3 |
| 151 | 23 | 67.6 | 36 | 15 | AAR58235 | [D-Asn33]-hPTH(1-3 |
| 152 | 23 | 67.6 | 36 | 15 | AAR58237 | [NMePhe34]-hPTH(1- |
| 153 | 23 | 67.6 | 36 | 15 | AAR58238 | [D-Asp30]-hPTH(1-3 |
| 154 | 23 | 67.6 | 36 | 15 | AAR58242 | [Lys(Isopropyl)13] |
| 155 | 23 | 67.6 | 36 | 15 | AAR58243 | Propargyl-[A1]-hPT |
| 156 | 23 | 67.6 | 36 | 15 | AAR58246 | Acetyl-hPTH(1-36)- |
| 157 | 23 | 67.6 | 36 | 15 | AAR58247 | [Hyp1]-hPTH(1-36)- |
| 158 | 23 | 67.6 | 36 | 15 | AAR58248 | N-Dimethyl-[Ala1]- |
| 159 | 23 | 67.6 | 36 | 15 | AAR58249 | [D-Ser1]-hPTH(1-36 |
| 160 | 23 | 67.6 | 36 | 15 | AAR58250 | [Lys(For)1]-hPTH(1 |
| 161 | 23 | 67.6 | 36 | 15 | AAR58251 | [D-glyceric acid1] |
| 162 | 23 | 67.6 | 36 | 15 | AAR58252 | [Asn1]-hPTH(1-36)- |
| 163 | 23 | 67.6 | 36 | 15 | AAR58253 | [4-aminobenzoic ac |
| 164 | 23 | 67.6 | 36 | 15 | AAR58196 | [D-Phe34, D-Ala36] |

| | | | | | | |
|-----|----|------|----|----|-----------|--------------------|
| 222 | 22 | 64.7 | 33 | 21 | AAAY98015 | Human amino-termin |
| 223 | 22 | 64.7 | 33 | 21 | AAAY98018 | Human amino-termin |
| 224 | 22 | 64.7 | 34 | 11 | AAR07922 | Human parathyroid |
| 225 | 22 | 64.7 | 34 | 11 | AAR08300 | Human parathyroid |
| 226 | 22 | 64.7 | 34 | 15 | AAR58193 | [L8,D10,K11,T33,A3 |
| 227 | 22 | 64.7 | 34 | 15 | AAR58194 | [A1,H5,L8,D10,K11, |
| 228 | 22 | 64.7 | 34 | 18 | AAW08121 | Human PTH derivati |
| 229 | 22 | 64.7 | 34 | 18 | AAW08115 | Human PTH derivati |
| 230 | 22 | 64.7 | 34 | 18 | AAW08116 | Human PTH derivati |
| 231 | 22 | 64.7 | 34 | 18 | AAW17955 | Human parathyroid |
| 232 | 22 | 64.7 | 34 | 18 | AAW17959 | Human parathyroid |
| 233 | 22 | 64.7 | 34 | 19 | AAW48392 | Human parathyroid |
| 234 | 22 | 64.7 | 34 | 21 | ABJ10772 | Human parathyroid |
| 235 | 22 | 64.7 | 34 | 21 | ABJ10773 | Human parathyroid |
| 236 | 22 | 64.7 | 34 | 22 | AAB96929 | Human parathyroid |
| 237 | 22 | 64.7 | 36 | 15 | AAR58191 | [Ala34]-hPTH(1-36) |
| 238 | 22 | 64.7 | 36 | 15 | AAR58203 | [Ala12]-hPTH(1-36) |
| 239 | 22 | 64.7 | 38 | 3 | AAP20248 | Parathyroid hormon |
| 240 | 22 | 64.7 | 38 | 15 | AAR58089 | [Arg12]-hPTH(1-38) |
| 241 | 22 | 64.7 | 38 | 15 | AAR58090 | [Ser12]-hPTH(1-38) |
| 242 | 21 | 61.8 | 28 | 13 | AAR22066 | Modified [D-Trp_12 |
| 243 | 21 | 61.8 | 32 | 17 | AAR88840 | Human parathyroid |
| 244 | 21 | 61.8 | 34 | 11 | AAR08303 | Human parathyroid |
| 245 | 21 | 61.8 | 34 | 15 | AAR58181 | [Thr33, Ala34]-hPT |
| 246 | 21 | 61.8 | 34 | 18 | AAW08112 | Human PTH derivati |
| 247 | 21 | 61.8 | 34 | 19 | AAW42614 | Human parathyroid |
| 248 | 21 | 61.8 | 34 | 22 | AAB96893 | Rat parathyroid ho |
| 249 | 21 | 61.8 | 34 | 22 | AAB96930 | Rat parathyroid ho |
| 250 | 21 | 61.8 | 36 | 15 | AAR58236 | [Ala33]-hPTH(1-36) |
| 251 | 21 | 61.8 | 36 | 15 | AAR58204 | [Gln13]-hPTH(1-36) |
| 252 | 21 | 61.8 | 36 | 15 | AAR58205 | [His13]-hPTH(1-36) |
| 253 | 21 | 61.8 | 36 | 15 | AAR58206 | [Leu13]-hPTH(1-36) |
| 254 | 21 | 61.8 | 36 | 15 | AAR58207 | [Ala13]-hPTH(1-36) |
| 255 | 21 | 61.8 | 38 | 15 | AAR58161 | [Pro3,Thr33]-hPTH(|
| 256 | 21 | 61.8 | 38 | 15 | AAR58162 | [Arg33]-hPTH(1-38) |
| 257 | 21 | 61.8 | 38 | 15 | AAR58163 | [Pro33]-hPTH(1-38) |
| 258 | 21 | 61.8 | 38 | 15 | AAR58164 | [Asp33]-hPTH(1-38) |
| 259 | 21 | 61.8 | 38 | 15 | AAR58165 | [Ile33]-hPTH(1-38) |
| 260 | 21 | 61.8 | 38 | 15 | AAR58166 | [Lys33]-hPTH(1-38) |
| 261 | 21 | 61.8 | 38 | 15 | AAR58075 | [Ser33]-hPTH(1-38) |
| 262 | 21 | 61.8 | 38 | 15 | AAR58076 | [Thr33]-hPTH(1-38) |
| 263 | 21 | 61.8 | 38 | 15 | AAR58077 | [Leu33]-hPTH(1-38) |
| 264 | 21 | 61.8 | 38 | 15 | AAR58078 | [Gly33]-hPTH(1-38) |
| 265 | 21 | 61.8 | 38 | 15 | AAR58084 | [Gln33]-hPTH(1-38) |
| 266 | 21 | 61.8 | 38 | 15 | AAR58091 | [Cys13]-hPTH(1-38) |
| 267 | 21 | 61.8 | 38 | 15 | AAR58092 | [Ile13]-hPTH(1-38) |
| 268 | 21 | 61.8 | 38 | 15 | AAR58093 | [Asn13]-hPTH(1-38) |
| 269 | 21 | 61.8 | 38 | 15 | AAR58094 | [Trp13]-hPTH(1-38) |
| 270 | 21 | 61.8 | 38 | 15 | AAR58095 | [Asp13]-hPTH(1-38) |
| 271 | 21 | 61.8 | 38 | 15 | AAR58096 | [Val13]-hPTH(1-38) |
| 272 | 21 | 61.8 | 38 | 15 | AAR58097 | [Thr13]-hPTH(1-38) |
| 273 | 21 | 61.8 | 38 | 15 | AAR58098 | [Ser13]-hPTH(1-38) |
| 274 | 21 | 61.8 | 38 | 15 | AAR58099 | [Tyr13]-hPTH(1-38) |
| 275 | 21 | 61.8 | 38 | 15 | AAR58100 | [Met13]-hPTH(1-38) |
| 276 | 21 | 61.8 | 38 | 15 | AAR58101 | [Gln13]-hPTH(1-38) |
| 277 | 21 | 61.8 | 38 | 15 | AAR58102 | [Leu13]-hPTH(1-38) |
| 278 | 21 | 61.8 | 38 | 15 | AAR58103 | [Ala13]-hPTH(1-38) |

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|-----|----|------|----|----|----------|--------------------|
| 279 | 21 | 61.8 | 38 | 15 | AAR58104 | [Gly13]-hPTH(1-38) |
| 280 | 20 | 58.8 | 30 | 6 | AAP50665 | Human parathyroid |
| 281 | 20 | 58.8 | 31 | 17 | AAR88830 | Human parathyroid |
| 282 | 20 | 58.8 | 31 | 19 | AAW42059 | Human parathyroid |
| 283 | 20 | 58.8 | 31 | 19 | AAW42051 | Human parathyroid |
| 284 | 20 | 58.8 | 31 | 20 | AAV02578 | N-terminal 31 resi |
| 285 | 20 | 58.8 | 31 | 22 | AAB81080 | Human parathyroid |
| 286 | 20 | 58.8 | 31 | 22 | AAB91097 | Parathyroid hormon |
| 287 | 20 | 58.8 | 31 | 23 | AAE23720 | Human parathyroid |
| 288 | 20 | 58.8 | 31 | 23 | AAU73039 | Parathyroid hormon |
| 289 | 20 | 58.8 | 32 | 23 | AAU73176 | Parathyroid hormon |
| 290 | 20 | 58.8 | 34 | 15 | AAR58232 | [Lys32]-hPTH(1-34) |
| 291 | 20 | 58.8 | 34 | 18 | AAW08129 | Human PTH derivati |
| 292 | 20 | 58.8 | 34 | 22 | AAB84771 | Parathyroid hormon |
| 293 | 20 | 58.8 | 34 | 22 | AAB84826 | Parathyroid hormon |
| 294 | 20 | 58.8 | 34 | 22 | AAB96916 | Parathyroid hormon |
| 295 | 20 | 58.8 | 34 | 22 | AAB96919 | Parathyroid hormon |
| 296 | 20 | 58.8 | 36 | 15 | AAR58234 | [Ala32]-hPTH(1-36) |
| 297 | 20 | 58.8 | 36 | 15 | AAR58209 | [Ala14]-hPTH(1-36) |
| 298 | 20 | 58.8 | 38 | 15 | AAR58037 | [Ser14]-hPTH(1-38) |
| 299 | 20 | 58.8 | 38 | 15 | AAR58105 | [Val14]-hPTH(1-38) |
| 300 | 20 | 58.8 | 38 | 15 | AAR58106 | [Ala14]-hPTH(1-38) |
| 301 | 20 | 58.8 | 38 | 15 | AAR58107 | [Lys14]-hPTH(1-38) |
| 302 | 20 | 58.8 | 38 | 15 | AAR58108 | [Arg14]-hPTH(1-38) |
| 303 | 20 | 58.8 | 38 | 15 | AAR58109 | [Thr14]-hPTH(1-38) |
| 304 | 20 | 58.8 | 38 | 15 | AAR58110 | [Ile14]-hPTH(1-38) |
| 305 | 20 | 58.8 | 38 | 15 | AAR58111 | [Tyr14]-hPTH(1-38) |
| 306 | 19 | 55.9 | 30 | 17 | AAR88832 | Human parathyroid |
| 307 | 19 | 55.9 | 30 | 23 | AAU73051 | Parathyroid hormon |
| 308 | 19 | 55.9 | 30 | 23 | AAU73052 | Parathyroid hormon |
| 309 | 19 | 55.9 | 30 | 23 | AAU73055 | Parathyroid hormon |
| 310 | 19 | 55.9 | 31 | 23 | AAU73177 | Parathyroid hormon |
| 311 | 19 | 55.9 | 34 | 18 | AAW17942 | Human parathyroid |
| 312 | 19 | 55.9 | 34 | 18 | AAW17948 | Human parathyroid |
| 313 | 19 | 55.9 | 34 | 18 | AAW17968 | Human parathyroid |
| 314 | 19 | 55.9 | 34 | 18 | AAW17952 | Human parathyroid |
| 315 | 19 | 55.9 | 34 | 19 | AAW67277 | Parathyroid hormon |
| 316 | 19 | 55.9 | 34 | 19 | AAW67283 | Parathyroid hormon |
| 317 | 19 | 55.9 | 34 | 19 | AAW67287 | Parathyroid hormon |
| 318 | 19 | 55.9 | 34 | 19 | AAW48394 | Human PTH/PTHrP hy |
| 319 | 19 | 55.9 | 36 | 15 | AAR58274 | [Ala15]-hPTH(1-36) |
| 320 | 19 | 55.9 | 36 | 15 | AAR58231 | [Ala31]-hPTH(1-36) |
| 321 | 19 | 55.9 | 38 | 15 | AAR58061 | [Ile15]-hPTH(1-38) |
| 322 | 19 | 55.9 | 38 | 15 | AAR58167 | [Ile31,Arg33]-hPTH |
| 323 | 19 | 55.9 | 38 | 15 | AAR58112 | [Tyr15]-hPTH(1-38) |
| 324 | 19 | 55.9 | 38 | 15 | AAR58113 | [Arg15]-hPTH(1-38) |
| 325 | 19 | 55.9 | 38 | 15 | AAR58114 | [Val15]-hPTH(1-38) |
| 326 | 18 | 52.9 | 28 | 13 | AAR22058 | Modified bovine PT |
| 327 | 18 | 52.9 | 28 | 23 | AAU73046 | Parathyroid hormon |
| 328 | 18 | 52.9 | 29 | 17 | AAR88836 | Human parathyroid |
| 329 | 18 | 52.9 | 29 | 23 | AAU73063 | Parathyroid hormon |
| 330 | 18 | 52.9 | 30 | 23 | AAU73178 | Parathyroid hormon |
| 331 | 18 | 52.9 | 32 | 22 | AAB91096 | Parathyroid hormon |
| 332 | 18 | 52.9 | 32 | 23 | AAE23739 | Bovine parathyroid |
| 333 | 18 | 52.9 | 32 | 23 | AAE18402 | Bovine PTH peptide |
| 334 | 18 | 52.9 | 32 | 23 | AAU73042 | Parathyroid hormon |
| 335 | 18 | 52.9 | 34 | 11 | AAR07918 | Bovine parathyroid |

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| 336 | 18 | 52.9 | 34 | 11 | AAR08299 | Bovine parathyroid |
| 337 | 18 | 52.9 | 34 | 14 | AAR41551 | [Thr16]hPTH (1-34) |
| 338 | 18 | 52.9 | 34 | 14 | AAR41552 | [Glu16]hPTH (1-34) |
| 339 | 18 | 52.9 | 34 | 14 | AAR41553 | [Lys16]hPTH (1-34) |
| 340 | 18 | 52.9 | 34 | 14 | AAR41571 | [D-Lys16]hPTH (1-34) |
| 341 | 18 | 52.9 | 34 | 14 | AAR41573 | [Gln16]hPTH (1-34) |
| 342 | 18 | 52.9 | 34 | 14 | AAR41574 | [Ser16]hPTH (1-34) |
| 343 | 18 | 52.9 | 34 | 14 | AAR41575 | [Gly16]hPTH (1-34) |
| 344 | 18 | 52.9 | 34 | 14 | AAR41576 | [Lys16]hPTH (1-34) |
| 345 | 18 | 52.9 | 34 | 17 | AAR99979 | Bovine parathyroid |
| 346 | 18 | 52.9 | 34 | 18 | AAW08124 | Human PTH derivati |
| 347 | 18 | 52.9 | 34 | 18 | AAW08111 | Human PTH derivati |
| 348 | 18 | 52.9 | 34 | 18 | AAW19995 | Cyclised bovine pa |
| 349 | 18 | 52.9 | 34 | 18 | AAW20001 | Cyclised bovine pa |
| 350 | 18 | 52.9 | 34 | 18 | AAW20007 | Cyclised bovine pa |
| 351 | 18 | 52.9 | 34 | 18 | AAW17953 | Human parathyroid |
| 352 | 18 | 52.9 | 34 | 18 | AAW17963 | Human PTH analogue |
| 353 | 18 | 52.9 | 34 | 19 | AAW61659 | Parathyroid hormon |
| 354 | 18 | 52.9 | 34 | 19 | AAW65976 | Bovine parathyroid |
| 355 | 18 | 52.9 | 34 | 19 | AAW42615 | Bovine parathyroid |
| 356 | 18 | 52.9 | 34 | 20 | AAW81872 | Bovine PTH N-termi |
| 357 | 18 | 52.9 | 34 | 22 | AAB84775 | Parathyroid hormon |
| 358 | 18 | 52.9 | 34 | 22 | AAB96922 | Parathyroid hormon |
| 359 | 18 | 52.9 | 34 | 23 | AAE23738 | Bovine parathyroid |
| 360 | 18 | 52.9 | 34 | 23 | AAE18394 | Bovine PTH peptide |
| 361 | 18 | 52.9 | 34 | 23 | AAU73034 | Parathyroid hormon |
| 362 | 18 | 52.9 | 36 | 15 | AAR58275 | [Ala16]-hPTH(1-36) |
| 363 | 18 | 52.9 | 36 | 15 | AAR58229 | [Ala30]-hPTH(1-36) |
| 364 | 18 | 52.9 | 37 | 22 | AAB86230 | Bovine parathyroid |
| 365 | 18 | 52.9 | 37 | 22 | AAB86233 | Canine parathyroid |
| 366 | 18 | 52.9 | 37 | 23 | ABB82204 | Bovine parathyroid |
| 367 | 18 | 52.9 | 38 | 15 | AAR58036 | [Gln16]-hPTH(1-38) |
| 368 | 18 | 52.9 | 38 | 15 | AAR58115 | [Lys16]-hPTH(1-38) |
| 369 | 18 | 52.9 | 38 | 15 | AAR58116 | [Ser16]-hPTH(1-38) |
| 370 | 18 | 52.9 | 38 | 15 | AAR58117 | [Leu16]-hPTH(1-38) |
| 371 | 18 | 52.9 | 38 | 15 | AAR58118 | [Ala16]-hPTH(1-38) |
| 372 | 18 | 52.9 | 38 | 15 | AAR58119 | [Gly16]-hPTH(1-38) |
| 373 | 17 | 50.0 | 28 | 13 | AAR22059 | Modified [Tyr ₃₄]b |
| 374 | 17 | 50.0 | 28 | 13 | AAR22060 | Modified [D-Trp ₁₂ |
| 375 | 17 | 50.0 | 28 | 17 | AAR88837 | Human parathyroid |
| 376 | 17 | 50.0 | 28 | 21 | AAV98048 | Human parathyroid |
| 377 | 17 | 50.0 | 28 | 21 | AAV98050 | Human parathyroid |
| 378 | 17 | 50.0 | 28 | 21 | AAV98052 | Human parathyroid |
| 379 | 17 | 50.0 | 28 | 22 | AAB91115 | Parathyroid hormon |
| 380 | 17 | 50.0 | 28 | 23 | AAE18405 | Bovine PTH peptide |
| 381 | 17 | 50.0 | 28 | 23 | AAU73047 | Parathyroid hormon |
| 382 | 17 | 50.0 | 28 | 23 | AAU73050 | Parathyroid hormon |
| 383 | 17 | 50.0 | 28 | 23 | AAU73064 | Parathyroid hormon |
| 384 | 17 | 50.0 | 29 | 12 | AAR11731 | Adenine-rich PTH-(|
| 385 | 17 | 50.0 | 29 | 23 | AAU73179 | Parathyroid hormon |
| 386 | 17 | 50.0 | 31 | 5 | AAP40510 | Bovine parathyroid |
| 387 | 17 | 50.0 | 31 | 21 | AAV96973 | Parathyroid hormon |
| 388 | 17 | 50.0 | 31 | 21 | AAV96974 | Parathyroid hormon |
| 389 | 17 | 50.0 | 34 | 11 | AAR07921 | Bovine parathyroid |
| 390 | 17 | 50.0 | 34 | 11 | AAR08302 | Bovine parathyroid |
| 391 | 17 | 50.0 | 34 | 14 | AAR41577 | [Lys16, Asp17]hPTH |
| 392 | 17 | 50.0 | 34 | 14 | AAR41578 | [Lys14,15,16,17]hP |

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| 393 | 17 | 50.0 | 34 | 14 | AAW41579 | [Lys15,15,17]hPTH |
| 394 | 17 | 50.0 | 34 | 14 | AAW41580 | [Lys16,17]hPTH (1- |
| 395 | 17 | 50.0 | 34 | 14 | AAW41581 | [Arg16,17]hPTH (1- |
| 396 | 17 | 50.0 | 34 | 14 | AAW41582 | [Arg15,16,17]hPTH |
| 397 | 17 | 50.0 | 34 | 17 | AAW14308 | Cyclic parathyroid |
| 398 | 17 | 50.0 | 34 | 17 | AAW14309 | Cyclic parathyroid |
| 399 | 17 | 50.0 | 34 | 17 | AAW14310 | Cyclic parathyroid |
| 400 | 17 | 50.0 | 34 | 17 | AAW14311 | Cyclic parathyroid |
| 401 | 17 | 50.0 | 34 | 17 | AAW14312 | Cyclic parathyroid |
| 402 | 17 | 50.0 | 34 | 17 | AAW14313 | Cyclic parathyroid |
| 403 | 17 | 50.0 | 34 | 17 | AAW14314 | Cyclic parathyroid |
| 404 | 17 | 50.0 | 34 | 17 | AAW14315 | Cyclic parathyroid |
| 405 | 17 | 50.0 | 34 | 18 | AAW08122 | Human PTH derivati |
| 406 | 17 | 50.0 | 34 | 18 | AAW08123 | Human PTH derivati |
| 407 | 17 | 50.0 | 34 | 18 | AAW17958 | Human parathyroid |
| 408 | 17 | 50.0 | 34 | 18 | AAW01610 | Parathyroid hormon |
| 409 | 17 | 50.0 | 34 | 19 | AAW67293 | Parathyroid hormon |
| 410 | 17 | 50.0 | 36 | 15 | AAW58190 | [Ala29]-hPTH(1-36) |
| 411 | 17 | 50.0 | 36 | 15 | AAW58212 | [Ala17]-hPTH(1-36) |
| 412 | 17 | 50.0 | 38 | 15 | AAW58120 | [Ala17]-hPTH(1-38) |
| 413 | 17 | 50.0 | 38 | 15 | AAW58121 | [Met17]-hPTH(1-38) |
| 414 | 17 | 50.0 | 38 | 15 | AAW58122 | [Ile17]-hPTH(1-38) |
| 415 | 16 | 47.1 | 28 | 21 | ABJ10775 | Human parathyroid |
| 416 | 16 | 47.1 | 34 | 13 | AAW22291 | Human parathyroid |
| 417 | 16 | 47.1 | 34 | 13 | AAW22295 | Human parathyroid |
| 418 | 16 | 47.1 | 34 | 15 | AAW58239 | Isopropyl-[Nle8,18 |
| 419 | 16 | 47.1 | 34 | 15 | AAW58241 | [Nle8,18,D-Asn33,D |
| 420 | 16 | 47.1 | 34 | 17 | AAW14316 | Cyclic parathyroid |
| 421 | 16 | 47.1 | 34 | 17 | AAW99981 | Porcine parathyroi |
| 422 | 16 | 47.1 | 34 | 18 | AAW17947 | Human parathyroid |
| 423 | 16 | 47.1 | 34 | 18 | AAW17951 | Human parathyroid |
| 424 | 16 | 47.1 | 34 | 19 | AAW67282 | Parathyroid hormon |
| 425 | 16 | 47.1 | 34 | 19 | AAW67286 | Parathyroid hormon |
| 426 | 16 | 47.1 | 34 | 19 | AAW67298 | Parathyroid hormon |
| 427 | 16 | 47.1 | 34 | 19 | AAW61660 | Parathyroid hormon |
| 428 | 16 | 47.1 | 34 | 19 | AAW65977 | Porcine parathyroi |
| 429 | 16 | 47.1 | 34 | 19 | AAW42616 | Porcine parathyroi |
| 430 | 16 | 47.1 | 34 | 20 | AAW92218 | Analogue of parath |
| 431 | 16 | 47.1 | 34 | 20 | AAW92219 | Analogue of parath |
| 432 | 16 | 47.1 | 34 | 20 | AAW03920 | Analogue of parath |
| 433 | 16 | 47.1 | 34 | 20 | AAW03921 | Analogue of parath |
| 434 | 16 | 47.1 | 34 | 20 | AAW03922 | Analogue of parath |
| 435 | 16 | 47.1 | 34 | 20 | AAW03923 | Analogue of parath |
| 436 | 16 | 47.1 | 34 | 20 | AAW03924 | Analogue of parath |
| 437 | 16 | 47.1 | 34 | 20 | AAW03925 | Analogue of parath |
| 438 | 16 | 47.1 | 34 | 20 | AAW03926 | Analogue of parath |
| 439 | 16 | 47.1 | 34 | 20 | AAW03927 | Analogue of parath |
| 440 | 16 | 47.1 | 34 | 20 | AAW03928 | Analogue of parath |
| 441 | 16 | 47.1 | 34 | 20 | AAW03929 | Analogue of parath |
| 442 | 16 | 47.1 | 34 | 20 | AAW03930 | Analogue of parath |
| 443 | 16 | 47.1 | 34 | 20 | AAW03931 | Analogue of parath |
| 444 | 16 | 47.1 | 34 | 20 | AAW03932 | Analogue of parath |
| 445 | 16 | 47.1 | 34 | 20 | AAW03933 | Analogue of parath |
| 446 | 16 | 47.1 | 34 | 20 | AAW92236 | Analogue of parath |
| 447 | 16 | 47.1 | 34 | 20 | AAW92237 | Analogue of parath |
| 448 | 16 | 47.1 | 34 | 20 | AAW92238 | Analogue of parath |
| 449 | 16 | 47.1 | 34 | 20 | AAW92239 | Analogue of parath |

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| 450 | 16 | 47.1 | 34 | 20 | AAW92240 | Analogue of parath |
| 451 | 16 | 47.1 | 34 | 20 | AAW92241 | Analogue of parath |
| 452 | 16 | 47.1 | 34 | 20 | AAW92242 | Analogue of parath |
| 453 | 16 | 47.1 | 34 | 20 | AAW92243 | Analogue of parath |
| 454 | 16 | 47.1 | 34 | 20 | AAW92244 | Analogue of parath |
| 455 | 16 | 47.1 | 34 | 20 | AAW92245 | Analogue of parath |
| 456 | 16 | 47.1 | 34 | 20 | AAW92246 | Analogue of parath |
| 457 | 16 | 47.1 | 34 | 20 | AAW92247 | Analogue of parath |
| 458 | 16 | 47.1 | 34 | 20 | AAW92248 | Analogue of parath |
| 459 | 16 | 47.1 | 34 | 20 | AAW92249 | Analogue of parath |
| 460 | 16 | 47.1 | 34 | 20 | AAW92250 | Analogue of parath |
| 461 | 16 | 47.1 | 34 | 20 | AAY03919 | Analogue of parath |
| 462 | 16 | 47.1 | 34 | 20 | AAW92220 | Analogue of parath |
| 463 | 16 | 47.1 | 34 | 20 | AAW92221 | Analogue of parath |
| 464 | 16 | 47.1 | 34 | 20 | AAW92222 | Analogue of parath |
| 465 | 16 | 47.1 | 34 | 20 | AAW92223 | Analogue of parath |
| 466 | 16 | 47.1 | 34 | 20 | AAW92224 | Analogue of parath |
| 467 | 16 | 47.1 | 34 | 20 | AAW92225 | Analogue of parath |
| 468 | 16 | 47.1 | 34 | 20 | AAW92226 | Analogue of parath |
| 469 | 16 | 47.1 | 34 | 20 | AAW92227 | Analogue of parath |
| 470 | 16 | 47.1 | 34 | 20 | AAW92228 | Analogue of parath |
| 471 | 16 | 47.1 | 34 | 20 | AAW92229 | Analogue of parath |
| 472 | 16 | 47.1 | 34 | 20 | AAW92230 | Analogue of parath |
| 473 | 16 | 47.1 | 34 | 20 | AAW92231 | Analogue of parath |
| 474 | 16 | 47.1 | 34 | 20 | AAW92232 | Analogue of parath |
| 475 | 16 | 47.1 | 34 | 20 | AAW92233 | Analogue of parath |
| 476 | 16 | 47.1 | 34 | 20 | AAW92234 | Analogue of parath |
| 477 | 16 | 47.1 | 34 | 20 | AAW92235 | Analogue of parath |
| 478 | 16 | 47.1 | 34 | 20 | AAY03947 | Analogue of parath |
| 479 | 16 | 47.1 | 34 | 20 | AAY03948 | Analogue of parath |
| 480 | 16 | 47.1 | 34 | 20 | AAW92204 | Analogue of parath |
| 481 | 16 | 47.1 | 34 | 20 | AAW92205 | Analogue of parath |
| 482 | 16 | 47.1 | 34 | 20 | AAW92207 | Analogue of parath |
| 483 | 16 | 47.1 | 34 | 20 | AAW92208 | Analogue of parath |
| 484 | 16 | 47.1 | 34 | 20 | AAW92209 | Analogue of parath |
| 485 | 16 | 47.1 | 34 | 20 | AAW92210 | Analogue of parath |
| 486 | 16 | 47.1 | 34 | 20 | AAW92211 | Analogue of parath |
| 487 | 16 | 47.1 | 34 | 20 | AAW92212 | Analogue of parath |
| 488 | 16 | 47.1 | 34 | 20 | AAW92213 | Analogue of parath |
| 489 | 16 | 47.1 | 34 | 20 | AAW92214 | Analogue of parath |
| 490 | 16 | 47.1 | 34 | 20 | AAW92215 | Analogue of parath |
| 491 | 16 | 47.1 | 34 | 20 | AAW92216 | Analogue of parath |
| 492 | 16 | 47.1 | 34 | 20 | AAW92217 | Analogue of parath |
| 493 | 16 | 47.1 | 34 | 20 | AAW92206 | Analogue of parath |
| 494 | 16 | 47.1 | 34 | 20 | AAW92203 | Analogue of parath |
| 495 | 16 | 47.1 | 34 | 20 | AAY03934 | Analogue of parath |
| 496 | 16 | 47.1 | 34 | 20 | AAY03935 | Analogue of parath |
| 497 | 16 | 47.1 | 34 | 20 | AAY03936 | Analogue of parath |
| 498 | 16 | 47.1 | 34 | 20 | AAY03937 | Analogue of parath |
| 499 | 16 | 47.1 | 34 | 20 | AAY03938 | Analogue of parath |
| 500 | 16 | 47.1 | 34 | 20 | AAY03939 | Analogue of parath |
| 501 | 16 | 47.1 | 34 | 20 | AAY03940 | Analogue of parath |
| 502 | 16 | 47.1 | 34 | 20 | AAY03941 | Analogue of parath |
| 503 | 16 | 47.1 | 34 | 20 | AAY03942 | Analogue of parath |
| 504 | 16 | 47.1 | 34 | 20 | AAY03943 | Analogue of parath |
| 505 | 16 | 47.1 | 34 | 20 | AAY03944 | Analogue of parath |
| 506 | 16 | 47.1 | 34 | 20 | AAY03945 | Analogue of parath |

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| 507 | 16 | 47.1 | 34 | 20 | AAV03946 | Analogue of parath |
| 508 | 16 | 47.1 | 34 | 20 | AAV03949 | Analogue of parath |
| 509 | 16 | 47.1 | 34 | 20 | AAV03950 | Analogue of parath |
| 510 | 16 | 47.1 | 34 | 20 | AAV03951 | Analogue of parath |
| 511 | 16 | 47.1 | 34 | 20 | AAV03952 | Analogue of parath |
| 512 | 16 | 47.1 | 34 | 20 | AAV03953 | Analogue of parath |
| 513 | 16 | 47.1 | 34 | 20 | AAV03954 | Analogue of parath |
| 514 | 16 | 47.1 | 34 | 20 | AAV03955 | Analogue of parath |
| 515 | 16 | 47.1 | 34 | 20 | AAV03956 | Analogue of parath |
| 516 | 16 | 47.1 | 34 | 20 | AAW92198 | Analogue of parath |
| 517 | 16 | 47.1 | 34 | 20 | AAW92199 | Analogue of parath |
| 518 | 16 | 47.1 | 34 | 20 | AAW92200 | Analogue of parath |
| 519 | 16 | 47.1 | 34 | 20 | AAW92201 | Analogue of parath |
| 520 | 16 | 47.1 | 34 | 20 | AAW92202 | Analogue of parath |
| 521 | 16 | 47.1 | 34 | 20 | AAW92183 | Analogue of parath |
| 522 | 16 | 47.1 | 34 | 20 | AAW92184 | Analogue of parath |
| 523 | 16 | 47.1 | 34 | 20 | AAW92185 | Analogue of parath |
| 524 | 16 | 47.1 | 34 | 20 | AAW92186 | Analogue of parath |
| 525 | 16 | 47.1 | 34 | 20 | AAW92187 | Analogue of parath |
| 526 | 16 | 47.1 | 34 | 20 | AAW92167 | Analogue of parath |
| 527 | 16 | 47.1 | 34 | 20 | AAW92188 | Analogue of parath |
| 528 | 16 | 47.1 | 34 | 20 | AAW92189 | Analogue of parath |
| 529 | 16 | 47.1 | 34 | 20 | AAW92190 | Analogue of parath |
| 530 | 16 | 47.1 | 34 | 20 | AAW92191 | Analogue of parath |
| 531 | 16 | 47.1 | 34 | 20 | AAW92192 | Analogue of parath |
| 532 | 16 | 47.1 | 34 | 20 | AAW92193 | Analogue of parath |
| 533 | 16 | 47.1 | 34 | 20 | AAW92194 | Analogue of parath |
| 534 | 16 | 47.1 | 34 | 20 | AAW92195 | Analogue of parath |
| 535 | 16 | 47.1 | 34 | 20 | AAW92196 | Analogue of parath |
| 536 | 16 | 47.1 | 34 | 20 | AAW92197 | Analogue of parath |
| 537 | 16 | 47.1 | 34 | 20 | AAW92166 | Analogue of parath |
| 538 | 16 | 47.1 | 34 | 20 | AAW92168 | Analogue of parath |
| 539 | 16 | 47.1 | 34 | 20 | AAW92169 | Analogue of parath |
| 540 | 16 | 47.1 | 34 | 20 | AAW92170 | Analogue of parath |
| 541 | 16 | 47.1 | 34 | 20 | AAW92171 | Analogue of parath |
| 542 | 16 | 47.1 | 34 | 20 | AAW92172 | Analogue of parath |
| 543 | 16 | 47.1 | 34 | 20 | AAW92173 | Analogue of parath |
| 544 | 16 | 47.1 | 34 | 20 | AAW92174 | Analogue of parath |
| 545 | 16 | 47.1 | 34 | 20 | AAW92175 | Analogue of parath |
| 546 | 16 | 47.1 | 34 | 20 | AAW92176 | Analogue of parath |
| 547 | 16 | 47.1 | 34 | 20 | AAW92177 | Analogue of parath |
| 548 | 16 | 47.1 | 34 | 20 | AAW92178 | Analogue of parath |
| 549 | 16 | 47.1 | 34 | 20 | AAW92179 | Analogue of parath |
| 550 | 16 | 47.1 | 34 | 20 | AAW92180 | Analogue of parath |
| 551 | 16 | 47.1 | 34 | 20 | AAW92181 | Analogue of parath |
| 552 | 16 | 47.1 | 34 | 20 | AAW92182 | Analogue of parath |
| 553 | 16 | 47.1 | 34 | 20 | AAW92152 | Analogue of parath |
| 554 | 16 | 47.1 | 34 | 20 | AAW92150 | Analogue of parath |
| 555 | 16 | 47.1 | 34 | 20 | AAW92151 | Analogue of parath |
| 556 | 16 | 47.1 | 34 | 20 | AAW92153 | Analogue of parath |
| 557 | 16 | 47.1 | 34 | 20 | AAW92154 | Analogue of parath |
| 558 | 16 | 47.1 | 34 | 20 | AAW92155 | Analogue of parath |
| 559 | 16 | 47.1 | 34 | 20 | AAW92156 | Analogue of parath |
| 560 | 16 | 47.1 | 34 | 20 | AAW92157 | Analogue of parath |
| 561 | 16 | 47.1 | 34 | 20 | AAW92158 | Analogue of parath |
| 562 | 16 | 47.1 | 34 | 20 | AAW92159 | Analogue of parath |
| 563 | 16 | 47.1 | 34 | 20 | AAW92160 | Analogue of parath |

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| 564 | 16 | 47.1 | 34 | 20 | AAW92161 | Analogue of parath |
| 565 | 16 | 47.1 | 34 | 20 | AAW92162 | Analogue of parath |
| 566 | 16 | 47.1 | 34 | 20 | AAW92163 | Analogue of parath |
| 567 | 16 | 47.1 | 34 | 20 | AAW92164 | Analogue of parath |
| 568 | 16 | 47.1 | 34 | 20 | AAW92165 | Analogue of parath |
| 569 | 16 | 47.1 | 34 | 20 | AAW92148 | Analogue of parath |
| 570 | 16 | 47.1 | 34 | 20 | AAW92149 | Analogue of parath |
| 571 | 16 | 47.1 | 34 | 20 | AAW81873 | Porcine PTH N-term |
| 572 | 16 | 47.1 | 34 | 21 | ABJ10735 | Human parathyroid |
| 573 | 16 | 47.1 | 34 | 21 | ABJ10739 | Human parathyroid |
| 574 | 16 | 47.1 | 34 | 21 | ABJ10740 | Human parathyroid |
| 575 | 16 | 47.1 | 34 | 21 | ABJ10742 | Human parathyroid |
| 576 | 16 | 47.1 | 34 | 21 | ABJ10743 | Human parathyroid |
| 577 | 16 | 47.1 | 34 | 22 | AAB91084 | Parathyroid hormon |
| 578 | 16 | 47.1 | 34 | 22 | AAB91085 | Parathyroid hormon |
| 579 | 16 | 47.1 | 34 | 22 | AAB91087 | Parathyroid hormon |
| 580 | 16 | 47.1 | 34 | 23 | AAU73036 | Parathyroid hormon |
| 581 | 16 | 47.1 | 35 | 2 | AAP10140 | h-PTH antigen. Sy |
| 582 | 16 | 47.1 | 36 | 15 | AAR58277 | [Nle18]-hPTH(1-36) |
| 583 | 16 | 47.1 | 36 | 15 | AAR58183 | [Gln18]-hPTH(1-36) |
| 584 | 16 | 47.1 | 36 | 15 | AAR58184 | [Tyr18]-hPTH(1-36) |
| 585 | 16 | 47.1 | 36 | 15 | AAR58042 | [L8,D10,K11,L18]-h |
| 586 | 16 | 47.1 | 36 | 15 | AAR58044 | [L8,D10,K11,A17,L1 |
| 587 | 16 | 47.1 | 36 | 15 | AAR58055 | [L8,Q18]-hPTH(1-36 |
| 588 | 16 | 47.1 | 36 | 15 | AAR58057 | [L8,D10,A16,Q18]-h |
| 589 | 16 | 47.1 | 36 | 15 | AAR58071 | [Aib3, Gln18]-hPTH |
| 590 | 16 | 47.1 | 36 | 15 | AAR55820 | [L8,D10,K11,Q18]-h |
| 591 | 16 | 47.1 | 36 | 15 | AAR55824 | [L8,D10,K11,A16,Q1 |
| 592 | 16 | 47.1 | 36 | 15 | AAR58027 | [A1,A3,L8,Q18]-hPT |
| 593 | 16 | 47.1 | 36 | 15 | AAR58031 | [L8,K11,Q18]-hPTH(|
| 594 | 16 | 47.1 | 36 | 15 | AAR58072 | Isopropyl-[L8,D10, |
| 595 | 16 | 47.1 | 36 | 15 | AAR58074 | [L8,Y18]-hPTH(1-36 |
| 596 | 16 | 47.1 | 36 | 15 | AAR58088 | [1-amino-cyclopent |
| 597 | 16 | 47.1 | 37 | 22 | AAB86232 | Porcine parathyroi |
| 598 | 16 | 47.1 | 38 | 15 | AAR58159 | [Val28]-hPTH(1-38) |
| 599 | 16 | 47.1 | 38 | 15 | AAR58160 | [Ile28]-hPTH(1-38) |
| 600 | 15 | 44.1 | 28 | 13 | AAR22061 | Modified [Nle_8,18 |
| 601 | 15 | 44.1 | 28 | 13 | AAR22062 | Modified [Nle_8,18 |
| 602 | 15 | 44.1 | 28 | 13 | AAR22067 | Modified [Nle_8,_1 |
| 603 | 15 | 44.1 | 28 | 13 | AAR22068 | Modified [Nle_8,_1 |
| 604 | 15 | 44.1 | 28 | 17 | AAR88838 | Human parathyroid |
| 605 | 15 | 44.1 | 28 | 21 | ABJ10774 | Human parathyroid |
| 606 | 15 | 44.1 | 28 | 22 | AAB81074 | Human parathyroid |
| 607 | 15 | 44.1 | 28 | 23 | AAE18404 | Bovine PTH peptide |
| 608 | 15 | 44.1 | 28 | 23 | AAU73045 | Parathyroid hormon |
| 609 | 15 | 44.1 | 28 | 23 | AAU73048 | Parathyroid hormon |
| 610 | 15 | 44.1 | 28 | 23 | AAU73049 | Parathyroid hormon |
| 611 | 15 | 44.1 | 29 | 17 | AAR88839 | Human parathyroid |
| 612 | 15 | 44.1 | 29 | 22 | AAB81075 | Human parathyroid |
| 613 | 15 | 44.1 | 30 | 17 | AAR88833 | Human parathyroid |
| 614 | 15 | 44.1 | 30 | 19 | AAW42052 | Human parathyroid |
| 615 | 15 | 44.1 | 30 | 22 | AAB91089 | Parathyroid hormon |
| 616 | 15 | 44.1 | 30 | 22 | AAB91092 | Parathyroid hormon |
| 617 | 15 | 44.1 | 30 | 23 | AAU73062 | Parathyroid hormon |
| 618 | 15 | 44.1 | 31 | 5 | AAP40511 | Bovine parathyroid |
| 619 | 15 | 44.1 | 31 | 5 | AAP40761 | Human parathyroid |
| 620 | 15 | 44.1 | 31 | 17 | AAR88831 | Human parathyroid |

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| 621 | 15 | 44.1 | 31 | 19 | AAW42056 | Human parathyroid |
| 622 | 15 | 44.1 | 31 | 19 | AAW42057 | Human parathyroid |
| 623 | 15 | 44.1 | 31 | 19 | AAW42060 | Human parathyroid |
| 624 | 15 | 44.1 | 31 | 19 | AAW42062 | Human parathyroid |
| 625 | 15 | 44.1 | 31 | 19 | AAW42067 | Human parathyroid |
| 626 | 15 | 44.1 | 31 | 19 | AAW42049 | Human parathyroid |
| 627 | 15 | 44.1 | 31 | 19 | AAW42050 | Human parathyroid |
| 628 | 15 | 44.1 | 31 | 19 | AAW42053 | Human parathyroid |
| 629 | 15 | 44.1 | 31 | 21 | AAU96975 | Parathyroid hormon |
| 630 | 15 | 44.1 | 31 | 23 | AAU73040 | Parathyroid hormon |
| 631 | 15 | 44.1 | 31 | 23 | AAU82640 | Analogue of human |
| 632 | 15 | 44.1 | 32 | 22 | AAB91088 | Parathyroid hormon |
| 633 | 15 | 44.1 | 32 | 22 | AAB91090 | Parathyroid hormon |
| 634 | 15 | 44.1 | 32 | 22 | AAB91091 | Parathyroid hormon |
| 635 | 15 | 44.1 | 32 | 23 | AAE18403 | Bovine PTH peptide |
| 636 | 15 | 44.1 | 32 | 23 | AAU73041 | Parathyroid hormon |
| 637 | 15 | 44.1 | 32 | 23 | AAU73043 | Parathyroid hormon |
| 638 | 15 | 44.1 | 34 | 6 | AAP50517 | Sequence of methio |
| 639 | 15 | 44.1 | 34 | 11 | AAR07924 | Bovine parathyroid |
| 640 | 15 | 44.1 | 34 | 11 | AAR07925 | Human parathyroid |
| 641 | 15 | 44.1 | 34 | 11 | AAR08305 | Bovine parathyroid |
| 642 | 15 | 44.1 | 34 | 11 | AAR08306 | Human parathyroid |
| 643 | 15 | 44.1 | 34 | 13 | AAR22298 | Human parathyroid |
| 644 | 15 | 44.1 | 34 | 13 | AAR22299 | Human parathyroid |
| 645 | 15 | 44.1 | 34 | 14 | AAR41554 | [Thr27]hPTH (1-34) |
| 646 | 15 | 44.1 | 34 | 14 | AAR41555 | [Asn27]hPTH (1-34) |
| 647 | 15 | 44.1 | 34 | 14 | AAR41558 | [Ser27]hPTH (1-34) |
| 648 | 15 | 44.1 | 34 | 14 | AAR41559 | [Gly27]hPTH (1-34) |
| 649 | 15 | 44.1 | 34 | 14 | AAR41560 | [His27]hPTH (1-34) |
| 650 | 15 | 44.1 | 34 | 15 | AAR45528 | Parathyroid hormon |
| 651 | 15 | 44.1 | 34 | 16 | AAR69055 | PTH analogue with |
| 652 | 15 | 44.1 | 34 | 17 | AAR88829 | Human parathyroid |
| 653 | 15 | 44.1 | 34 | 17 | AAR88834 | Human parathyroid |
| 654 | 15 | 44.1 | 34 | 18 | AAW13352 | Truncated parathyr |
| 655 | 15 | 44.1 | 34 | 18 | AAW12651 | Parathyroid hormon |
| 656 | 15 | 44.1 | 34 | 18 | AAW08130 | Human PTH derivati |
| 657 | 15 | 44.1 | 34 | 18 | AAW20004 | Cyclised [Nle 8,18 |
| 658 | 15 | 44.1 | 34 | 18 | AAW19997 | Cyclised [Nle 8,18 |
| 659 | 15 | 44.1 | 34 | 18 | AAW19998 | Cyclised [Nle 8,18 |
| 660 | 15 | 44.1 | 34 | 18 | AAW20003 | Cyclised [Nle 8,18 |
| 661 | 15 | 44.1 | 34 | 18 | AAW20009 | Cyclised [Nle 8,18 |
| 662 | 15 | 44.1 | 34 | 18 | AAW20010 | Cyclised [Nle 8,18 |
| 663 | 15 | 44.1 | 34 | 18 | AAW17940 | Human PTH analogue |
| 664 | 15 | 44.1 | 34 | 18 | AAW17969 | Human parathyroid |
| 665 | 15 | 44.1 | 34 | 18 | AAW17970 | Human PTH analogue |
| 666 | 15 | 44.1 | 34 | 18 | AAW17964 | Human PTH analogue |
| 667 | 15 | 44.1 | 34 | 18 | AAW17954 | Human parathyroid |
| 668 | 15 | 44.1 | 34 | 18 | AAW17956 | Human parathyroid |
| 669 | 15 | 44.1 | 34 | 18 | AAW17962 | Human PTH analogue |
| 670 | 15 | 44.1 | 34 | 19 | AAW67275 | Parathyroid hormon |
| 671 | 15 | 44.1 | 34 | 19 | AAW67292 | Parathyroid hormon |
| 672 | 15 | 44.1 | 34 | 19 | AAW67297 | Parathyroid hormon |
| 673 | 15 | 44.1 | 34 | 19 | AAW61725 | Parathyroid hormon |
| 674 | 15 | 44.1 | 34 | 19 | AAW66053 | Parathyroid hormon |
| 675 | 15 | 44.1 | 34 | 19 | AAW42602 | Parathyroid hormon |
| 676 | 15 | 44.1 | 34 | 19 | AAW42054 | Human parathyroid |
| 677 | 15 | 44.1 | 34 | 19 | AAW42055 | Human parathyroid |

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| 678 | 15 | 44.1 | 34 | 19 | AAW48395 | Human PTH/PTHrP hy |
| 679 | 15 | 44.1 | 34 | 20 | AAW74396 | Modified parathyro |
| 680 | 15 | 44.1 | 34 | 20 | AAW81945 | Synthetic PTH and |
| 681 | 15 | 44.1 | 34 | 21 | ABJ10705 | Human parathyroid |
| 682 | 15 | 44.1 | 34 | 21 | ABJ10707 | Human parathyroid |
| 683 | 15 | 44.1 | 34 | 21 | ABJ10708 | Human parathyroid |
| 684 | 15 | 44.1 | 34 | 21 | ABJ10709 | Human parathyroid |
| 685 | 15 | 44.1 | 34 | 21 | ABJ10710 | Human parathyroid |
| 686 | 15 | 44.1 | 34 | 21 | ABJ10711 | Human parathyroid |
| 687 | 15 | 44.1 | 34 | 21 | ABJ10715 | Human parathyroid |
| 688 | 15 | 44.1 | 34 | 21 | ABJ10716 | Human parathyroid |
| 689 | 15 | 44.1 | 34 | 21 | ABJ10718 | Human parathyroid |
| 690 | 15 | 44.1 | 34 | 21 | ABJ10720 | Human parathyroid |
| 691 | 15 | 44.1 | 34 | 21 | ABJ10721 | Human parathyroid |
| 692 | 15 | 44.1 | 34 | 21 | ABJ10723 | Human parathyroid |
| 693 | 15 | 44.1 | 34 | 21 | ABJ10725 | Human parathyroid |
| 694 | 15 | 44.1 | 34 | 21 | ABJ10726 | Human parathyroid |
| 695 | 15 | 44.1 | 34 | 21 | ABJ10728 | Human parathyroid |
| 696 | 15 | 44.1 | 34 | 21 | ABJ10731 | Human parathyroid |
| 697 | 15 | 44.1 | 34 | 21 | ABJ10732 | Human parathyroid |
| 698 | 15 | 44.1 | 34 | 21 | ABJ10734 | Human parathyroid |
| 699 | 15 | 44.1 | 34 | 21 | ABJ10738 | Human parathyroid |
| 700 | 15 | 44.1 | 34 | 21 | ABJ10741 | Human parathyroid |
| 701 | 15 | 44.1 | 34 | 21 | ABJ10744 | Human parathyroid |
| 702 | 15 | 44.1 | 34 | 21 | ABJ10745 | Human parathyroid |
| 703 | 15 | 44.1 | 34 | 21 | ABJ10746 | Human parathyroid |
| 704 | 15 | 44.1 | 34 | 21 | ABJ10747 | Human parathyroid |
| 705 | 15 | 44.1 | 34 | 21 | ABJ10748 | Human parathyroid |
| 706 | 15 | 44.1 | 34 | 21 | ABJ10749 | Human parathyroid |
| 707 | 15 | 44.1 | 34 | 21 | ABJ10750 | Human parathyroid |
| 708 | 15 | 44.1 | 34 | 21 | ABJ10751 | Human parathyroid |
| 709 | 15 | 44.1 | 34 | 21 | ABJ10752 | Human parathyroid |
| 710 | 15 | 44.1 | 34 | 21 | ABJ10753 | Human parathyroid |
| 711 | 15 | 44.1 | 34 | 21 | ABJ10754 | Human parathyroid |
| 712 | 15 | 44.1 | 34 | 21 | ABJ10755 | Human parathyroid |
| 713 | 15 | 44.1 | 34 | 21 | ABJ10756 | Human parathyroid |
| 714 | 15 | 44.1 | 34 | 21 | ABJ10761 | Human parathyroid |
| 715 | 15 | 44.1 | 34 | 21 | ABJ10762 | Human parathyroid |
| 716 | 15 | 44.1 | 34 | 21 | ABJ10763 | Human parathyroid |
| 717 | 15 | 44.1 | 34 | 21 | ABJ10764 | Human parathyroid |
| 718 | 15 | 44.1 | 34 | 21 | ABJ10765 | Human parathyroid |
| 719 | 15 | 44.1 | 34 | 21 | ABJ10766 | Human parathyroid |
| 720 | 15 | 44.1 | 34 | 21 | ABJ10767 | Human parathyroid |
| 721 | 15 | 44.1 | 34 | 21 | ABJ10768 | Human parathyroid |
| 722 | 15 | 44.1 | 34 | 21 | ABJ10770 | Human parathyroid |
| 723 | 15 | 44.1 | 34 | 21 | ABJ10771 | Human parathyroid |
| 724 | 15 | 44.1 | 34 | 21 | ABJ10777 | Human parathyroid |
| 725 | 15 | 44.1 | 34 | 23 | AAE18396 | Bovine PTH peptide |
| 726 | 15 | 44.1 | 34 | 23 | AAE18397 | Human PTH peptide |
| 727 | 15 | 44.1 | 34 | 23 | AAU73031 | Parathyroid hormon |
| 728 | 15 | 44.1 | 34 | 23 | AAU73033 | Parathyroid hormon |
| 729 | 15 | 44.1 | 34 | 23 | AAU73035 | Parathyroid hormon |
| 730 | 15 | 44.1 | 35 | 16 | AAR74518 | Parathyroid hormon |
| 731 | 15 | 44.1 | 35 | 16 | AAR74519 | Parathyroid hormon |
| 732 | 15 | 44.1 | 35 | 16 | AAR74520 | Parathyroid hormon |
| 733 | 15 | 44.1 | 35 | 16 | AAR74527 | Human parathyroid |
| 734 | 15 | 44.1 | 35 | 16 | AAR74464 | Parathyroid hormon |

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| 735 | 15 | 44.1 | 35 | 16 | AAR74465 | Parathyroid hormon |
| 736 | 15 | 44.1 | 35 | 16 | AAR74466 | Parathyroid hormon |
| 737 | 15 | 44.1 | 35 | 16 | AAR74467 | Parathyroid hormon |
| 738 | 15 | 44.1 | 35 | 16 | AAR74468 | Parathyroid hormon |
| 739 | 15 | 44.1 | 35 | 16 | AAR74469 | Parathyroid hormon |
| 740 | 15 | 44.1 | 35 | 16 | AAR74470 | Parathyroid hormon |
| 741 | 15 | 44.1 | 35 | 16 | AAR74471 | Parathyroid hormon |
| 742 | 15 | 44.1 | 35 | 16 | AAR74472 | Parathyroid hormon |
| 743 | 15 | 44.1 | 35 | 16 | AAR74473 | Parathyroid hormon |
| 744 | 15 | 44.1 | 35 | 16 | AAR74474 | Parathyroid hormon |
| 745 | 15 | 44.1 | 35 | 16 | AAR74475 | Parathyroid hormon |
| 746 | 15 | 44.1 | 35 | 16 | AAR74476 | Parathyroid hormon |
| 747 | 15 | 44.1 | 35 | 16 | AAR74477 | Parathyroid hormon |
| 748 | 15 | 44.1 | 35 | 16 | AAR74478 | Parathyroid hormon |
| 749 | 15 | 44.1 | 35 | 16 | AAR74479 | Parathyroid hormon |
| 750 | 15 | 44.1 | 35 | 16 | AAR74448 | Parathyroid hormon |
| 751 | 15 | 44.1 | 35 | 16 | AAR74449 | Parathyroid hormon |
| 752 | 15 | 44.1 | 35 | 16 | AAR74450 | Parathyroid hormon |
| 753 | 15 | 44.1 | 35 | 16 | AAR74451 | Parathyroid hormon |
| 754 | 15 | 44.1 | 35 | 16 | AAR74452 | Parathyroid hormon |
| 755 | 15 | 44.1 | 35 | 16 | AAR74453 | Parathyroid hormon |
| 756 | 15 | 44.1 | 35 | 16 | AAR74454 | Parathyroid hormon |
| 757 | 15 | 44.1 | 35 | 16 | AAR74455 | Parathyroid hormon |
| 758 | 15 | 44.1 | 35 | 16 | AAR74456 | Parathyroid hormon |
| 759 | 15 | 44.1 | 35 | 16 | AAR74457 | Parathyroid hormon |
| 760 | 15 | 44.1 | 35 | 16 | AAR74458 | Parathyroid hormon |
| 761 | 15 | 44.1 | 35 | 16 | AAR74459 | Parathyroid hormon |
| 762 | 15 | 44.1 | 35 | 16 | AAR74460 | Parathyroid hormon |
| 763 | 15 | 44.1 | 35 | 16 | AAR74461 | Parathyroid hormon |
| 764 | 15 | 44.1 | 35 | 16 | AAR74462 | Parathyroid hormon |
| 765 | 15 | 44.1 | 35 | 16 | AAR74463 | Parathyroid hormon |
| 766 | 15 | 44.1 | 35 | 16 | AAR74432 | Parathyroid hormon |
| 767 | 15 | 44.1 | 35 | 16 | AAR74433 | Parathyroid hormon |
| 768 | 15 | 44.1 | 35 | 16 | AAR74434 | Parathyroid hormon |
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| 770 | 15 | 44.1 | 35 | 16 | AAR74436 | Parathyroid hormon |
| 771 | 15 | 44.1 | 35 | 16 | AAR74437 | Parathyroid hormon |
| 772 | 15 | 44.1 | 35 | 16 | AAR74438 | Parathyroid hormon |
| 773 | 15 | 44.1 | 35 | 16 | AAR74439 | Parathyroid hormon |
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| 775 | 15 | 44.1 | 35 | 16 | AAR74441 | Parathyroid hormon |
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| 777 | 15 | 44.1 | 35 | 16 | AAR74443 | Parathyroid hormon |
| 778 | 15 | 44.1 | 35 | 16 | AAR74444 | Parathyroid hormon |
| 779 | 15 | 44.1 | 35 | 16 | AAR74445 | Parathyroid hormon |
| 780 | 15 | 44.1 | 35 | 16 | AAR74446 | Parathyroid hormon |
| 781 | 15 | 44.1 | 35 | 16 | AAR74447 | Parathyroid hormon |
| 782 | 15 | 44.1 | 35 | 16 | AAR74429 | Parathyroid hormon |
| 783 | 15 | 44.1 | 35 | 16 | AAR74430 | Parathyroid hormon |
| 784 | 15 | 44.1 | 35 | 16 | AAR74431 | Parathyroid hormon |
| 785 | 15 | 44.1 | 35 | 16 | AAR74398 | Parathyroid hormon |
| 786 | 15 | 44.1 | 35 | 16 | AAR74399 | Parathyroid hormon |
| 787 | 15 | 44.1 | 35 | 16 | AAR74400 | Parathyroid hormon |
| 788 | 15 | 44.1 | 35 | 16 | AAR74394 | Parathyroid hormon |
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| 790 | 15 | 44.1 | 35 | 16 | AAR74396 | Parathyroid hormon |
| 791 | 15 | 44.1 | 35 | 16 | AAR74397 | Parathyroid hormon |

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| 792 | 15 | 44.1 | 35 | 23 | AAU73175 | Parathyroid hormon |
| 793 | 15 | 44.1 | 36 | 15 | AAR58222 | [His27]-hPTH(1-36) |
| 794 | 15 | 44.1 | 36 | 15 | AAR58223 | [Phe27]-hPTH(1-36) |
| 795 | 15 | 44.1 | 36 | 15 | AAR58224 | [Nle27]-hPTH(1-36) |
| 796 | 15 | 44.1 | 36 | 15 | AAR58225 | [Asn27]-hPTH(1-36) |
| 797 | 15 | 44.1 | 36 | 15 | AAR58226 | [Ala27]-hPTH(1-36) |
| 798 | 15 | 44.1 | 36 | 15 | AAR58214 | [Ala19]-hPTH(1-36) |
| 799 | 15 | 44.1 | 36 | 15 | AAR58041 | [L8,D10,K11,S14,I1 |
| 800 | 15 | 44.1 | 36 | 15 | AAR58043 | [L8,Q16,D17,L18,R1 |
| 801 | 15 | 44.1 | 36 | 15 | AAR58046 | [L8,A16,D17,L18,A1 |
| 802 | 15 | 44.1 | 36 | 15 | AAR58047 | [L8,D10,A16,D17,L1 |
| 803 | 15 | 44.1 | 36 | 15 | AAR58050 | [L8,A16,D17,Q18,A1 |
| 804 | 15 | 44.1 | 36 | 15 | AAR58051 | [L8,A16,A17,Q18,A1 |
| 805 | 15 | 44.1 | 36 | 15 | AAR58052 | [L8,A17,Q18,A19]-h |
| 806 | 15 | 44.1 | 36 | 15 | AAR58067 | [L8,A16,A17,A18,A1 |
| 807 | 15 | 44.1 | 36 | 15 | AAR58069 | Isopropyl-[L8,K(Is |
| 808 | 15 | 44.1 | 36 | 15 | AAR58070 | Isopropyl-[L8,K(Is |
| 809 | 15 | 44.1 | 36 | 15 | AAR55822 | [L8,D10,K11,A16,Q1 |
| 810 | 15 | 44.1 | 36 | 15 | AAR55825 | [L8,A16,Q18,A19]-h |
| 811 | 15 | 44.1 | 36 | 15 | AAR58086 | [1-amino-cyclopent |
| 812 | 15 | 44.1 | 38 | 15 | AAR58136 | [Arg19]-hPTH(1-38) |
| 813 | 15 | 44.1 | 38 | 15 | AAR58154 | [Val27]-hPTH(1-38) |
| 814 | 15 | 44.1 | 38 | 15 | AAR58155 | [Ile27]-hPTH(1-38) |
| 815 | 15 | 44.1 | 38 | 15 | AAR58156 | [Leu27]-hPTH(1-38) |
| 816 | 15 | 44.1 | 38 | 15 | AAR58157 | [Arg27]-hPTH(1-38) |
| 817 | 15 | 44.1 | 38 | 15 | AAR58158 | [Ala27]-hPTH(1-38) |
| 818 | 15 | 44.1 | 38 | 15 | AAR58123 | [Ser19]-hPTH(1-38) |
| 819 | 15 | 44.1 | 38 | 15 | AAR58124 | [Lys19]-hPTH(1-38) |
| 820 | 15 | 44.1 | 38 | 15 | AAR58125 | [Leu19]-hPTH(1-38) |
| 821 | 15 | 44.1 | 38 | 15 | AAR58126 | [Ala19]-hPTH(1-38) |
| 822 | 15 | 44.1 | 38 | 15 | AAR58127 | [Tyr19]-hPTH(1-38) |
| 823 | 15 | 44.1 | 38 | 15 | AAR58128 | [Met19]-hPTH(1-38) |
| 824 | 15 | 44.1 | 38 | 15 | AAR58129 | [His19]-hPTH(1-38) |
| 825 | 15 | 44.1 | 38 | 15 | AAR58130 | [Val19]-hPTH(1-38) |
| 826 | 15 | 44.1 | 38 | 15 | AAR58131 | [Gly19]-hPTH(1-38) |
| 827 | 15 | 44.1 | 38 | 15 | AAR58132 | [Pro19]-hPTH(1-38) |
| 828 | 15 | 44.1 | 38 | 15 | AAR58133 | [Asp19]-hPTH(1-38) |
| 829 | 15 | 44.1 | 38 | 15 | AAR58134 | [Ile19]-hPTH(1-38) |
| 830 | 14 | 41.2 | 28 | 23 | AAU73066 | Parathyroid hormon |
| 831 | 14 | 41.2 | 30 | 23 | AAU73057 | Parathyroid hormon |
| 832 | 14 | 41.2 | 33 | 17 | AAW15814 | [Leu(8),Trp(10),Al |
| 833 | 14 | 41.2 | 34 | 14 | AAR41556 | [Gln26,27]hPTH(1- |
| 834 | 14 | 41.2 | 34 | 14 | AAR41566 | [Arg 26,27]hPTH(1 |
| 835 | 14 | 41.2 | 34 | 14 | AAR41567 | [Gln26]hPTH(1-34) |
| 836 | 14 | 41.2 | 34 | 15 | AAR55817 | [L8,Q18,T33,A34]-h |
| 837 | 14 | 41.2 | 34 | 15 | AAR55819 | [L8,A16,Q18,T33,A3 |
| 838 | 14 | 41.2 | 34 | 15 | AAR55821 | [L8,D10,K11,Q18,T3 |
| 839 | 14 | 41.2 | 34 | 15 | AAR55823 | [L8,D10,K11,A16,Q1 |
| 840 | 14 | 41.2 | 34 | 15 | AAR58021 | [L8,D10,A16,Q18,T3 |
| 841 | 14 | 41.2 | 34 | 15 | AAR58034 | Isopropyl-[L8,K(Is |
| 842 | 14 | 41.2 | 34 | 17 | AAW15813 | [Leu(8),Trp(10),Al |
| 843 | 14 | 41.2 | 34 | 17 | AAW15815 | [Leu(8),Trp(10),DL |
| 844 | 14 | 41.2 | 34 | 17 | AAW15828 | N-alpha-acylated [|
| 845 | 14 | 41.2 | 34 | 18 | AAW08132 | Human PTH derivati |
| 846 | 14 | 41.2 | 34 | 18 | AAW17960 | Human PTH analogue |
| 847 | 14 | 41.2 | 34 | 20 | AAV02587 | Parathyroid hormon |
| 848 | 14 | 41.2 | 34 | 21 | ABJ10757 | Human parathyroid |

| | | | | | | |
|-----|----|------|----|----|----------|---------------------|
| 849 | 14 | 41.2 | 35 | 16 | AAR74515 | Parathyroid hormon |
| 850 | 14 | 41.2 | 35 | 16 | AAR74516 | Parathyroid hormon |
| 851 | 14 | 41.2 | 35 | 16 | AAR74517 | Parathyroid hormon |
| 852 | 14 | 41.2 | 35 | 16 | AAR74480 | Parathyroid hormon |
| 853 | 14 | 41.2 | 35 | 16 | AAR74401 | Parathyroid hormon |
| 854 | 14 | 41.2 | 35 | 16 | AAR74409 | Parathyroid hormon |
| 855 | 14 | 41.2 | 35 | 16 | AAR74412 | Parathyroid hormon |
| 856 | 14 | 41.2 | 36 | 15 | AAR58290 | [Ala26] -hPTH(1-36) |
| 857 | 14 | 41.2 | 36 | 15 | AAR58279 | [Lys20] -hPTH(1-36) |
| 858 | 14 | 41.2 | 36 | 15 | AAR58218 | [Gln26] -hPTH(1-36) |
| 859 | 14 | 41.2 | 36 | 15 | AAR58219 | [Nle26] -hPTH(1-36) |
| 860 | 14 | 41.2 | 38 | 15 | AAR58137 | [Phe20] -hPTH(1-38) |
| 861 | 14 | 41.2 | 38 | 15 | AAR58153 | [Arg26] -hPTH(1-38) |
| 862 | 13 | 38.2 | 32 | 22 | AAB84835 | Parathyroid hormon |
| 863 | 13 | 38.2 | 32 | 22 | AAB96906 | Parathyroid hormon |
| 864 | 13 | 38.2 | 34 | 13 | AAR22297 | Human parathyroid |
| 865 | 13 | 38.2 | 34 | 14 | AAR34456 | Human parathyroid |
| 866 | 13 | 38.2 | 34 | 14 | AAR34457 | Human parathyroid |
| 867 | 13 | 38.2 | 34 | 14 | AAR41557 | [Gln25,26,27]hPTH |
| 868 | 13 | 38.2 | 34 | 15 | AAR58195 | [S14,I15,Q16,D17,L |
| 869 | 13 | 38.2 | 34 | 15 | AAR58045 | [L8,Q16,D17,L18,R1 |
| 870 | 13 | 38.2 | 34 | 15 | AAR58049 | [L8,D10,K11,Q16,D1 |
| 871 | 13 | 38.2 | 34 | 15 | AAR58056 | [L8,D10,K11,A16,Q1 |
| 872 | 13 | 38.2 | 34 | 15 | AAR58058 | [L8,D10,K11,A16,Q1 |
| 873 | 13 | 38.2 | 34 | 15 | AAR55818 | [L8,A16,Q18,A19,T3 |
| 874 | 13 | 38.2 | 34 | 18 | AAW08131 | Human PTH derivati |
| 875 | 13 | 38.2 | 34 | 21 | ABJ10758 | Human parathyroid |
| 876 | 13 | 38.2 | 34 | 22 | AAB84828 | Parathyroid hormon |
| 877 | 13 | 38.2 | 34 | 22 | AAB96921 | Parathyroid hormon |
| 878 | 13 | 38.2 | 35 | 16 | AAR74512 | Parathyroid hormon |
| 879 | 13 | 38.2 | 35 | 16 | AAR74513 | Parathyroid hormon |
| 880 | 13 | 38.2 | 35 | 16 | AAR74514 | Parathyroid hormon |
| 881 | 13 | 38.2 | 35 | 16 | AAR74511 | Parathyroid hormon |
| 882 | 13 | 38.2 | 35 | 16 | AAR74481 | Parathyroid hormon |
| 883 | 13 | 38.2 | 35 | 16 | AAR74482 | Parathyroid hormon |
| 884 | 13 | 38.2 | 35 | 16 | AAR74483 | Parathyroid hormon |
| 885 | 13 | 38.2 | 35 | 16 | AAR74408 | Parathyroid hormon |
| 886 | 13 | 38.2 | 36 | 15 | AAR58287 | [Phe25] -hPTH(1-36) |
| 887 | 13 | 38.2 | 36 | 15 | AAR58288 | [Lys25] -hPTH(1-36) |
| 888 | 13 | 38.2 | 36 | 15 | AAR58289 | [Ala25] -hPTH(1-36) |
| 889 | 13 | 38.2 | 36 | 15 | AAR58192 | [Gln25] -hPTH(1-36) |
| 890 | 13 | 38.2 | 36 | 15 | AAR58216 | [Ala21] -hPTH(1-36) |
| 891 | 13 | 38.2 | 38 | 15 | AAR58138 | [Ala21] -hPTH(1-38) |
| 892 | 13 | 38.2 | 38 | 15 | AAR58139 | [Gly21] -hPTH(1-38) |
| 893 | 13 | 38.2 | 38 | 15 | AAR58140 | [Phe21] -hPTH(1-38) |
| 894 | 13 | 38.2 | 38 | 15 | AAR58141 | [Leu21] -hPTH(1-38) |
| 895 | 13 | 38.2 | 38 | 15 | AAR58142 | [Asn21] -hPTH(1-38) |
| 896 | 13 | 38.2 | 38 | 15 | AAR58143 | [Gln21] -hPTH(1-38) |
| 897 | 13 | 38.2 | 38 | 15 | AAR58144 | [Ser21] -hPTH(1-38) |
| 898 | 12 | 35.3 | 28 | 23 | AAU73065 | Parathyroid hormon |
| 899 | 12 | 35.3 | 28 | 23 | AAU73067 | Parathyroid hormon |
| 900 | 12 | 35.3 | 29 | 13 | AAR22070 | Modified rPTH(7-34 |
| 901 | 12 | 35.3 | 30 | 23 | AAU73056 | Parathyroid hormon |
| 902 | 12 | 35.3 | 30 | 23 | AAU73058 | Parathyroid hormon |
| 903 | 12 | 35.3 | 30 | 23 | AAU73059 | Parathyroid hormon |
| 904 | 12 | 35.3 | 34 | 11 | AAR07917 | Rat parathyroid ho |
| 905 | 12 | 35.3 | 34 | 11 | AAR08298 | Rat parathyroid ho |

| | | | | | | |
|-----|----|------|----|----|----------|--------------------|
| 906 | 12 | 35.3 | 34 | 16 | AAR62432 | Accelerator peptid |
| 907 | 12 | 35.3 | 34 | 17 | AAR99980 | Rat parathyroid ho |
| 908 | 12 | 35.3 | 34 | 18 | AAW19996 | Cyclised rat parat |
| 909 | 12 | 35.3 | 34 | 18 | AAW20002 | Cyclised rat parat |
| 910 | 12 | 35.3 | 34 | 18 | AAW20008 | Cyclised rat parat |
| 911 | 12 | 35.3 | 34 | 18 | AAW17949 | Human parathyroid |
| 912 | 12 | 35.3 | 34 | 18 | AAW17945 | Human parathyroid |
| 913 | 12 | 35.3 | 34 | 18 | AAW17950 | Human PTH analogue |
| 914 | 12 | 35.3 | 34 | 19 | AAW67280 | Parathyroid hormon |
| 915 | 12 | 35.3 | 34 | 19 | AAW67284 | Parathyroid hormon |
| 916 | 12 | 35.3 | 34 | 19 | AAW67285 | Parathyroid hormon |
| 917 | 12 | 35.3 | 34 | 19 | AAW67288 | Parathyroid hormon |
| 918 | 12 | 35.3 | 34 | 19 | AAW67289 | Parathyroid hormon |
| 919 | 12 | 35.3 | 34 | 19 | AAW67294 | Parathyroid hormon |
| 920 | 12 | 35.3 | 34 | 19 | AAW67295 | Parathyroid hormon |
| 921 | 12 | 35.3 | 34 | 19 | AAW67296 | Parathyroid hormon |
| 922 | 12 | 35.3 | 34 | 19 | AAW67303 | Parathyroid hormon |
| 923 | 12 | 35.3 | 34 | 19 | AAW67304 | Parathyroid hormon |
| 924 | 12 | 35.3 | 34 | 19 | AAW48396 | Human PTH/PTHrP hy |
| 925 | 12 | 35.3 | 34 | 21 | ABJ10759 | Human parathyroid |
| 926 | 12 | 35.3 | 34 | 22 | AAB84777 | Native human parat |
| 927 | 12 | 35.3 | 34 | 22 | AAB96897 | Rat parathyroid ho |
| 928 | 12 | 35.3 | 34 | 22 | AAB91100 | Parathyroid hormon |
| 929 | 12 | 35.3 | 34 | 23 | AAU73037 | Parathyroid hormon |
| 930 | 12 | 35.3 | 34 | 24 | ABP71499 | Rat parathyroid ho |
| 931 | 12 | 35.3 | 35 | 16 | AAR74507 | Parathyroid hormon |
| 932 | 12 | 35.3 | 35 | 16 | AAR74508 | Parathyroid hormon |
| 933 | 12 | 35.3 | 35 | 16 | AAR74509 | Parathyroid hormon |
| 934 | 12 | 35.3 | 35 | 16 | AAR74510 | Parathyroid hormon |
| 935 | 12 | 35.3 | 35 | 16 | AAR74484 | Parathyroid hormon |
| 936 | 12 | 35.3 | 35 | 16 | AAR74485 | Parathyroid hormon |
| 937 | 12 | 35.3 | 35 | 16 | AAR74486 | Parathyroid hormon |
| 938 | 12 | 35.3 | 36 | 15 | AAR58208 | [A13,Q26,F27,D-F34 |
| 939 | 12 | 35.3 | 36 | 15 | AAR58217 | [Ala22]-hPTH(1-36) |
| 940 | 12 | 35.3 | 36 | 15 | AAR58053 | [L8,A17,Q18,A19,R2 |
| 941 | 12 | 35.3 | 36 | 15 | AAR58060 | [L8,A16,Q18,A19,R2 |
| 942 | 12 | 35.3 | 36 | 15 | AAR58064 | [L8,S13,A16,Q18,A1 |
| 943 | 12 | 35.3 | 36 | 15 | AAR58032 | [L8,A16,D17,L18,R1 |
| 944 | 12 | 35.3 | 36 | 15 | AAR58073 | Isopropyl-[L8,S13, |
| 945 | 12 | 35.3 | 37 | 22 | AAB86231 | Rat parathyroid ho |
| 946 | 12 | 35.3 | 38 | 15 | AAR58145 | [Gly22]-hPTH(1-38) |
| 947 | 12 | 35.3 | 38 | 15 | AAR58146 | [Leu22]-hPTH(1-38) |
| 948 | 12 | 35.3 | 38 | 15 | AAR58147 | [His22]-hPTH(1-38) |
| 949 | 12 | 35.3 | 38 | 15 | AAR58148 | [Ala22]-hPTH(1-38) |
| 950 | 12 | 35.3 | 38 | 15 | AAR58149 | [Ile22]-hPTH(1-38) |
| 951 | 12 | 35.3 | 38 | 15 | AAR58150 | [Val22]-hPTH(1-38) |
| 952 | 12 | 35.3 | 38 | 15 | AAR58151 | [Ser22]-hPTH(1-38) |
| 953 | 12 | 35.3 | 38 | 15 | AAR58152 | [Arg22]-hPTH(1-38) |
| 954 | 11 | 32.4 | 28 | 9 | AAP82184 | Sequence of parath |
| 955 | 11 | 32.4 | 28 | 13 | AAR22071 | Modified [Tyr_34]r |
| 956 | 11 | 32.4 | 28 | 13 | AAR22072 | Modified [D-Trp_12 |
| 957 | 11 | 32.4 | 28 | 13 | AAR22073 | Modified [Nle_8,_1 |
| 958 | 11 | 32.4 | 28 | 13 | AAR22074 | Modified [Nle_8,_1 |
| 959 | 11 | 32.4 | 28 | 23 | AAU73105 | Parathyroid hormon |
| 960 | 11 | 32.4 | 28 | 23 | AAU73106 | Parathyroid hormon |
| 961 | 11 | 32.4 | 30 | 22 | AAB84834 | Parathyroid hormon |
| 962 | 11 | 32.4 | 30 | 22 | AAB96905 | Parathyroid hormon |

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|------|----|------|----|----|----------|--------------------|
| 963 | 11 | 32.4 | 30 | 23 | AAU73054 | Parathyroid hormon |
| 964 | 11 | 32.4 | 30 | 23 | AAU73136 | Parathyroid hormon |
| 965 | 11 | 32.4 | 30 | 23 | AAU73137 | Parathyroid hormon |
| 966 | 11 | 32.4 | 32 | 22 | AAB91094 | Parathyroid hormon |
| 967 | 11 | 32.4 | 33 | 9 | AAP82176 | Sequence of parath |
| 968 | 11 | 32.4 | 34 | 7 | AAP61414 | Peptide with parat |
| 969 | 11 | 32.4 | 34 | 8 | AAP71281 | Parathyroid hormon |
| 970 | 11 | 32.4 | 34 | 11 | AAR07920 | Rat parathyroid ho |
| 971 | 11 | 32.4 | 34 | 11 | AAR07923 | Rat parathyroid ho |
| 972 | 11 | 32.4 | 34 | 11 | AAR08301 | Rat parathyroid ho |
| 973 | 11 | 32.4 | 34 | 11 | AAR08304 | Rat parathyroid ho |
| 974 | 11 | 32.4 | 34 | 14 | AAR34358 | Human parathyroid |
| 975 | 11 | 32.4 | 34 | 14 | AAR34337 | Bovine parathyroid |
| 976 | 11 | 32.4 | 34 | 14 | AAR34338 | Bovine parathyroid |
| 977 | 11 | 32.4 | 34 | 14 | AAR34339 | Bovine parathyroid |
| 978 | 11 | 32.4 | 34 | 14 | AAR34340 | Bovine parathyroid |
| 979 | 11 | 32.4 | 34 | 14 | AAR34341 | Bovine parathyroid |
| 980 | 11 | 32.4 | 34 | 14 | AAR34342 | Bovine parathyroid |
| 981 | 11 | 32.4 | 34 | 14 | AAR34343 | Bovine parathyroid |
| 982 | 11 | 32.4 | 34 | 14 | AAR34344 | Bovine parathyroid |
| 983 | 11 | 32.4 | 34 | 14 | AAR34345 | Bovine parathyroid |
| 984 | 11 | 32.4 | 34 | 14 | AAR34346 | Bovine parathyroid |
| 985 | 11 | 32.4 | 34 | 14 | AAR34347 | Bovine parathyroid |
| 986 | 11 | 32.4 | 34 | 14 | AAR34348 | Bovine parathyroid |
| 987 | 11 | 32.4 | 34 | 14 | AAR34349 | Bovine parathyroid |
| 988 | 11 | 32.4 | 34 | 14 | AAR34350 | Bovine parathyroid |
| 989 | 11 | 32.4 | 34 | 14 | AAR34351 | Bovine parathyroid |
| 990 | 11 | 32.4 | 34 | 14 | AAR34352 | Bovine parathyroid |
| 991 | 11 | 32.4 | 34 | 14 | AAR34353 | Human parathyroid |
| 992 | 11 | 32.4 | 34 | 14 | AAR34354 | Human parathyroid |
| 993 | 11 | 32.4 | 34 | 14 | AAR34355 | Human parathyroid |
| 994 | 11 | 32.4 | 34 | 14 | AAR34356 | Human parathyroid |
| 995 | 11 | 32.4 | 34 | 14 | AAR34357 | Human parathyroid |
| 996 | 11 | 32.4 | 34 | 14 | AAR34359 | Human parathyroid |
| 997 | 11 | 32.4 | 34 | 14 | AAR34360 | Human parathyroid |
| 998 | 11 | 32.4 | 34 | 14 | AAR34361 | Human parathyroid |
| 999 | 11 | 32.4 | 34 | 14 | AAR34362 | Human parathyroid |
| 1000 | 11 | 32.4 | 34 | 14 | AAR34363 | Human parathyroid |

ALIGNMENTS

RESULT 1

AAR22296

ID AAR22296 standard; Peptide; 34 AA.

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AC AAR22296;

XX

DT 25-MAR-2003 (updated)

DT 03-AUG-1992 (first entry)

XX

DE Human parathyroid hormone 1-34 [Lys 11].

XX

KW hPTH; protease resistant; osteoporosis; hypoparathyroidism;

KW hypertension.

XX

OS Synthetic.
 XX
 PN EP477885-A.
 XX
 PD 01-APR-1992.
 XX
 PF 25-SEP-1991; 91EP-0116303.
 XX
 PR 06-SEP-1991; 91JP-0227232.
 PR 28-SEP-1990; 90JP-0257490.
 XX
 PA (TAKE) TAKEDA CHEM IND LTD.
 XX
 PI Nakagawa S, Fukuda T, Kawase M, Yamazaki I;
 XX
 DR WPI; 1992-106285/14.
 XX
 PT New peptide(s) are parathyroid hormone derivs. - used in hormone
 PT therapy, for treating osteoporosis hyperparathyroidism and
 PT hypertension
 XX
 PS Claim 9; Page 14; 14pp; English.
 XX
 CC The peptide is an analogue of human parathyroid hormone fragment
 CC 1-34. The peptide modification defined increase resistance to
 CC proteases and therefore persistence in the blood. The peptide is
 CC used in therapy of osteoporosis, hypoparathyroidism and hypertension.
 CC The peptide may be synthesised by the Merrifield solid phase
 CC method in an automatic apparatus.
 CC See also AAR22290-99.
 CC (Updated on 25-MAR-2003 to correct PA field.)
 XX
 SQ Sequence 34 AA;

Query Match 100.0%; Score 34; DB 13; Length 34;
 Best Local Similarity 100.0%; Pred. No. 6.4e-29;
 Matches 34; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 SVSEIQLMHNKGKHLNSMERVEWLRKKLQDVHNF 34
 ||||||||||||||||||||||||||||||||||
 Db 1 SVSEIQLMHNKGKHLNSMERVEWLRKKLQDVHNF 34

RESULT 2

AAU73030

ID AAU73030 standard; Peptide; 34 AA.

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AC AAU73030;

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DT 12-MAR-2002 (first entry)

XX

DE Parathyroid hormone PTH/PTHrP modulating domain #12.

XX

KW Human; parathyroid hormone; PTH; parathyroid hormone-related protein;
 KW PTHrP; bone resorption inhibitor; osteoprotegerin; OPG; OPG-L antibody;
 KW calcitonin; bisphosphonate; oestrogen; oestrogen receptor; tibolone;
 KW osteopenia; hyperthyroidism; hypercalcaemia; tumour metastasis; bone;

KW breast cancer; prostate cancer; cachexia; anorexia; osteoporosis;
 KW Paget's disease; osteomyelitis; osteonecrosis; bone cell death;
 KW Gaucher's disease; sickle cell anaemia; systemic lupus erythematosus;
 KW rheumatoid arthritis; periodontal disease; alopecia; fracture repair;
 KW immunoglobulin G; IgG.
 XX
 OS Homo sapiens.
 XX
 PN WO200181415-A2.
 XX
 PD 01-NOV-2001.
 XX
 PF 27-APR-2001; 2001WO-US13528.
 XX
 PR 27-APR-2000; 2000US-200053P.
 PR 28-JUN-2000; 2000US-214860P.
 PR 06-FEB-2001; 2001US-266673P.
 PR 26-APR-2001; 2001US-0843221.
 XX
 PA (AMGE-) AMGEN INC.
 XX
 PI Kostenuik P, Liu C, Lacey DL;
 XX
 DR WPI; 2002-066435/09.
 XX
 PT Composition, useful for treating osteopenia, comprises parathyroid
 PT hormone and parathyroid hormone-related protein receptor modulators -
 XX
 PS Claim 39; Page 26; 107pp; English.
 XX
 CC The invention relates to a composition (I) comprising modulators of
 CC parathyroid hormone (PTH) and parathyroid hormone-related protein (PTHrP)
 CC which comprise a PTH/PTHrP modulating domain and a vehicle. (I)
 CC comprising PTH agonist optionally with a bone resorption inhibitor, such
 CC as osteoprotegrin (OPG), OPG-L antibody, calcitonin, bisphosphonates,
 CC oestrogens, oestrogen receptor modulators and tibolone is useful for
 CC treating osteopenia. (I) is useful for therapeutic and prophylactic
 CC purposes. Antagonists of PTH receptor are useful in treating primary and
 CC secondary hyperthyroidism, hypercalcaemia, tumour metastases,
 CC particularly breast and prostate cancer, cachexia and anorexia,
 CC osteopenia, including various forms of osteoporosis, Paget's disease of
 CC bone, osteomyelitis, osteonecrosis or bone cell death, associated with
 CC traumatic injury or nontraumatic necrosis associated with Gaucher's
 CC disease, sickle cell anaemia, systemic lupus erythematosus, rheumatoid
 CC arthritis, periodontal disease and alopecia. PTH receptor agonists are
 CC useful as therapeutic agents in conditions including fracture repair
 CC (including healing of non-union fractures), osteopenia, including various
 CC forms of osteoporosis. AAU73018-AAU73181 represent parathyroid hormone
 CC and parathyroid hormone related protein (PTH/PTHrP) modulators and
 CC related amino acid sequences of the invention.
 XX
 SQ Sequence 34 AA;

Query Match 100.0%; Score 34; DB 23; Length 34;
 Best Local Similarity 100.0%; Pred. No. 6.4e-29;
 Matches 34; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 SVSEIQLMHNKGKHLNSMERVEWLRKKLQDVHNF 34
|||||||
Db 1 SVSEIQLMHNKGKHLNSMERVEWLRKKLQDVHNF 34

RESULT 3

AAU73053

ID AAU73053 standard; Peptide; 30 AA.

XX

AC AAU73053;

XX

DT 12-MAR-2002 (first entry)

XX

DE Parathyroid hormone PTH/PTHrP modulating domain #35.

XX

KW Human; parathyroid hormone; PTH; parathyroid hormone-related protein;
KW PTHrP; bone resorption inhibitor; osteoprotegrin; OPG; OPG-L antibody;
KW calcitonin; bisphosphonate; oestrogen; oestrogen receptor; tibolone;
KW osteopenia; hyperthyroidism; hypercalcaemia; tumour metastasis; bone;
KW breast cancer; prostate cancer; cachexia; anorexia; osteoporosis;
KW Paget's disease; osteomyelitis; osteonecrosis; bone cell death;
KW Gaucher's disease; sickle cell anaemia; systemic lupus erythematosus;
KW rheumatoid arthritis; periodontal disease; alopecia; fracture repair;
KW immunoglobulin G; IgG.

XX

OS Homo sapiens.

XX

PN WO200181415-A2.

XX

PD 01-NOV-2001.

XX

PF 27-APR-2001; 2001WO-US13528.

XX

PR 27-APR-2000; 2000US-200053P.

PR 28-JUN-2000; 2000US-214860P.

PR 06-FEB-2001; 2001US-266673P.

PR 26-APR-2001; 2001US-0843221.

XX

PA (AMGE-) AMGEN INC.

XX

PI Kostenuik P, Liu C, Lacey DL;

XX

DR WPI; 2002-066435/09.

XX

PT Composition, useful for treating osteopenia, comprises parathyroid
PT hormone and parathyroid hormone-related protein receptor modulators -

XX

PS Disclosure; Page 27; 107pp; English.

XX

CC The invention relates to a composition (I) comprising modulators of
CC parathyroid hormone (PTH) and parathyroid hormone-related protein (PTHrP)
CC which comprise a PTH/PTHrP modulating domain and a vehicle. (I)
CC comprising PTH agonist optionally with a bone resorption inhibitor, such
CC as osteoprotegrin (OPG), OPG-L antibody, calcitonin, bisphosphonates,
CC oestrogens, oestrogen receptor modulators and tibolone is useful for
CC treating osteopenia. (I) is useful for therapeutic and prophylactic
CC purposes. Antagonists of PTH receptor are useful in treating primary and

CC secondary hyperthyroidism, hypercalcaemia, tumour metastases,
 CC particularly breast and prostate cancer, cachexia and anorexia,
 CC osteopenia, including various forms of osteoporosis, Paget's disease of
 CC bone, osteomyelitis, osteonecrosis or bone cell death, associated with
 CC traumatic injury or nontraumatic necrosis associated with Gaucher's
 CC disease, sickle cell anaemia, systemic lupus erythematosus, rheumatoid
 CC arthritis, periodontal disease and alopecia. PTH receptor agonists are
 CC useful as therapeutic agents in conditions including fracture repair
 CC (including healing of non-union fractures), osteopenia, including various
 CC forms of osteoporosis. AAU73018-AAU73181 represent parathyroid hormone
 CC and parathyroid hormone related protein (PTH/PTHrP) modulators and
 CC related amino acid sequences of the invention.
 XX
 SQ Sequence 30 AA;

Query Match 88.2%; Score 30; DB 23; Length 30;
 Best Local Similarity 100.0%; Pred. No. 1e-24;
 Matches 30; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 SVSEIQLMHNKGKHLNSMERVEWLRKKLQD 30
 ||||||||||||||||||||||||||||
 Db 1 SVSEIQLMHNKGKHLNSMERVEWLRKKLQD 30

RESULT 4

AAU73174

ID AAU73174 standard; Peptide; 35 AA.

XX

AC AAU73174;

XX

DT 12-MAR-2002 (first entry)

XX

DE Parathyroid hormone PTH/PTHrP modulating domain #156.

XX

KW Human; parathyroid hormone; PTH; parathyroid hormone-related protein;
 KW PTHrP; bone resorption inhibitor; osteoprotegrin; OPG; OPG-L antibody;
 KW calcitonin; bisphosphonate; oestrogen; oestrogen receptor; tibolone;
 KW osteopenia; hyperthyroidism; hypercalcaemia; tumour metastasis; bone;
 KW breast cancer; prostate cancer; cachexia; anorexia; osteoporosis;
 KW Paget's disease; osteomyelitis; osteonecrosis; bone cell death;
 KW Gaucher's disease; sickle cell anaemia; systemic lupus erythematosus;
 KW rheumatoid arthritis; periodontal disease; alopecia; fracture repair;
 KW immunoglobulin G; IgG.

XX

OS Synthetic.

XX

PN WO200181415-A2.

XX

PD 01-NOV-2001.

XX

PF 27-APR-2001; 2001WO-US13528.

XX

PR 27-APR-2000; 2000US-200053P.

PR 28-JUN-2000; 2000US-214860P.

PR 06-FEB-2001; 2001US-266673P.

PR 26-APR-2001; 2001US-0843221.

XX

PA (AMGE-) AMGEN INC.
 XX
 PI Kostenuik P, Liu C, Lacey DL;
 XX
 DR WPI; 2002-066435/09.
 XX
 PT Composition, useful for treating osteopenia, comprises parathyroid
 PT hormone and parathyroid hormone-related protein receptor modulators -
 XX
 PS Disclosure; Page 63; 107pp; English.
 XX
 CC The invention relates to a composition (I) comprising modulators of
 CC parathyroid hormone (PTH) and parathyroid hormone-related protein (PTHrP)
 CC which comprise a PTH/PTHrP modulating domain and a vehicle. (I)
 CC comprising PTH agonist optionally with a bone resorption inhibitor, such
 CC as osteoprotegerin (OPG), OPG-L antibody, calcitonin, bisphosphonates,
 CC oestrogens, oestrogen receptor modulators and tibolone is useful for
 CC treating osteopenia. (I) is useful for therapeutic and prophylactic
 CC purposes. Antagonists of PTH receptor are useful in treating primary and
 CC secondary hyperthyroidism, hypercalcaemia, tumour metastases,
 CC particularly breast and prostate cancer, cachexia and anorexia,
 CC osteopenia, including various forms of osteoporosis, Paget's disease of
 CC bone, osteomyelitis, osteonecrosis or bone cell death, associated with
 CC traumatic injury or nontraumatic necrosis associated with Gaucher's
 CC disease, sickle cell anaemia, systemic lupus erythematosus, rheumatoid
 CC arthritis, periodontal disease and alopecia. PTH receptor agonists are
 CC useful as therapeutic agents in conditions including fracture repair
 CC (including healing of non-union fractures), osteopenia, including various
 CC forms of osteoporosis. AAU73018-AAU73181 represent parathyroid hormone
 CC and parathyroid hormone related protein (PTH/PTHrP) modulators and
 CC related amino acid sequences of the invention.
 XX
 SQ Sequence 35 AA;

Query Match 88.2%; Score 30; DB 23; Length 35;
 Best Local Similarity 100.0%; Pred. No. 1.1e-24;
 Matches 30; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 SVSEIQLMHNKGKHLNSMERVEWLRKKLQD 30
 |||||
 Db 1 SVSEIQLMHNKGKHLNSMERVEWLRKKLQD 30

RESULT 5
 AAW08108

ID AAW08108 standard; peptide; 34 AA.
 XX
 AC AAW08108;
 XX
 DT 10-OCT-1997 (first entry)
 XX
 DE Human parathyroid hormone derivative, [Asp10,Lys11]hPTH(1-34).
 XX
 KW Human; parathyroid hormone; PTH; cAMP-producing activity;
 KW bone formation; osteoporosis; hypoparathyroidism; hypertension;
 KW climacteric disturbance.
 XX

OS Synthetic.
 XX
 PN EP748817-A2.
 XX
 PD 18-DEC-1996.
 XX
 PF 13-JUN-1996; 96EP-0109475.
 XX
 PR 15-JUN-1995; 95JP-0148652.
 XX
 PA (TAKE) TAKEDA CHEM IND LTD.
 XX
 PI Fukuda T, Habashita J, Nakagawa S, Taketomi S;
 XX
 DR WPI; 1997-036114/04.
 XX
 PT New parathyroid hormone derivs. - useful in treatment of bone
 PT diseases, hypoparathyroidism and hypertension
 XX
 PS Claim 27; Page 26; 42pp; English.
 XX
 CC The sequences given in AAW08108-32 represent derivatives of human
 CC parathyroid hormone (PTH). These peptides are human PTH (1-34)
 CC derivative peptides. They have potent cAMP-producing activity and
 CC bone formation activity. They may be used in treatment of bone
 CC diseases including osteoporosis, hypoparathyroidism, hypertension
 CC and climacteric disturbance. The peptides are low in toxicity and
 CC are safe.
 XX
 SQ Sequence 34 AA;

Query Match 70.6%; Score 24; DB 18; Length 34;
 Best Local Similarity 100.0%; Pred. No. 2.5e-18;
 Matches 24; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 11 KGKHLNSMERVEWLRKKLQDVHNF 34
 |||||
 Db 11 KGKHLNSMERVEWLRKKLQDVHNF 34

RESULT 6

AAR22064

ID AAR22064 standard; Protein; 28 AA.

XX

AC AAR22064;

XX

DT 14-JUL-1992 (first entry)

XX

DE Modified hPTH(7-34)NH2.

XX

KW Parathyroid hormone; analogue; osteoporosis; hyperthyroidism;
 KW tumours; hypercalcaemia; renal failure; human.

XX

OS Synthetic.

XX

FH Key Location/Qualifiers

FT Modified-site 7

FT /label= OTHER
 FT /note= "OTHER = see comments"
 FT Modified-site 28
 FT /label= NH2
 XX
 PN US5093233-A.
 XX
 PD 03-MAR-1992.
 XX
 PF 25-APR-1990; 90US-0514394.
 XX
 PR 25-APR-1990; 90US-0514394.
 XX
 PA (MERI) MERCK & CO INC.
 XX
 PI Rosenblatt M, Roubini E, Chorev M, Nutt RF;
 XX
 DR WPI; 1992-096233/12.
 XX
 PT New parathyroid hormone analogues - useful for treatment and in
 PT vitro diagnosis of PTH-dependent tumours, immune disorders,
 PT osteoporosis and hyperparathyroidism.
 XX
 PS Claim 1; Column 10; 6pp; English.
 XX
 CC The peptide is modified at Lys13 (of the parent PTH) in the epsilon
 CC amino acid gp. by N,N-diisobutyl or 3-phenylpropanoyl. The PTH
 CC analogue binds with high affinity to the peptide hormone receptor
 CC without activating the 2nd messenger mol. The modification of the
 CC Lys residue stabilises the bioactive conformation of PTH to enhance
 CC the activity. The peptide may be used in in vitro bioassays to
 CC measure naturally occurring PTH and to diagnose the etiology of or
 CC to treat osteoporosis or hypercalcaemia. It may also be used to
 CC treat hyperthyroidism and diseases caused by aberrant prodn. of
 CC hormone-like substances, such as tumours. It may also be used to
 CC treat immune diseases such as inflammation. It is prepd. by solid
 CC phase synthesis.
 CC See also AAR22058-75.
 XX
 SQ Sequence 28 AA;

 Query Match 67.6%; Score 23; DB 13; Length 28;
 Best Local Similarity 100.0%; Pred. No. 2.5e-17;
 Matches 23; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 12 GKHLNSMERVEWLRKKLQDVHNF 34
 ||||||||||||||||||
 Db 6 GKHLNSMERVEWLRKKLQDVHNF 28

RESULT 7
 ABJ10776
 ID ABJ10776 standard; Peptide; 28 AA.
 XX
 AC ABJ10776;
 XX
 DT 02-DEC-2002 (first entry)

XX
 DE Human parathyroid hormone analogue #72.
 XX
 KW Human; parathyroid hormone; parathyroid hormone-related protein;
 KW PTH; PTHrP; analogue; abnormal CNS function; pancreatic function;
 KW mineral metabolism; male infertility; abnormal blood pressure;
 KW hypothalamic disease.
 XX
 OS Homo sapiens.
 OS Synthetic.
 XX
 FH Key Location/Qualifiers
 FT Misc-difference 2
 FT /note= "D-form residue"
 FT Modified-site 28
 FT /note= "C-terminal amide"
 XX
 PN W09957139-A2.
 XX
 PD 11-NOV-1999.
 XX
 PF 03-MAY-1999; 99WO-US09521.
 XX
 PR 05-MAY-1998; 98US-0072956.
 XX
 PA (SCRC) SOC CONSEILS RECH & APPL SCI.
 XX
 PI Chorev M, Dong ZX, Rosenblatt M;
 XX
 DR WPI; 2000-038790/03.
 XX
 PT New parathyroid hormone analogs, used for treating e.g. abnormal CNS or
 PT pancreatic functions, abnormal mineral metabolism and homeostasis, male
 PT infertility, abnormal blood pressure or hypothalamic disease -
 XX
 PS Claim 11; Page 40; 49pp; English.
 XX
 CC The present invention provides a number of parathyroid hormone (PTH) or
 CC parathyroid hormone-related protein (PTHrP) analogues. These act as PTH2
 CC receptor agonists or antagonists and can be used in the treatment of
 CC disorders resulting from altered or excessive action of the PTH2
 CC receptor, e.g. abnormal CNS functions, abnormal pancreatic functions,
 CC divergence from normal mineral metabolism and homeostasis, male
 CC infertility, abnormal blood pressure or a hypothalamic disease. The
 CC present sequence is a peptide analogue of the invention.
 XX
 SQ Sequence 28 AA;

 Query Match 67.6%; Score 23; DB 21; Length 28;
 Best Local Similarity 100.0%; Pred. No. 2.5e-17;
 Matches 23; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

 QY 12 GKHLNSMERVEWLRKKLQDVHNF 34
 |||||
 Db 6 GKHLNSMERVEWLRKKLQDVHNF 28

RESULT 8

AAE23734

ID AAE23734 standard; peptide; 28 AA.

XX

AC AAE23734;

XX

DT 10-SEP-2002 (first entry)

XX

DE Human parathyroid hormone (hPTH) peptide (7-34).

XX

KW Human parathyroid hormone; hPTH; PTH-related peptide; PTHrP; eczema;
KW hyperproliferative skin disorder; psoriasis; ichthyosis; skin cancer;
KW acne; actinic keratosis; alopecia; gene therapy.

XX

OS Homo sapiens.

XX

PN WO200228420-A2.

XX

PD 11-APR-2002.

XX

PF 05-OCT-2001; 2001WO-US31082.

XX

PR 06-OCT-2000; 2000US-238134P.

XX

PA (HOLI/) HOLICK M F.

XX

PI Holick MF;

XX

DR WPI; 2002-452304/48.

DR N-PSDB; AAD37995.

XX

PT Regulating mammalian skin or hair cell proliferation and
PT differentiation by administering nucleic acids encoding peptides
PT derived from N-terminal region of human parathyroid hormone (hPTH) or
PT hPTH-related protein -

XX

PS Claim 35; Fig 38; 56pp; English.

XX

CC The invention relates to a method for regulating proliferation or
CC enhancing differentiation of mammalian skin or hair cell. The method
CC involves administering nucleic acids encoding peptides derived from
CC N-terminal region of human parathyroid hormone (hPTH) or hPTH-related
CC peptide (PTHrP). The method is used for inhibiting hyperproliferative
CC skin disorders such as psoriasis, ichthyosis, eczema, acne, actinic
CC keratosis, skin cancer, for inhibiting hair growth or preventing hair
CC regrowth. It is useful for stimulating cell growth, rejuvenating aged
CC skin, preventing skin wrinkles, treating skin wrinkles, enhancing wound
CC healing, stimulating hair growth, maintaining hair growth, treating or
CC preventing female or male pattern baldness, for treating chemotherapy
CC induced alopecia and also for stimulating epidermal cell growth or
CC hair follicle cell growth. The method is also used in gene therapy.
CC The present sequence is hPTH peptide.

XX

SQ Sequence 28 AA;

Query Match 67.6%; Score 23; DB 23; Length 28;
Best Local Similarity 100.0%; Pred. No. 2.5e-17;

Matches 23; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 12 GKHLNSMERVEWLRKKLQDVHNF 34
 |||||
 Db 6 GKHLNSMERVEWLRKKLQDVHNF 28

RESULT 9

AAU73044

ID AAU73044 standard; Peptide; 28 AA.

XX

AC AAU73044;

XX

DT 12-MAR-2002 (first entry)

XX

DE Parathyroid hormone PTH/PTHrP modulating domain #26.

XX

KW Human; parathyroid hormone; PTH; parathyroid hormone-related protein;
KW PTHrP; bone resorption inhibitor; osteoprotegrin; OPG; OPG-L antibody;
KW calcitonin; bisphosphonate; oestrogen; oestrogen receptor; tibolone;
KW osteopenia; hyperthyroidism; hypercalcaemia; tumour metastasis; bone;
KW breast cancer; prostate cancer; cachexia; anorexia; osteoporosis;
KW Paget's disease; osteomyelitis; osteonecrosis; bone cell death;
KW Gaucher's disease; sickle cell anaemia; systemic lupus erythematosus;
KW rheumatoid arthritis; periodontal disease; alopecia; fracture repair;
KW immunoglobulin G; IgG.

XX

OS Homo sapiens.

XX

PN WO200181415-A2.

XX

PD 01-NOV-2001.

XX

PF 27-APR-2001; 2001WO-US13528.

XX

PR 27-APR-2000; 2000US-200053P.

PR 28-JUN-2000; 2000US-214860P.

PR 06-FEB-2001; 2001US-266673P.

PR 26-APR-2001; 2001US-0843221.

XX

PA (AMGE-) AMGEN INC.

XX

PI Kostenuik P, Liu C, Lacey DL;

XX

DR WPI; 2002-066435/09.

XX

PT Composition, useful for treating osteopenia, comprises parathyroid
PT hormone and parathyroid hormone-related protein receptor modulators -

XX

PS Disclosure; Page 27; 107pp; English.

XX

CC The invention relates to a composition (I) comprising modulators of
CC parathyroid hormone (PTH) and parathyroid hormone-related protein (PTHrP)
CC which comprise a PTH/PTHrP modulating domain and a vehicle. (I)
CC comprising PTH agonist optionally with a bone resorption inhibitor, such
CC as osteoprotegerin (OPG), OPG-L antibody, calcitonin, bisphosphonates,
CC oestrogens, oestrogen receptor modulators and tibolone is useful for

CC treating osteopenia. (I) is useful for therapeutic and prophylactic
 CC purposes. Antagonists of PTH receptor are useful in treating primary and
 CC secondary hyperthyroidism, hypercalcaemia, tumour metastases,
 CC particularly breast and prostate cancer, cachexia and anorexia,
 CC osteopenia, including various forms of osteoporosis, Paget's disease of
 CC bone, osteomyelitis, osteonecrosis or bone cell death, associated with
 CC traumatic injury or nontraumatic necrosis associated with Gaucher's
 CC disease, sickle cell anaemia, systemic lupus erythematosus, rheumatoid
 CC arthritis, periodontal disease and alopecia. PTH receptor agonists are
 CC useful as therapeutic agents in conditions including fracture repair
 CC (including healing of non-union fractures), osteopenia, including various
 CC forms of osteoporosis. AAU73018-AAU73181 represent parathyroid hormone
 CC and parathyroid hormone related protein (PTH/PTHrP) modulators and
 CC related amino acid sequences of the invention.

XX

SQ Sequence 28 AA;

Query Match 67.6%; Score 23; DB 23; Length 28;
 Best Local Similarity 100.0%; Pred. No. 2.5e-17;
 Matches 23; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 12 GKHLNSMERVEWLRKKLQDVHNF 34
 |||||
 Db 6 GKHLNSMERVEWLRKKLQDVHNF 28

RESULT 10

AAE23752

ID AAE23752 standard; peptide; 30 AA.

XX

AC AAE23752;

XX

DT 10-SEP-2002 (first entry)

XX

DE Human parathyroid hormone (hPTH) peptide (5-34).

XX

KW Human parathyroid hormone; hPTH; PTH-related peptide; PTHrP; eczema;
 KW hyperproliferative skin disorder; psoriasis; ichthyosis; skin cancer;
 KW acne; actinic keratosis; alopecia; gene therapy.

XX

OS Homo sapiens.

XX

PN WO200228420-A2.

XX

PD 11-APR-2002.

XX

PF 05-OCT-2001; 2001WO-US31082.

XX

PR 06-OCT-2000; 2000US-238134P.

XX

PA (HOLI/) HOLICK M F.

XX

PI Holick MF;

XX

DR WPI; 2002-452304/48.

XX

PT Regulating mammalian skin or hair cell proliferation and

PT differentiation by administering nucleic acids encoding peptides
PT derived from N-terminal region of human parathyroid hormone (hPTH) or
PT hPTH-related protein -

XX

PS Claim 35; Fig 42; 56pp; English.

XX

CC The invention relates to a method for regulating proliferation or
CC enhancing differentiation of mammalian skin or hair cell. The method
CC involves administering nucleic acids encoding peptides derived from
CC N-terminal region of human parathyroid hormone (hPTH) or hPTH-related
CC peptide (PTHrP). The method is used for inhibiting hyperproliferative
CC skin disorders such as psoriasis, ichthyosis, eczema, acne, actinic
CC keratosis, skin cancer, for inhibiting hair growth or preventing hair
CC regrowth. It is useful for stimulating cell growth, rejuvenating aged
CC skin, preventing skin wrinkles, treating skin wrinkles, enhancing wound
CC healing, stimulating hair growth, maintaining hair growth, treating or
CC preventing female or male pattern baldness, for treating chemotherapy
CC induced alopecia and also for stimulating epidermal cell growth or
CC hair follicle cell growth. The method is also used in gene therapy.
CC The present sequence is hPTH peptide.

XX

SQ Sequence 30 AA;

Query Match 67.6%; Score 23; DB 23; Length 30;
Best Local Similarity 100.0%; Pred. No. 2.6e-17;
Matches 23; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 12 GKHLNSMERVEWLRKKLQDVHNF 34
| | | | | | | | | | | | | | | | | |
Db 8 GKHLNSMERVEWLRKKLQDVHNF 30

RESULT 11

AAB07468

ID AAB07468 standard; protein; 32 AA.

XX

AC AAB07468;

XX

DT 20-OCT-2000 (first entry)

XX

DE Antigenic peptide derived from human parathyroid hormone.

XX

KW Human; parathyroid hormone; PTH; hyperparathyroidism; bone disease.

XX

OS Homo sapiens.

XX

PN WO200042437-A1.

XX

PD 20-JUL-2000.

XX

PF 13-JAN-2000; 2000WO-US00855.

XX

PR 14-JAN-1999; 99US-0231422.

PR 26-JUN-1999; 99US-0344639.

XX

PA (SCAN-) SCANTIBODIES LAB INC.

XX

DR WPI; 2000-476147/41.

XX

PT Differentiating between normal parathyroid function and
PT hyperparathyroidism comprises determining and comparing whole
PT parathyroid hormone, parathyroid hormone inhibitory peptide fragment
PT and/or total parathyroid hormone levels -

XX

PS Disclosure; Page 6; 46pp; English.

XX

CC The present sequence represents an antigenic fragment derived from
CC human parathyroid hormone (PTH). It was used to raise antibodies.
CC PTH peptide fragments can function as PTH antagonists. The
CC specification describes a method for differentiating between a
CC person having substantially normal parathyroid function and having
CC hyperparathyroidism. The method comprises determining and comparing
CC at least two of the following parameters: whole parathyroid
CC hormone level, parathyroid hormone inhibitory peptide fragment level
CC and total parathyroid hormone level. The method is used for monitoring
CC (treatments of) parathyroid related bone disease and the effects of
CC therapeutic treatment for hyperparathyroidism.

XX

SQ Sequence 32 AA;

Query Match 67.6%; Score 23; DB 21; Length 32;

Best Local Similarity 100.0%; Pred. No. 2.8e-17;

Matches 23; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 12 GKHLNSMERVEWLRKKLQDVHNF 34

|||||

Db 6 GKHLNSMERVEWLRKKLQDVHNF 28

RESULT 12

AAE23735

ID AAE23735 standard; peptide; 32 AA.

XX

AC AAE23735;

XX

DT 10-SEP-2002 (first entry)

XX

DE Human parathyroid hormone (hPTH) peptide (5-36).

XX

KW Human parathyroid hormone; hPTH; PTH-related peptide; PTHrP; eczema;
KW hyperproliferative skin disorder; psoriasis; ichthyosis; skin cancer;
KW acne; actinic keratosis; alopecia; gene therapy.

XX

OS Homo sapiens.

XX

PN WO200228420-A2.

XX

PD 11-APR-2002.

XX

PF 05-OCT-2001; 2001WO-US31082.

XX

PR 06-OCT-2000; 2000US-238134P.

XX

PA (HOLI/) HOLICK M F.

XX
 PI Holick MF;
 XX
 DR WPI; 2002-452304/48.
 DR N-PSDB; AAD37995.
 XX
 PT Regulating mammalian skin or hair cell proliferation and
 PT differentiation by administering nucleic acids encoding peptides
 PT derived from N-terminal region of human parathyroid hormone (hPTH) or
 PT hPTH-related protein -
 XX
 PS Claim 35; Fig 40; 56pp; English.
 XX
 CC The invention relates to a method for regulating proliferation or
 CC enhancing differentiation of mammalian skin or hair cell. The method
 CC involves administering nucleic acids encoding peptides derived from
 CC N-terminal region of human parathyroid hormone (hPTH) or hPTH-related
 CC peptide (PTHrP). The method is used for inhibiting hyperproliferative
 CC skin disorders such as psoriasis, ichthyosis, eczema, acne, actinic
 CC keratosis, skin cancer, for inhibiting hair growth or preventing hair
 CC regrowth. It is useful for stimulating cell growth, rejuvenating aged
 CC skin, preventing skin wrinkles, treating skin wrinkles, enhancing wound
 CC healing, stimulating hair growth, maintaining hair growth, treating or
 CC preventing female or male pattern baldness, for treating chemotherapy
 CC induced alopecia and also for stimulating epidermal cell growth or
 CC hair follicle cell growth. The method is also used in gene therapy.
 CC The present sequence is hPTH peptide.
 XX
 SQ Sequence 32 AA;

Query Match 67.6%; Score 23; DB 23; Length 32;
 Best Local Similarity 100.0%; Pred. No. 2.8e-17;
 Matches 23; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 12 GKHLNSMERVEWLRKKLQDVHNF 34
 ||||||||||||||||||
 Db 8 GKHLNSMERVEWLRKKLQDVHNF 30

RESULT 13

AAP30022

ID AAP30022 standard; peptide; 34 AA.

XX

AC AAP30022;

XX

DT 25-MAR-2003 (updated)

DT 01-SEP-1992 (first entry)

XX

DE Human parathyroid-(1-34) amide.

XX

KW PTH; parathyroid gland; antibodies.

XX

OS Synthetic.

XX

FH Key Location/Qualifiers

FT Modified-site 34

FT /note= "amidated"

XX
 PN JP58096052-A.
 XX
 PD 07-JUN-1983.
 XX
 PF 30-NOV-1983; 83JP-0193212.
 XX
 PR 31-MAR-1981; 81JP-0048887.
 XX
 PA (TOXN) TOYO JOZO KK.
 XX
 DR WPI; 1983-709291/28.
 XX
 PT High activity human parathyroid hormone amide prodn. - by
 PT condensing protected aminoacid(s) and/or peptide(s) useful for
 PT lowering parathyroid gland function
 XX
 PS Claim 1; Page 1; 20pp; Japanese.
 XX
 CC The human parathyroid hormone, hPTH(1-34)-amide was prepd. by
 CC the following steps: Firstly the carboxy gp. at the C-terminal
 CC phenylalanine was converted into its amide form. The protected
 CC individual amino acids were condensed, in order, by liquid phase
 CC synthesis. The protecting groups were removed from the N-terminal
 CC amino gp. and other functional gps. by acidolysis, and the
 CC resulting hPTH(1-34)-amide purified by gel filtration
 CC chromatography using a Sephadex G-25, G-50 or LH-20 column or by
 CC column chromatography with carboxymethyl cellulose or ion exchange
 CC resin. The peptide amide is useful in lowering the activity of the
 CC parathyroid gland and in the prepn. of antibodies for diagnosis of
 CC parathyroid gland function.
 CC (Updated on 25-MAR-2003 to correct PR field.)
 XX
 SQ Sequence 34 AA;

Query Match 67.6%; Score 23; DB 4; Length 34;
 Best Local Similarity 100.0%; Pred. No. 2.9e-17;
 Matches 23; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 12 GKHLNSMERVEWLRKKLQDVHNF 34
 |||||
 Db 12 GKHLNSMERVEWLRKKLQDVHNF 34

RESULT 14

AAP50377

ID AAP50377 standard; peptide; 34 AA.

XX

AC AAP50377;

XX

DT 25-MAR-2003 (updated)

DT 08-MAR-1992 (first entry)

XX

DE [Met(O)8,18]hPTH-(1-34).

XX

KW Human parathyroid hormone; calcium regulation.

XX

OS Homo sapiens.
 XX
 FH Key Location/Qualifiers
 FT Modified-site 8
 FT /label= oxidised methionine
 FT Modified-site 18
 FT /label= oxidised methionine
 XX
 PN JP59204159-A.
 XX
 PD 19-NOV-1984.
 XX
 PF 28-APR-1983; 83JP-0075607.
 XX
 PR 28-APR-1983; 83JP-0075607.
 XX
 PA (TOXN) TOYO JOZO KK.
 XX
 DR WPI; 1985-003560/01.
 XX
 PT New (Met(O)8,18)hPTH-(1-34) peptide - increases calcium level in
 PT blood and decreases level in urine.
 XX
 PS Claim 1; Page 1; 3pp; Japanese.
 XX
 CC Unmodified hPTH(1-34) increases Ca in blood, decreases P in blood,
 CC decreases Ca in urine and increases P in urine by increasing cAMP in
 CC urine and enhancing vitamin D hydroxylase activity in kidneys. The
 CC modified derivative only has the effect of lowering Ca levels in
 CC urine and can be used when only this particular effect is required.
 CC (Updated on 25-MAR-2003 to correct PA field.)
 CC (Updated on 25-MAR-2003 to correct DR field.)
 XX
 SQ Sequence 34 AA;

Query Match 67.6%; Score 23; DB 6; Length 34;
 Best Local Similarity 100.0%; Pred. No. 2.9e-17;
 Matches 23; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 12 GKHLNSMERVEWLRKKLQDVHNF 34
 |||||
 Db 12 GKHLNSMERVEWLRKKLQDVHNF 34

RESULT 15

AAP60031

ID AAP60031 standard; peptide; 34 AA.

XX

AC AAP60031;

XX

DT 25-MAR-2003 (updated)

DT 06-JUL-1991 (first entry)

XX

DE Sequence of the first 34 AA residues of a parathyroid hormone
 DE obtainable from a human or animal.

XX

KW Osteoporosis therapy.

XX
 OS Homo sapiens/animal.
 XX
 PN EP197514-A.
 XX
 PD 15-OCT-1986.
 XX
 PF 03-APR-1986; 86EP-0104562.
 XX
 PR 04-APR-1985; 85US-0720018.
 PR 05-DEC-1986; 86US-0939308.
 PR 21-MAY-1987; 87US-0052383.
 XX
 PA (GEHO) GEN HOSPITAL CORP.
 XX
 PI Potts JT, Neer RM, Slovik DM;
 XX
 DR WPI; 1986-273437/42.
 XX
 PT Compsn. and kits for increasing bone mass in osteoporosis -
 PT contg. parathyroid hormone or fragment with hydroxylated
 PT vitamin/D cpd. or calcium salt
 XX
 PS Claim 4; Page 24; 26pp; English.
 XX
 CC The peptide is used in a pharmaceutical compsn. together with a
 CC hydroxylated vitamin D compound, or a non-toxic calcium salt, pref.
 CC CaCO3. The compsn. pref. contains 100-700 (pref. 200-600, esp. 400-
 CC 500) units of the peptide. The vitamin D compound is pref. 1-alpha-
 CC hydroxy vitamin D2 or 1-alpha,25-dihydroxy vitamin D2.
 CC (Updated on 25-MAR-2003 to correct PA field.)
 XX
 SQ Sequence 34 AA;

Query Match 67.6%; Score 23; DB 7; Length 34;
 Best Local Similarity 100.0%; Pred. No. 2.9e-17;
 Matches 23; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 12 GKHLNSMERVEWLRKKLQDVHNF 34
 |||||
 Db 12 GKHLNSMERVEWLRKKLQDVHNF 34

RESULT 16

AAR07919

ID AAR07919 standard; protein; 34 AA.

XX

AC AAR07919;

XX

DT 18-FEB-1991 (first entry)

XX

DE Human parathyroid hormone analogue, hPTH(7-34).

XX

KW Osteoporosis; hypercalcemia; hyperparathyroidism; hypertension.

XX

OS Homo sapiens.

XX

PN US4968669-A.
 XX
 PD 06-NOV-1990.
 XX
 PF 21-APR-1989; 89US-0341597.
 XX
 PR 21-APR-1989; 89US-0341597.
 PR 09-MAY-1988; 88US-0191512.
 XX
 PA (MERI) MERCK & CO INC.
 XX
 PI Rosenblatt M, Chorev M;
 XX
 DR WPI; 1990-354642/47.
 XX
 PT New para:thyroid hormone analogues - which inhibit hormone
 PT activity by binding receptors while not producing second
 PT messenger molecules
 XX
 PS Claim 1; Column 8; 6pp; English.
 XX
 CC Peptide analogues have high affinity for PTH cell surface receptors,
 CC but do not stimulate production of secondary messenger molecules.
 CC They may be used in inhibition of PTH action, and in diagnosis and
 CC treatment of osteoporosis, hypercalcemia and hyperparathyroidism.
 CC Analogues may also be used in treatment of tumours and other cells
 CC overproducing peptide hormone-like substances, and immune diseases
 CC eg. allergic inflammation and hyperactive lymphocytes.
 CC Naturally occurring PTH levels may also be measured in vitro.
 XX
 SQ Sequence 34 AA;

Query Match 67.6%; Score 23; DB 11; Length 34;
 Best Local Similarity 100.0%; Pred. No. 2.9e-17;
 Matches 23; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 12 GKHLNSMERVEWLRKKLQDVHNF 34
 |||||
 Db 12 GKHLNSMERVEWLRKKLQDVHNF 34

RESULT 17

AAR22283

ID AAR22283 standard; peptide; 34 AA.
 XX
 AC AAR22283;
 XX
 DT 29-JUL-1992 (first entry)
 XX
 DE Parathyroid hormone analogue N-terminus [1-34].
 XX
 KW Human; hPTH; wound healing; hair growth; hyperproliferation skin;
 KW disorders; psoriasis; cancer; burns.
 XX
 OS Homo sapiens.
 XX
 PN WO9204039-A.

XX
 PD 19-MAR-1992.
 XX
 PF 30-AUG-1991; 91WO-US06218.
 XX
 PR 30-AUG-1990; 90US-0575219.
 XX
 PA (HOLI/) HOLICK M F.
 XX
 PI Holick MF;
 XX
 DR WPI; 1992-114063/14.
 XX
 PT Use of peptide having homology with parathyroid hormone - for
 PT enhancement of cell proliferation for wound healing
 XX
 PS Disclosure; Fig 1; 34pp; English.
 XX
 CC The peptide can be easily synthesised by recombinant DNA or solid
 CC phase peptide synthesis techniques. The peptide has > 50 percent
 CC homology with the N-terminal 1-34 amino acids of human parathyroid
 CC hormone or hypercalcaemic region. It is esp. PTH (7-34). The
 CC peptide may be used in a method for the treatment of hyperprolifer-
 CC ation skin disorders e.g. psoriasis, cancers, burns or skin
 CC ulcerations by inhibition of cell proliferation and enhancement of
 CC cell differentiation (agonist activity). They are also used to
 CC enhance cell proliferation (antagonist activity) for wound healing.
 CC They are also applicable in the promotion of new hair growth or
 CC stimulation of the rate of hair growth e.g. following chemotherapy
 CC or for treating alopecia e.g. male pattern baldness.
 XX
 SQ Sequence 34 AA;

 Query Match 67.6%; Score 23; DB 13; Length 34;
 Best Local Similarity 100.0%; Pred. No. 2.9e-17;
 Matches 23; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

 Qy 12 GKHLNSMERVEWLRKKLQDVHNF 34
 ||||||||||||||||
 Db 12 GKHLNSMERVEWLRKKLQDVHNF 34

RESULT 18

AAR22292

ID AAR22292 standard; Peptide; 34 AA.
 XX
 AC AAR22292;
 XX
 DT 25-MAR-2003 (updated)
 DT 03-AUG-1992 (first entry)
 XX
 DE Human parathyroid hormone 1-34 [Phe 11].
 XX
 KW hPTH; protease resistant; osteoporosis; hypoparathyroidism;
 KW hypertension.
 XX
 OS Synthetic.

XX
 PN EP477885-A.
 XX
 PD 01-APR-1992.
 XX
 PF 25-SEP-1991; 91EP-0116303.
 XX
 PR 06-SEP-1991; 91JP-0227232.
 PR 28-SEP-1990; 90JP-0257490.
 XX
 PA (TAKE) TAKEDA CHEM IND LTD.
 XX
 PI Nakagawa S, Fukuda T, Kawase M, Yamazaki I;
 XX
 DR WPI; 1992-106285/14.
 XX
 PT New peptide(s) are parathyroid hormone derivs. - used in hormone
 PT therapy, for treating osteoporosis hyperparathyroidism and
 PT hypertension
 XX
 PS Claim 9; Page 14; 14pp; English.
 XX
 CC The peptide is an analogue of human parathyroid hormone fragment
 CC 1-34. The peptide modification defined increase resistance to
 CC proteases and therefore persistence in the blood. The peptide is
 CC used in therapy of osteoporosis, hypoparathyroidism and hypertension.
 CC The peptide may be synthesised by the Merrifield solid phase
 CC method in an automatic apparatus.
 CC See also AAR22290-99.
 CC (Updated on 25-MAR-2003 to correct PA field.)
 XX
 SQ Sequence 34 AA;

Query Match 67.6%; Score 23; DB 13; Length 34;
 Best Local Similarity 100.0%; Pred. No. 2.9e-17;
 Matches 23; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 12 GKHLNSMERVEWLRKKLQDVHNF 34
 ||||||||||||||||||
 Db 12 GKHLNSMERVEWLRKKLQDVHNF 34

RESULT 19

AAR22293

ID AAR22293 standard; Peptide; 34 AA.
 XX
 AC AAR22293;
 XX
 DT 25-MAR-2003 (updated)
 DT 03-AUG-1992 (first entry)
 XX
 DE Human parathyroid hormone 1-34 [Leu 8].
 XX
 KW hPTH; protease resistant; osteoporosis; hypoparathyroidism;
 KW hypertension.
 XX
 OS Synthetic.

XX
 PN EP477885-A.
 XX
 PD 01-APR-1992.
 XX
 PF 25-SEP-1991; 91EP-0116303.
 XX
 PR 06-SEP-1991; 91JP-0227232.
 PR 28-SEP-1990; 90JP-0257490.
 XX
 PA (TAKE) TAKEDA CHEM IND LTD.
 XX
 PI Nakagawa S, Fukuda T, Kawase M, Yamazaki I;
 XX
 DR WPI; 1992-106285/14.
 XX
 PT New peptide(s) are parathyroid hormone derivs. - used in hormone
 PT therapy, for treating osteoporosis hyperparathyroidism and
 PT hypertension
 XX
 PS Claim 9; Page 14; 14pp; English.
 XX
 CC The peptide is an analogue of human parathyroid hormone fragment
 CC 1-34. The peptide modification defined increase resistance to
 CC proteases and therefore persistence in the blood. The peptide is
 CC used in therapy of osteoporosis, hypoparathyroidism and hypertension.
 CC The peptide may be synthesised by the Merrifield solid phase
 CC method in an automatic apparatus.
 CC See also AAR22290-99.
 CC (Updated on 25-MAR-2003 to correct PA field.)
 XX
 SQ Sequence 34 AA;

Query Match 67.6%; Score 23; DB 13; Length 34;
 Best Local Similarity 100.0%; Pred. No. 2.9e-17;
 Matches 23; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 12 GKHLNSMERVEWLRKKLQDVHNF 34
 |||||
 Db 12 GKHLNSMERVEWLRKKLQDVHNF 34

RESULT 20

AAR22294

ID AAR22294 standard; Peptide; 34 AA.

XX

AC AAR22294;

XX

DT 25-MAR-2003 (updated)

DT 03-AUG-1992 (first entry)

XX

DE Human parathyroid hormone 1-34 [Ser 11].

XX

KW hPTH; protease resistant; osteoporosis; hypoparathyroidism;
 KW hypertension.

XX

OS Synthetic.

XX
 PN EP477885-A.
 XX
 PD 01-APR-1992.
 XX
 PF 25-SEP-1991; 91EP-0116303.
 XX
 PR 06-SEP-1991; 91JP-0227232.
 PR 28-SEP-1990; 90JP-0257490.
 XX
 PA (TAKE) TAKEDA CHEM IND LTD.
 XX
 PI Nakagawa S, Fukuda T, Kawase M, Yamazaki I;
 XX
 DR WPI; 1992-106285/14.
 XX
 PT New peptide(s) are parathyroid hormone derivs. - used in hormone
 PT therapy, for treating osteoporosis hyperparathyroidism and
 PT hypertension
 XX
 PS Claim 9; Page 14; 14pp; English.
 XX
 CC The peptide is an analogue of human parathyroid hormone fragment
 CC 1-34. The peptide modification defined increase resistance to
 CC proteases and therefore persistence in the blood. The peptide is
 CC used in therapy of osteoporosis, hypoparathyroidism and hypertension.
 CC The peptide may be synthesised by the Merrifield solid phase
 CC method in an automatic apparatus.
 CC See also AAR22290-99.
 CC (Updated on 25-MAR-2003 to correct PA field.)
 XX
 SQ Sequence 34 AA;

Query Match 67.6%; Score 23; DB 13; Length 34;
 Best Local Similarity 100.0%; Pred. No. 2.9e-17;
 Matches 23; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 12 GKHLNSMERVEWLRKKLQDVHNF 34
 |||||
 Db 12 GKHLNSMERVEWLRKKLQDVHNF 34

RESULT 21

AAR41549

ID AAR41549 standard; protein; 34 AA.

XX

AC AAR41549;

XX

DT 25-MAR-2003 (updated)

DT 11-APR-1994 (first entry)

XX

DE [D-Ser3]hPTH (1-34)NH2.

XX

KW PTH; parathyroid hormone; protease resistance; osteoporosis;
 KW hypoparathyroidism; hypertension.

XX

OS Homo sapiens.

XX
 FH Key Location/Qualifiers
 FT Misc-difference 3
 FT /note = "D-form residue"
 FT Modified-site 34
 FT /note = "C terminal is amidated"
 XX
 PN EP561412-A1.
 XX
 PD 22-SEP-1993.
 XX
 PF 18-MAR-1993; 93EP-0104500.
 XX
 PR 19-MAR-1992; 92JP-0063517.
 PR 18-FEB-1993; 93JP-0029283.
 XX
 PA (TAKE) TAKEDA CHEM IND LTD.
 XX
 PI Fukuda T, Nakagawa S, Taketomi S;
 XX
 DR WPI; 1993-296712/38.
 XX
 PT New parathyroid hormone derivs. - used for the treatment of
 PT osteoporosis hypoparathyroidism and hypertension
 XX
 PS Example 1; Page 17; 37pp; English.
 XX
 CC Human parathyroid hormone (PTH) analogues (AAR41548 - generic sequence;
 CC AAR41549-R41582 - specific examples) show increased resistance to
 CC proteases and a greater persistency of activity within the blood is
 CC obtained. The proteins can be used to treat a number of bone and blood
 CC disorders. This analogue was used as a test compound.
 CC (Updated on 25-MAR-2003 to correct PN field.)
 XX
 SQ Sequence 34 AA;

Query Match 67.6%; Score 23; DB 14; Length 34;
 Best Local Similarity 100.0%; Pred. No. 2.9e-17;
 Matches 23; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 12 GKHLNSMERVEWLRKKLQDVHNF 34
 |||||
 Db 12 GKHLNSMERVEWLRKKLQDVHNF 34

RESULT 22

AAR41550

ID AAR41550 standard; protein; 34 AA.

XX

AC AAR41550;

XX

DT 25-MAR-2003 (updated)

DT 11-APR-1994 (first entry)

XX

DE [D-Ala3]hPTH (1-34).

XX

KW PTH; parathyroid hormone; protease resistance; osteoporosis;

KW hypoparathyroidism; hypertension.
 XX
 OS Homo sapiens.
 XX
 FH Key Location/Qualifiers
 FT Misc-difference 3
 FT /note = "D-form residue"
 XX
 PN EP561412-A1.
 XX
 PD 22-SEP-1993.
 XX
 PF 18-MAR-1993; 93EP-0104500.
 XX
 PR 19-MAR-1992; 92JP-0063517.
 PR 18-FEB-1993; 93JP-0029283.
 XX
 PA (TAKE) TAKEDA CHEM IND LTD.
 XX
 PI Fukuda T, Nakagawa S, Taketomi S;
 XX
 DR WPI; 1993-296712/38.
 XX
 PT New parathyroid hormone derivs. - used for the treatment of
 PT osteoporosis hypoparathyroidism and hypertension
 XX
 PS Example 1; Page 17; 37pp; English.
 XX
 CC Human parathyroid hormone (PTH) analogues (AAR41548 - generic sequence;
 CC AAR41549-R41582 - specific examples) show increased resistance to
 CC proteases and a greater persistency of activity within the blood is
 CC obtained. The proteins can be used to treat a number of bone and blood
 CC disorders. This analogue has a relative biological activity to hPTH(1-34)
 CC of 2.17.
 CC (Updated on 25-MAR-2003 to correct PN field.)
 XX
 SQ Sequence 34 AA;

Query Match 67.6%; Score 23; DB 14; Length 34;
 Best Local Similarity 100.0%; Pred. No. 2.9e-17;
 Matches 23; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 12 GKHLNSMERVEWLRKKLQDVHNF 34
 |||||
 Db 12 GKHLNSMERVEWLRKKLQDVHNF 34

RESULT 23

AAR41570

ID AAR41570 standard; protein; 34 AA.

XX

AC AAR41570;

XX

DT 25-MAR-2003 (updated)

DT 11-APR-1994 (first entry)

XX

DE [Gln25]hPTH (1-34).

XX
 KW PTH; parathyroid hormone; protease resistance; osteoporosis;
 KW hypoparathyroidism; hypertension.
 XX
 OS Homo sapiens.
 XX
 PN EP561412-A1.
 XX
 PD 22-SEP-1993.
 XX
 PF 18-MAR-1993; 93EP-0104500.
 XX
 PR 19-MAR-1992; 92JP-0063517.
 PR 18-FEB-1993; 93JP-0029283.
 XX
 PA (TAKE) TAKEDA CHEM IND LTD.
 XX
 PI Fukuda T, Nakagawa S, Taketomi S;
 XX
 DR WPI; 1993-296712/38.
 XX
 PT New parathyroid hormone derivs. - used for the treatment of
 PT osteoporosis hypoparathyroidism and hypertension
 XX
 PS Example 1; Page 27; 37pp; English.
 XX
 CC Human parathyroid hormone (PTH) analogues (AAR41548 - generic sequence;
 CC AAR41549-R41582 - specific examples) show increased resistance to
 CC proteases and a greater persistency of activity within the blood is
 CC obtained. The proteins can be used to treat a number of bone and blood
 CC disorders. This analogue was used as a test compound.
 CC (Updated on 25-MAR-2003 to correct PN field.)
 XX
 SQ Sequence 34 AA;

Query Match 67.6%; Score 23; DB 14; Length 34;
 Best Local Similarity 100.0%; Pred. No. 2.9e-17;
 Matches 23; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 12 GKHLNSMERVEWLRKKLQDVHNF 34
 |||||
 Db 12 GKHLNSMERVEWLRKKLQDVHNF 34

RESULT 24

AAR49697

ID AAR49697 standard; Protein; 34 AA.

XX

AC AAR49697;

XX

DT 14-SEP-1994 (first entry)

XX

DE Sequence of variant of human parathyroid hormone [Ala8]hPTH(1-34).

XX

KW Parathyroid hormone; bone-stimulating; non-vasoactive compound;
 KW osteoporosis; therapy.

XX

OS Synthetic.
 XX
 PN CA2098639-A.
 XX
 PD 20-DEC-1993.
 XX
 PF 17-JUN-1993; 93CA-2098639.
 XX
 PR 19-JUN-1992; 92US-0900680.
 XX
 PA (ALLX) ALLELIX BIOPHARMACEUTICALS INC.
 PA (GLAX) GLAXO CANADA INC.
 XX
 PI Bozzato RP, Kronis KA;
 XX
 DR WPI; 1994-074853/10.
 XX
 PT New Met8-substd. variants of parathyroid hormone - stimulate bone
 PT and are non-vasoactive, useful for treating, e.g. osteoporosis
 XX
 PS Claim 13; Fig 2; 31pp; English.
 XX
 CC AAQ58564 is the sequence of wild-type human parathyroid hormone. In
 CC the cpds of the invention, Met 8 is replaced with Cys, Val or Ala.
 CC In addition, Met 18 may be replaced with Leu. Moreover truncated
 CC variants of 34 AAs with Ala or Cys substituted for Met 8 are also
 CC claimed. The variants have reduced vasoactivity relative to Met 8-
 CC contg. hPTH and are useful for the treatment of bone disorders, such
 CC as osteoporosis. Dosage is 1 microgram - 100 milligram (pref. 1-
 CC microgram - 1000 microgram)/kg.
 XX
 SQ Sequence 34 AA;

Query Match 67.6%; Score 23; DB 15; Length 34;
 Best Local Similarity 100.0%; Pred. No. 2.9e-17;
 Matches 23; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 12 GKHLNSMERVEWLRKKLQDVHNF 34
 |||||
 Db 12 GKHLNSMERVEWLRKKLQDVHNF 34

RESULT 25

AAR49698

ID AAR49698 standard; Protein; 34 AA.

XX

AC AAR49698;

XX

DT 14-SEP-1994 (first entry)

XX

DE Sequence of variant of human parathyroid hormone [Cys8]hPTH(1-34).

XX

KW Parathyroid hormone; bone-stimulating; non-vasoactive compound;
 KW osteoporosis; therapy.

XX

OS Synthetic.

XX

PN CA2098639-A.
 XX
 PD 20-DEC-1993.
 XX
 PF 17-JUN-1993; 93CA-2098639.
 XX
 PR 19-JUN-1992; 92US-0900680.
 XX
 PA (ALLX) ALLELIX BIOPHARMACEUTICALS INC.
 PA (GLAX) GLAXO CANADA INC.
 XX
 PI Bozzato RP, Kronis KA;
 XX
 DR WPI; 1994-074853/10.
 XX
 PT New Met8-substd. variants of parathyroid hormone - stimulate bone
 PT and are non-vasoactive, useful for treating, e.g. osteoporosis
 XX
 PS Claim 14; Fig 2; 31pp; English.
 XX
 CC AAQ58564 is the sequence of wild-type human parathyroid hormone. In
 CC the cpds of the invention, Met 8 is replaced with Cys, Val or Ala.
 CC In addition, Met 18 may be replaced with Leu. Moreover truncated
 CC variants of 34 AAs with Ala or Cys substituted for Met 8 are also
 CC claimed. The variants have reduced vasoactivity relative to Met 8-
 CC contg. hPTH and are useful for the treatment of bone disorders, such
 CC as osteoporosis. Dosage is 1 microgram - 100 milligram (pref. 1-
 CC microgram - 1000 microgram)/kg.
 XX
 SQ Sequence 34 AA;

 Query Match 67.6%; Score 23; DB 15; Length 34;
 Best Local Similarity 100.0%; Pred. No. 2.9e-17;
 Matches 23; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

 QY 12 GKHLNSMERVEWLRKKLQDVHNF 34
 ||||||||||||||||||
 Db 12 GKHLNSMERVEWLRKKLQDVHNF 34

 RESULT 26
 AAR58291
 ID AAR58291 standard; peptide; 34 AA.
 XX
 AC AAR58291;
 XX
 DT 20-SEP-1994 (first entry)
 XX
 DE [Lys(For)26, Lys(For)27]-hPTH(1-34)-NH2.
 XX
 KW Human parathyroid hormone; hPTH; variant; analogue;
 KW calcium; depletion; fixation; resorption; osteopathy; osteoporosis;
 KW hypoparathyroidism.
 XX
 OS Synthetic.
 XX
 FH Key Location/Qualifiers

FT Modified-site 26
 FT /label= Other
 FT /note= "Formyl-Lys."
 FT Modified-site 27
 FT /label= Other
 FT /note= "Formyl-Lys."
 FT Modified-site 34
 FT /note= "in amide form"
 XX
 PN GB2269176-A.
 XX
 PD 02-FEB-1994.
 XX
 PF 12-JUL-1993; 93GB-0014384.
 XX
 PR 15-JUL-1992; 92GB-0015009.
 PR 18-DEC-1992; 92GB-0026415.
 PR 23-DEC-1992; 92GB-0026859.
 PR 23-DEC-1992; 92GB-0026861.
 PR 28-JAN-1993; 93GB-0001691.
 PR 28-JAN-1993; 93GB-0001692.
 PR 14-APR-1993; 93GB-0007673.
 PR 19-APR-1993; 93GB-0008033.
 XX
 PA (SANO) SANDOZ LTD.
 PA (BAUE/) BAUER W.
 PA (SANO) SANDOZ PATENT GMBH.
 PA (SANO) SANDOZ-ERFINDUNGEN VERW GES MBH.
 XX
 PI Albert R, Bauer W, Breckenridge R, Cardinaux F;
 PI Gombert F, Gram H, Lewis I, Ramage P, Schneider H;
 PI Waelchli R, Rainer A;
 XX
 DR WPI; 1994-018352/03.
 XX
 PT New active para-thyroid hormone variants - used for treating or
 PT preventing osteoporosis etc.
 XX
 PS Example 289; Page 47; 92pp; English.
 XX
 CC This peptide is an example of a highly generic formula covering
 CC parathyroid hormone variants useful for treating or preventing bone
 CC conditions associated with calcium depletion/resorption, in cases
 CC where calcium fixation is required (esp. osteoporosis) or to treat
 CC hypoparathyroidism.
 XX
 SQ Sequence 34 AA;

 Query Match 67.6%; Score 23; DB 15; Length 34;
 Best Local Similarity 100.0%; Pred. No. 2.9e-17;
 Matches 23; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

 Qy 12 GKHLNSMERVEWLRKKLQDVHNF 34
 |||||
 Db 12 GKHLNSMERVEWLRKKLQDVHNF 34

RESULT 27

AAR58228

ID AAR58228 standard; peptide; 34 AA.

XX

AC AAR58228;

XX

DT 20-SEP-1994 (first entry)

XX

DE [D-Asp30]-hPTH(1-34)-NH2.

XX

KW Human parathyroid hormone; hPTH; variant; analogue;
KW calcium; depletion; fixation; resorption; osteopathy; osteoporosis;
KW hypoparathyroidism.

XX

OS Synthetic.

XX

FH Key Location/Qualifiers

FT Misc-difference 30

FT /note= "D-form residue."

FT Modified-site 34

FT /note= "in amide form"

XX

PN GB2269176-A.

XX

PD 02-FEB-1994.

XX

PF 12-JUL-1993; 93GB-0014384.

XX

PR 15-JUL-1992; 92GB-0015009.

PR 18-DEC-1992; 92GB-0026415.

PR 23-DEC-1992; 92GB-0026859.

PR 23-DEC-1992; 92GB-0026861.

PR 28-JAN-1993; 93GB-0001691.

PR 28-JAN-1993; 93GB-0001692.

PR 14-APR-1993; 93GB-0007673.

PR 19-APR-1993; 93GB-0008033.

XX

PA (SANO) SANDOZ LTD.

PA (BAUE/) BAUER W.

PA (SANO) SANDOZ PATENT GMBH.

PA (SANO) SANDOZ-ERFINDUNGEN VERW GES MBH.

XX

PI Albert R, Bauer W, Breckenridge R, Cardinaux F;

PI Gombert F, Gram H, Lewis I, Ramage P, Schneider H;

PI Waelchli R, Rainer A;

XX

DR WPI; 1994-018352/03.

XX

PT New active para-thyroid hormone variants - used for treating or
PT preventing osteoporosis etc.

XX

PS Example 226; Page 45; 92pp; English.

XX

CC This peptide is an example of a highly generic formula covering
CC parathyroid hormone variants useful for treating or preventing bone
CC conditions associated with calcium depletion/resorption, in cases
CC where calcium fixation is required (esp. osteoporosis) or to treat

CC hypoparathyroidism.

XX

SQ Sequence 34 AA;

Query Match 67.6%; Score 23; DB 15; Length 34;

Best Local Similarity 100.0%; Pred. No. 2.9e-17;

Matches 23; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 12 GKHLNSMERVEWLRKKLQDVHNF 34

|||||

Db 12 GKHLNSMERVEWLRKKLQDVHNF 34

RESULT 28

AAR58016

ID AAR58016 standard; peptide; 34 AA.

XX

AC AAR58016;

XX

DT 20-SEP-1994 (first entry)

XX

DE N-alpha-Isopropyl-hPTH(1-34)-NH2 parathyroid hormone variant.

XX

KW Human parathyroid hormone; hPTH; variant; analogue;

KW calcium; depletion; fixation; resorption; osteopathy; osteoporosis;

KW hypoparathyroidism.

XX

OS Synthetic.

XX

FH Key Location/Qualifiers

FT Modified-site 1

FT /note= "N-alpha-isopropyl-Ser"

FT Modified-site 34

FT /note= "in amide form"

XX

PN GB2269176-A.

XX

PD 02-FEB-1994.

XX

PF 12-JUL-1993; 93GB-0014384.

XX

PR 15-JUL-1992; 92GB-0015009.

PR 18-DEC-1992; 92GB-0026415.

PR 23-DEC-1992; 92GB-0026859.

PR 23-DEC-1992; 92GB-0026861.

PR 28-JAN-1993; 93GB-0001691.

PR 28-JAN-1993; 93GB-0001692.

PR 14-APR-1993; 93GB-0007673.

PR 19-APR-1993; 93GB-0008033.

XX

PA (SANO) SANDOZ LTD.

PA (BAUE/) BAUER W.

PA (SANO) SANDOZ PATENT GMBH.

PA (SANO) SANDOZ-ERFINDUNGEN VERW GES MBH.

XX

PI Albert R, Bauer W, Breckenridge R, Cardinaux F;

PI Gombert F, Gram H, Lewis I, Ramage P, Schneider H;

PI Waelchli R, Rainer A;
 XX
 DR WPI; 1994-018352/03.
 XX
 PT New active para-thyroid hormone variants - used for treating or
 PT preventing osteoporosis etc.
 XX
 PS Example 1; Page 30; 92pp; English.
 XX
 CC This peptide is an example of a highly generic formula covering
 CC parathyroid hormone variants useful for treating or preventing bone
 CC conditions associated with calcium depletion/resorption, in cases
 CC where calcium fixation is required (esp. osteoporosis) or to treat
 CC hypoparathyroidism.
 XX
 SQ Sequence 34 AA;

Query Match 67.6%; Score 23; DB 15; Length 34;
 Best Local Similarity 100.0%; Pred. No. 2.9e-17;
 Matches 23; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 12 GKHLNSMERVEWLRKKLQDVHNF 34
 ||||||||||||||||||
 Db 12 GKHLNSMERVEWLRKKLQDVHNF 34

RESULT 29

AAR58017

ID AAR58017 standard; peptide; 34 AA.
 XX
 AC AAR58017;
 XX
 DT 20-SEP-1994 (first entry)
 XX
 DE [Lys(N-epsilon-Isopropyl)26,27]-human parathyroid hormone(1-34)-NH2.
 XX
 KW Human parathyroid hormone; hPTH; variant; analogue;
 KW calcium; depletion; fixation; resorption; osteopathy; osteoporosis;
 KW hypoparathyroidism.
 XX
 OS Synthetic.
 XX

| FH | Key | Location/Qualifiers |
|----|---------------|----------------------------------|
| FT | Modified-site | 26 |
| FT | | /note= "N-epsilon-Isopropyl-Lys" |
| FT | Modified-site | 27 |
| FT | | /note= "N-epsilon-Isopropyl-Lys" |
| FT | Modified-site | 34 |
| FT | | /note= "in amide form" |

 XX
 PN GB2269176-A.
 XX
 PD 02-FEB-1994.
 XX
 PF 12-JUL-1993; 93GB-0014384.
 XX
 PR 15-JUL-1992; 92GB-0015009.

PR 18-DEC-1992; 92GB-0026415.
PR 23-DEC-1992; 92GB-0026859.
PR 23-DEC-1992; 92GB-0026861.
PR 28-JAN-1993; 93GB-0001691.
PR 28-JAN-1993; 93GB-0001692.
PR 14-APR-1993; 93GB-0007673.
PR 19-APR-1993; 93GB-0008033.

XX

PA (SANO) SANDOZ LTD.
PA (BAUE/) BAUER W.
PA (SANO) SANDOZ PATENT GMBH.
PA (SANO) SANDOZ-ERFINDUNGEN VERW GES MBH.

XX

PI Albert R, Bauer W, Breckenridge R, Cardinaux F;
PI Gombert F, Gram H, Lewis I, Ramage P, Schneider H;
PI Waelchli R, Rainer A;

XX

DR WPI; 1994-018352/03.

XX

PT New active para-thyroid hormone variants - used for treating or
PT preventing osteoporosis etc.

XX

PS Example 2; Page 32; 92pp; English.

XX

CC This peptide is an example of a highly generic formula covering
CC parathyroid hormone variants useful for treating or preventing bone
CC conditions associated with calcium depletion/resorption, in cases
CC where calcium fixation is required (esp. osteoporosis) or to treat
CC hypoparathyroidism.

XX

SQ Sequence 34 AA;

Query Match 67.6%; Score 23; DB 15; Length 34;
Best Local Similarity 100.0%; Pred. No. 2.9e-17;
Matches 23; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 12 GKHLNSMERVEWLRKKLQDVHNF 34
| | | | | | | | | | | | | | | | | |
Db 12 GKHLNSMERVEWLRKKLQDVHNF 34

RESULT 30

AAR55724

ID AAR55724 standard; peptide; 34 AA.

XX

AC AAR55724;

XX

DT 25-MAR-2003 (updated)

DT 16-NOV-1994 (first entry)

XX

DE Parathormone N-terminal sequence.

XX

KW Parathormone; parathyroid hormone; fatty acyl-peptide; conjugate;
KW antiproliferative; tumor; psoriasis; docosahexaenoic acid; DHA;
KW eicosapentaenoic acid; EPA; antitumor.

XX

OS Synthetic.

XX
 PN WO9412530-A1.
 XX
 PD 09-JUN-1994.
 XX
 PF 29-NOV-1993; 93WO-HU00065.
 XX
 PR 30-NOV-1992; 92US-0984293.
 XX
 PA (BIOS-) BIOSIGNAL KUTATO FEJLESZTO KFT.
 PA (SYNT-) SYNTHETIC PEPTIDES INC.
 XX
 PI Balogh A, Cachia PJ, Hodges RS, Horvath A, Keri G;
 PI Szederkenyi F, Vadasz Z;
 XX
 DR WPI; 1994-200194/24.
 XX
 PT New fatty acyl-peptide conjugates for inhibiting cell
 PT proliferation - more active than free peptide, partic. for
 PT treating tumours, virus-infected cells, psoriasis, etc.
 XX
 PS Disclosure; Fig. 1; 45pp; English.
 XX
 CC The peptides given in AAR55718-48 can each be conjugated through an
 CC amide linkage with a polyunsaturated fatty acid moiety, such as
 CC docosahexaenoic acid (DHA) or eicosapentanoic acid, to improve
 CC antiproliferative activity. The parathormone N-terminal fragment
 CC inhibits osteoblast proliferation.
 CC (Updated on 25-MAR-2003 to correct PN field.)
 XX
 SQ Sequence 34 AA;

Query Match 67.6%; Score 23; DB 15; Length 34;
 Best Local Similarity 100.0%; Pred. No. 2.9e-17;
 Matches 23; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 12 GKHLNSMERVEWLRKKLQDVHNF 34
 ||||||||||||||||||
 Db 12 GKHLNSMERVEWLRKKLQDVHNF 34

RESULT 31

AAR74521

ID AAR74521 standard; Peptide; 34 AA.

XX

AC AAR74521;

XX

DT 25-MAR-2003 (updated)

DT 04-DEC-1995 (first entry)

XX

DE Human parathyroid hormone (1-34).

XX

KW Analogue; truncated human parathyroid hormone; PTH; hPTH; substitution;

KW osteoporosis; hypercalcaemia; hyperparathroidism;

KW metabolic bone disease; human; veterinary medicine;

KW iontophoretic transdermal transport; recombinant E.coli.

XX

OS Homo sapiens.
 XX
 PN WO9511988-A1.
 XX
 PD 04-MAY-1995.
 XX
 PF 25-OCT-1994; 94WO-US12205.
 XX
 PR 25-OCT-1993; 93US-0142551.
 XX
 PA (AFFY-) AFFYMAX TECHNOLOGIES NV.
 XX
 PI Oldenburg KR, Selick HE;
 XX
 DR WPI; 1995-178880/23.
 XX
 PT New active analogues of parathyroid hormone - with increased
 PT activity, stability in serum etc., esp. for treating
 PT osteoporosis, also related DNA and vectors
 XX
 PS Disclosure; Page 1; 109pp; English.
 XX
 CC This sequence represents residues 1-34 of human parathyroid hormone
 CC (RPTH). This sequence was used in the production of analogues of the
 CC truncated form of PTH. These analogues have increased activity and
 CC longer serum half life than native PTH due to eg. substitution of Met
 CC residues with Leu residues and replacing the carboxy Phe with Tyr. The
 CC carboxy terminal may also be modified by the addition of a homoserine
 CC residue or analogue, or by the addition of residues 35-84 of wild type
 CC PTH (see AAR74410). These PTH analogues may be used in the treatment of
 CC osteoporosis or hypercalcaemia, hyperparathroidism or other metabolic
 CC bone diseases in human or veterinary medicine. These peptides may also
 CC have increased iontophoretic transdermal transport compared to wild type
 CC PTH and can be produced in high yield in recombinant E.coli.
 CC (Updated on 25-MAR-2003 to correct PN field.)
 XX
 SQ Sequence 34 AA;

Query Match 67.6%; Score 23; DB 16; Length 34;
 Best Local Similarity 100.0%; Pred. No. 2.9e-17;
 Matches 23; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 12 GKHLNSMERVEWLRKKLQDVHNF 34
 |||||
 Db 12 GKHLNSMERVEWLRKKLQDVHNF 34

RESULT 32
 AAW99449
 ID AAW99449 standard; peptide; 34 AA.
 XX
 AC AAW99449;
 XX
 DT 08-JUN-1999 (first entry)
 XX
 DE Human parathyroid hormone aal-34.
 XX

KW Parathyroid hormone; PTH; parathormone; premature birth; pregnancy;
 KW spontaneous abortion; uterine contraction; human.
 XX
 OS Homo sapiens.
 XX
 PN US5880093-A.
 XX
 PD 09-MAR-1999.
 XX
 PF 05-APR-1995; 95US-0411726.
 XX
 PR 28-SEP-1992; 92IT-MI02331.
 XX
 PA (BAGN/) BAGNOLI F.
 XX
 PI Bagnoli F;
 XX
 DR WPI; 1996-162392/17.
 XX
 PT Use of composition containing parathormone or fragments - for
 PT preventing premature birth or spontaneous abortion or for treating
 PT unwanted uterine contractions
 XX
 PS Disclosure; Column 7-8; 11pp; English.
 XX
 CC Peptides AAW99448-W99452 represent all or part of the parathyroid
 CC hormone (PTH; parathormone) sequence or related peptide. The peptides
 CC are used for preventing premature birth, spontaneous abortion or unwanted
 CC uterine contractions in a pregnant human patient.
 CC (Note: this patent is the first Major Country Equivalent to Italian
 CC Patent IT1255388).
 XX
 SQ Sequence 34 AA;

Query Match 67.6%; Score 23; DB 17; Length 34;
 Best Local Similarity 100.0%; Pred. No. 2.9e-17;
 Matches 23; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 12 GKHLNSMERVEWLRKKLQDVHNF 34
 |||||
 Db 12 GKHLNSMERVEWLRKKLQDVHNF 34

RESULT 33

AAW15812

ID AAW15812 standard; peptide; 34 AA.

XX

AC AAW15812;

XX

DT 25-MAR-2003 (updated)

DT 05-JUN-1997 (first entry)

XX

DE [Trp(10)]-hPTH(1-34)-OH.

XX

KW human parathyroid hormone; human parathyroid hormone related peptide;

KW hPTH; hPTHrP; antagonist; hyperparathyroidism; hypercalcaemia;

KW tumour; dermatological disorders; hair growth promoter.

XX
 OS Synthetic.
 XX
 PN WO9603437-A1.
 XX
 PD 08-FEB-1996.
 XX
 PF 27-JUL-1995; 95WO-EP02993.
 XX
 PR 28-JUL-1994; 94GB-0015255.
 PR 28-JUL-1994; 94GB-0015254.
 XX
 PA (SANO) SANDOZ LTD.
 PA (SANO) SANDOZ PATENT GMBH.
 PA (SANO) SANDOZ-ERFINDUNGEN VERW GES MBH.
 XX
 PI Cardinaux F, Feyen JHM, Gamse R, Gombert FO;
 XX
 DR WPI; 1996-117003/12.
 XX
 PT New parathyroid hormone or parathyroid hormone related peptide cpds.
 PT - useful for preventing or treating conditions associated with
 PT increased plasma calcium, tumour growth and dermatological disorders
 XX
 PS Example 9; Page 9; 32pp; English.
 XX
 CC New parathyroid hormone (PTH) or parathyroid hormone related peptide
 CC (PTHrP) compounds are claimed in which (i) at least one of the amino
 CC acid residues naturally occurring in positions 2 and 10 is replaced
 CC by tryptophan or another amino acid residue bearing an aromatic or
 CC heteroaromatic group on its side chain, and (ii) optionally at least
 CC one of the amino acid residues naturally occurring in positions 3 and 6
 CC is further replaced by tryptophan or another amino acid residue bearing
 CC an aromatic or heteroaromatic group on its side chain. The peptides are
 CC PTH or PTHrP antagonists useful for preventing or treating conditions
 CC associated with increased plasma calcium caused by excessive release of
 CC PTH or PTHrP (e.g. hyperparathyroidism, or hypercalcemia associated with
 CC malignancy); for preventing or treating tumour growth stimulated by
 CC PTHrP; for treating dermatological disorders; and for promoting hair
 CC growth. They may be used in combination with a further active agent,
 CC e.g. a bone resorption inhibitor or cytostatic agent.
 CC The present sequence is a specific example of the new peptides.
 CC (Updated on 25-MAR-2003 to correct PA field.)
 XX
 SQ Sequence 34 AA;

Query Match 67.6%; Score 23; DB 17; Length 34;
 Best Local Similarity 100.0%; Pred. No. 2.9e-17;
 Matches 23; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 12 GKHLNSMERVEWLRKKLQDVHNF 34
 |||||
 Db 12 GKHLNSMERVEWLRKKLQDVHNF 34

RESULT 34
 AAR99978

ID AAR99978 standard; peptide; 34 AA.
 XX
 AC AAR99978;
 XX
 DT 30-APR-1997 (first entry)
 XX
 DE Human parathyroid hormone peptide fragment (1-34).
 XX
 KW cyclic parathyroid hormone fragment; calcium-regulating activity;
 KW osteoporosis; inhibit proliferation; epidermal cell; psoriasis;
 KW improved half life; calcium retention; bone.
 XX
 OS Synthetic.
 XX
 PN DE19508672-A1.
 XX
 PD 12-SEP-1996.
 XX
 PF 10-MAR-1995; 95DE-1008672.
 XX
 PR 10-MAR-1995; 95DE-1008672.
 XX
 PA (BOEF) BOEHRINGER MANNHEIM GMBH.
 XX
 PI Dony C, Esswein A, Hoffmann E, Honold K, Schaefer W;
 XX
 DR WPI; 1996-413519/42.
 XX
 PT Cyclic parathyroid hormone fragments with lactam bridge - have good
 PT in vivo half life and are useful for treating osteoporosis and
 PT preventing epidermal cell proliferation
 XX
 PS Disclosure; Page 9; 14pp; German.
 XX
 CC New cyclic parathyroid hormone fragments (CPTH) have the amino acid
 CC sequence of h, b, p, r or cPTH(1-34), opt. extended by up to 4 amino
 CC acids (aa) at the C-terminus and opt. shortened by up to 3 amino acids at
 CC the N-terminus, and are cyclised between positions 13 and 17. One of
 CC these positions is occupied by L- or D- Orn or Lys, and the other by L-
 CC or D- Glu or Asp. CPTH have calcium-regulating activity (esp. for
 CC treating osteoporosis and inhibit proliferation of epidermal cells (for
 CC treating psoriasis). The CPTH have an improved half life in vivo than
 CC known PTH fragments, increased mitogenicity and DNA-synthesising
 CC capacity, reduced catabolic, calcium-mobilising activity and increased
 CC activity for calcium retention and incorporation into bone. The
 CC present sequence is that of human PTH peptide fragment (1-34).
 XX
 SQ Sequence 34 AA;

Query Match 67.6%; Score 23; DB 17; Length 34;
 Best Local Similarity 100.0%; Pred. No. 2.9e-17;
 Matches 23; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 12 GKHLNSMERVEWLRKKLQDVHNF 34
 |||||
 Db 12 GKHLNSMERVEWLRKKLQDVHNF 34

RESULT 35

AAR98951

ID AAR98951 standard; peptide; 34 AA.

XX

AC AAR98951;

XX

DT 15-JAN-1997 (first entry)

XX

DE Target peptide (PTH(1-34)) used in fusion protein construct.

XX

KW Fusion protein construct; isolation; purification;
KW growth hormone releasing factor; glucagon-like peptide 1;
KW parathyroid hormone; inclusion body; carbonic anhydrase.

XX

OS Synthetic.

XX

PN WO9617942-A1.

XX

PD 13-JUN-1996.

XX

PF 07-DEC-1995; 95WO-US15800.

XX

PR 07-DEC-1994; 94US-0350530.

XX

PA (BION-) BIONEBRASKA INC.

XX

PI De LA MOTTE RS, Henriksen DB, Holmquist B, Manning SD;

PI Partridge BE, Stout JS, Wagner FW;

XX

DR WPI; 1996-287186/29.

XX

PT Isolation and purificn of peptide(s) from fusion protein constructs

PT - which include a carbonic anhydrase and a variable fused

PT polypeptide

XX

PS Claim 18; Page 48; 67pp; English.

XX

CC A new method for the isolation and/or purification of a recombinant
CC peptide employs a fusion protein construct (FPC) comprising a
CC carbonic anhydrase and a variable fused polypeptide containing a
CC target peptide. The method comprises precipitating either the FPC or
CC a fragment of the FPC including the carbonic anhydrase. An
CC alternative method of producing the peptide comprises expressing the
CC FPC as part of an inclusion body. The target peptides of the FPC are
CC derived from growth hormone releasing factor (GRF), glucagon-like
CC peptide 1 (GLP1) or parathyroid hormone (PTH). This sequence
CC corresponds to amino acids 1-34 of PTH.

XX

SQ Sequence 34 AA;

Query Match 67.6%; Score 23; DB 17; Length 34;

Best Local Similarity 100.0%; Pred. No. 2.9e-17;

Matches 23; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 12 GKHLNSMERVEWLRKKLQDVHNF 34

|||||

Db 12 GKHLNSMERVEWLRKKLQDVHNF 34

RESULT 36

AAR98966

ID AAR98966 standard; Peptide; 34 AA.

XX

AC AAR98966;

XX

DT 02-DEC-1996 (first entry)

XX

DE PTH(1-34).

XX

KW PTH; parathyroid hormone; parathormone; C-amide;

KW C-amidated peptide; alpha-carboxamide; recombinant protein;

KW fusion protein; transpeptidation.

XX

OS Not specified.

XX

PN WO9617941-A2.

XX

PD 13-JUN-1996.

XX

PF 07-DEC-1995; 95WO-US15799.

XX

PR 07-DEC-1994; 94US-0350528.

XX

PA (BION-) BIONEBRASKA INC.

XX

PI Heriksen DB, Holmquist B, Patridge BE, Stout JS;

PI Wagner FW;

XX

DR WPI; 1996-287185/29.

XX

PT Production of C-terminal alpha-carboxamidated peptide(s) - by

PT cleavage and transpeptidation of recombinant multicopy peptide(s) or

PT fusion constructs

XX

PS Claim 12; Page 70; 93pp; English.

XX

CC GLP1(7-35), GRF(1-44) and PTH(1-34) peptides (AAR98964-66) can be

CC produced as C-terminal amidated peptides utilising novel recombinant

CC protein constructs (see also AAR98967-72) in which single or multiple

CC copies of the peptide are linked by intraconnecting peptides that

CC permit the construct to be selectively reacted to produce product

CC peptides having a C-terminal alpha-carboxamide. Expression cassettes

CC (see also AAT34865-70) can be incorporated into vectors allowing prodn.

CC of the recombinant proteins in transformed E. coli host cells.

XX

SQ Sequence 34 AA;

Query Match 67.6%; Score 23; DB 17; Length 34;

Best Local Similarity 100.0%; Pred. No. 2.9e-17;

Matches 23; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 12 GKHLNSMERVEWLRKKLQDVHNF 34

||||||||||||||||||||

RESULT 37

AAR88835

ID AAR88835 standard; peptide; 34 AA.

XX

AC AAR88835;

XX

DT 07-OCT-1996 (first entry)

XX

DE Human parathyroid hormone analogue, cyclo-PTH(1-34)-NH₂.

XX

KW Parathyroid hormone; PTH; analogue; osteoporosis; bone cell;

KW calcium regulation; reduced PKC activity; protein kinase C;

KW increased adenylyl cyclase activity; cAMPase; cyclic; bone loss.

XX

OS Synthetic.

XX

FH Key Location/Qualifiers

FT Modified-site 10

FT /note= "forms peptide bond with Lys at posn. 26"

FT Modified-site 14

FT /note= "forms peptide bond with Asp at posn. 30"

FT Modified-site 26

FT /note= "forms peptide bond with Asn at posn. 10"

FT Modified-site 30

FT /note= "forms peptide bond with His at posn. 14"

FT Modified-site 34

FT /note= "amidated"

XX

PN CA2126299-A.

XX

PD 21-DEC-1995.

XX

PF 20-JUN-1994; 94CA-2126299.

XX

PR 20-JUN-1994; 94CA-2126299.

XX

PA (WILL/) WILLICK G E.

XX

PI Neugebauer W, Sung WL, Surewicz W, Whitfield JF;

PI Willick GE;

XX

DR WPI; 1996-151754/16.

XX

PT New human parathyroid hormone analogues - which have increased

PT adenylyl cyclase activating activity, used for treating osteoporosis

XX

PS Claim 3; Fig 8; 21pp; English.

XX

CC AAR88829-R88841 are human parathyroid hormone (hPTH) analogues. The

CC analogues increase G-protein coupled adenylyl cyclase (cAMPase)

CC activity and reduce protein kinase C (PKC) activity. The analogues

CC can reverse the loss of bone and increase bone mass and density

CC without undesirable effects. They are useful for the treatment of

CC osteoporosis and other bone related disorders and disorders

CC involving bone cell calcium regulation.

XX

SQ Sequence 34 AA;

Query Match 67.6%; Score 23; DB 17; Length 34;

Best Local Similarity 100.0%; Pred. No. 2.9e-17;

Matches 23; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 12 GKHLNSMERVEWLRKKLQDVHNF 34

|||||

Db 12 GKHLNSMERVEWLRKKLQDVHNF 34

RESULT 38

AAW24273

ID AAW24273 standard; protein; 34 AA.

XX

AC AAW24273;

XX

DT 17-OCT-1997 (first entry)

XX

DE Wild type parathyroid hormone.

XX

KW Analogue; parathyroid hormone; PTH; hirudin; hirulog;

KW electrotransportability; alpha-helix; beta-sheet.

XX

OS Homo sapiens.

XX

PN W09639423-A2.

XX

PD 12-DEC-1996.

XX

PF 06-JUN-1996; 96WO-US09647.

XX

PR 06-JUN-1995; 95US-0468275.

XX

PA (ALZA) ALZA CORP.

XX

PI Holladay LA, Oldenburg KR;

XX

DR WPI; 1997-043058/04.

XX

PT Prepn. of analogues of parent poly-peptide(s), esp. parathyroid

PT hormone and hirulog - which exhibit better or enhanced

PT electro-transportability through a body surface

XX

PS Claim 7; Fig 1A; 55pp; English.

XX

CC The sequences given in AAW24273-76 represent wildtype and analogues of

CC parathyroid hormone (PTH). The analogues exhibit better/enhanced

CC electrotransportability through a body surface, and are characterised

CC by substituting one or more amino acid residues of the parent

CC polypeptide to disrupt one or more alpha-helical and/or beta-sheet

CC segments of the parent polypeptide. An electrotransport device can

CC deliver the polypeptide analogue through a body surface by electro-

CC transport by including providing a therapeutically effective amount

CC of the polypeptide analogue in a donor reservoir of the electrotransport

CC device. The electrotransport flux of a polypeptide is increased by
CC reducing the potential of the polypeptide for forming alpha-helix or
CC beta-sheet segment.

XX

SQ Sequence 34 AA;

Query Match 67.6%; Score 23; DB 18; Length 34;
Best Local Similarity 100.0%; Pred. No. 2.9e-17;
Matches 23; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 12 GKHLNSMERVEWLRKKLQDVHNF 34
|||
Db 12 GKHLNSMERVEWLRKKLQDVHNF 34

RESULT 39

AAW08120

ID AAW08120 standard; peptide; 34 AA.

XX

AC AAW08120;

XX

DT 10-OCT-1997 (first entry)

XX

DE Human PTH derivative, [Aad10]hPTH(1-34).

XX

KW Human; parathyroid hormone; PTH; cAMP-producing activity;
KW bone formation; osteoporosis; hypoparathyroidism; hypertension;
KW climacteric disturbance.

XX

OS Synthetic.

XX

FH Key Location/Qualifiers

FT Modified-site 10

FT /label= Aad

XX

PN EP748817-A2.

XX

PD 18-DEC-1996.

XX

PF 13-JUN-1996; 96EP-0109475.

XX

PR 15-JUN-1995; 95JP-0148652.

XX

PA (TAKE) TAKEDA CHEM IND LTD.

XX

PI Fukuda T, Habashita J, Nakagawa S, Taketomi S;

XX

DR WPI; 1997-036114/04.

XX

PT New parathyroid hormone derivs. - useful in treatment of bone
PT diseases, hypoparathyroidism and hypertension

XX

PS Example 1; Page 29; 42pp; English.

XX

CC The sequences given in AAW08108-32 represent derivatives of human
CC parathyroid hormone (PTH). These peptides are human PTH (1-34)
CC derivative peptides. They have potent cAMP-producing activity and

CC bone formation activity. They may be used in treatment of bone
CC diseases including osteoporosis, hypoparathyroidism, hypertension
CC and climacteric disturbance. The peptides are low in toxicity and
CC are safe.

XX

SQ Sequence 34 AA;

Query Match 67.6%; Score 23; DB 18; Length 34;
Best Local Similarity 100.0%; Pred. No. 2.9e-17;
Matches 23; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 12 GKHLNSMERVEWLRKKLQDVHNF 34

|||||

Db 12 GKHLNSMERVEWLRKKLQDVHNF 34

RESULT 40

AAW08109

ID AAW08109 standard; peptide; 34 AA.

XX

AC AAW08109;

XX

DT 10-OCT-1997 (first entry)

XX

DE Human parathyroid hormone derivative, [Glu10]hPTH(1-34).

XX

KW Human; parathyroid hormone; PTH; cAMP-producing activity;
KW bone formation; osteoporosis; hypoparathyroidism; hypertension;
KW climacteric disturbance.

XX

OS Synthetic.

XX

PN EP748817-A2.

XX

PD 18-DEC-1996.

XX

PF 13-JUN-1996; 96EP-0109475.

XX

PR 15-JUN-1995; 95JP-0148652.

XX

PA (TAKE) TAKEDA CHEM IND LTD.

XX

PI Fukuda T, Habashita J, Nakagawa S, Taketomi S;

XX

DR WPI; 1997-036114/04.

XX

PT New parathyroid hormone derivs. - useful in treatment of bone
PT diseases, hypoparathyroidism and hypertension

XX

PS Claim 28; Page 26; 42pp; English.

XX

CC The sequences given in AAW08108-32 represent derivatives of human
CC parathyroid hormone (PTH). These peptides are human PTH (1-34)
CC derivative peptides. They have potent cAMP-producing activity and
CC bone formation activity. They may be used in treatment of bone
CC diseases including osteoporosis, hypoparathyroidism, hypertension
CC and climacteric disturbance. The peptides are low in toxicity and

CC are safe.

XX

SQ Sequence 34 AA;

Query Match 67.6%; Score 23; DB 18; Length 34;

Best Local Similarity 100.0%; Pred. No. 2.9e-17;

Matches 23; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 12 GKHLNSMERVEWLRKKLQDVHNF 34

||||||||||||||||

Db 12 GKHLNSMERVEWLRKKLQDVHNF 34

Search completed: January 14, 2004, 10:34:21

Job time : 34.5171 secs

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OM protein - protein search, using sw model

Run on: January 14, 2004, 10:28:59 ; Search time 11.5452 Seconds
(without alignments)
124.604 Million cell updates/sec

Title: US-09-843-221A-163
Perfect score: 34
Sequence: 1 SVSEIQLMHNKGKHLNSMERVEWLRKKLQDVHNF 34

Scoring table: OLIGO
Gapop 60.0 , Gapext 60.0

Searched: 328717 seqs, 42310858 residues

Word size : 0

Total number of hits satisfying chosen parameters: 25778

Minimum DB seq length: 28
Maximum DB seq length: 40

Post-processing: Listing first 1000 summaries

Database : Issued_Patents_AA:*
1: /cgn2_6/ptodata/1/iaa/5A_COMB.pep:*
2: /cgn2_6/ptodata/1/iaa/5B_COMB.pep:*
3: /cgn2_6/ptodata/1/iaa/6A_COMB.pep:*
4: /cgn2_6/ptodata/1/iaa/6B_COMB.pep:*
5: /cgn2_6/ptodata/1/iaa/PCTUS_COMB.pep:*
6: /cgn2_6/ptodata/1/iaa/backfiles1.pep:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

| Result | | % | | | | | |
|--------|-------|-------|-------|--------|------------------|----|-------------------|
| No. | Score | Query | Match | Length | DB | ID | Description |
| 1 | 24 | 70.6 | 34 | 3 | US-09-044-536A-8 | | Sequence 8, Appli |
| 2 | 23 | 67.6 | 33 | 1 | US-08-256-363-1 | | Sequence 1, Appli |
| 3 | 23 | 67.6 | 34 | 1 | US-07-765-373-1 | | Sequence 1, Appli |
| 4 | 23 | 67.6 | 34 | 1 | US-08-033-099-1 | | Sequence 1, Appli |
| 5 | 23 | 67.6 | 34 | 1 | US-08-262-495C-1 | | Sequence 1, Appli |
| 6 | 23 | 67.6 | 34 | 1 | US-07-915-247A-1 | | Sequence 1, Appli |
| 7 | 23 | 67.6 | 34 | 1 | US-08-443-863-1 | | Sequence 1, Appli |
| 8 | 23 | 67.6 | 34 | 1 | US-08-448-070-1 | | Sequence 1, Appli |
| 9 | 23 | 67.6 | 34 | 1 | US-08-488-105-7 | | Sequence 7, Appli |
| 10 | 23 | 67.6 | 34 | 1 | US-08-468-275-6 | | Sequence 6, Appli |
| 11 | 23 | 67.6 | 34 | 1 | US-08-256-363-2 | | Sequence 2, Appli |

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| 12 | 23 | 67.6 | 34 | 1 | US-08-449-500-1 | Sequence 1, Appli |
| 13 | 23 | 67.6 | 34 | 1 | US-08-449-317A-1 | Sequence 1, Appli |
| 14 | 23 | 67.6 | 34 | 2 | US-08-142-551B-2 | Sequence 2, Appli |
| 15 | 23 | 67.6 | 34 | 2 | US-08-477-022-1 | Sequence 1, Appli |
| 16 | 23 | 67.6 | 34 | 2 | US-08-449-447-1 | Sequence 1, Appli |
| 17 | 23 | 67.6 | 34 | 2 | US-08-835-231-13 | Sequence 13, Appl |
| 18 | 23 | 67.6 | 34 | 2 | US-08-184-328-1 | Sequence 1, Appli |
| 19 | 23 | 67.6 | 34 | 2 | US-08-411-726-2 | Sequence 2, Appli |
| 20 | 23 | 67.6 | 34 | 2 | US-08-691-647C-5 | Sequence 5, Appli |
| 21 | 23 | 67.6 | 34 | 2 | US-08-521-097-1 | Sequence 1, Appli |
| 22 | 23 | 67.6 | 34 | 3 | US-09-044-536A-1 | Sequence 1, Appli |
| 23 | 23 | 67.6 | 34 | 3 | US-09-044-536A-9 | Sequence 9, Appli |
| 24 | 23 | 67.6 | 34 | 3 | US-09-044-536A-10 | Sequence 10, Appl |
| 25 | 23 | 67.6 | 34 | 3 | US-09-044-536A-11 | Sequence 11, Appl |
| 26 | 23 | 67.6 | 34 | 3 | US-09-044-536A-12 | Sequence 12, Appl |
| 27 | 23 | 67.6 | 34 | 3 | US-09-044-536A-13 | Sequence 13, Appl |
| 28 | 23 | 67.6 | 34 | 3 | US-09-044-536A-14 | Sequence 14, Appl |
| 29 | 23 | 67.6 | 34 | 3 | US-09-044-536A-15 | Sequence 15, Appl |
| 30 | 23 | 67.6 | 34 | 3 | US-08-904-760B-22 | Sequence 22, Appl |
| 31 | 23 | 67.6 | 34 | 3 | US-09-108-661-13 | Sequence 13, Appl |
| 32 | 23 | 67.6 | 34 | 4 | US-09-007-466-6 | Sequence 6, Appli |
| 33 | 23 | 67.6 | 34 | 4 | US-09-406-813-1 | Sequence 1, Appli |
| 34 | 23 | 67.6 | 34 | 4 | US-08-952-980B-6 | Sequence 6, Appli |
| 35 | 23 | 67.6 | 34 | 4 | US-09-228-990-1 | Sequence 1, Appli |
| 36 | 23 | 67.6 | 34 | 4 | US-09-447-800-1 | Sequence 1, Appli |
| 37 | 23 | 67.6 | 34 | 4 | US-09-447-800-2 | Sequence 2, Appli |
| 38 | 23 | 67.6 | 34 | 4 | US-09-447-800-5 | Sequence 5, Appli |
| 39 | 23 | 67.6 | 34 | 4 | US-09-447-800-8 | Sequence 8, Appli |
| 40 | 23 | 67.6 | 34 | 4 | US-09-536-785A-22 | Sequence 22, Appl |
| 41 | 23 | 67.6 | 34 | 4 | US-09-442-989-26 | Sequence 26, Appl |
| 42 | 23 | 67.6 | 34 | 5 | PCT-US95-15800-22 | Sequence 22, Appl |
| 43 | 23 | 67.6 | 35 | 1 | US-08-256-363-3 | Sequence 3, Appli |
| 44 | 23 | 67.6 | 36 | 1 | US-08-112-024-2 | Sequence 2, Appli |
| 45 | 23 | 67.6 | 36 | 1 | US-08-256-363-4 | Sequence 4, Appli |
| 46 | 23 | 67.6 | 37 | 1 | US-08-440-117-1 | Sequence 1, Appli |
| 47 | 23 | 67.6 | 37 | 3 | US-09-068-738A-16 | Sequence 16, Appl |
| 48 | 23 | 67.6 | 38 | 1 | US-08-112-024-1 | Sequence 1, Appli |
| 49 | 23 | 67.6 | 38 | 1 | US-08-232-849-1 | Sequence 1, Appli |
| 50 | 23 | 67.6 | 38 | 2 | US-08-625-586-1 | Sequence 1, Appli |
| 51 | 23 | 67.6 | 38 | 3 | US-09-128-401-1 | Sequence 1, Appli |
| 52 | 23 | 67.6 | 38 | 5 | PCT-US95-15800-29 | Sequence 29, Appl |
| 53 | 22 | 64.7 | 33 | 4 | US-09-447-800-3 | Sequence 3, Appli |
| 54 | 22 | 64.7 | 33 | 4 | US-09-447-800-6 | Sequence 6, Appli |
| 55 | 22 | 64.7 | 33 | 4 | US-09-447-800-9 | Sequence 9, Appli |
| 56 | 22 | 64.7 | 34 | 3 | US-08-903-497A-1 | Sequence 1, Appli |
| 57 | 22 | 64.7 | 34 | 4 | US-09-635-076-1 | Sequence 1, Appli |
| 58 | 21 | 61.8 | 34 | 3 | US-09-044-536A-26 | Sequence 26, Appl |
| 59 | 21 | 61.8 | 34 | 4 | US-09-449-632-24 | Sequence 24, Appl |
| 60 | 20 | 58.8 | 31 | 1 | US-08-262-495C-3 | Sequence 3, Appli |
| 61 | 20 | 58.8 | 31 | 2 | US-08-691-647C-1 | Sequence 1, Appli |
| 62 | 20 | 58.8 | 31 | 2 | US-08-691-647C-6 | Sequence 6, Appli |
| 63 | 20 | 58.8 | 31 | 3 | US-08-904-760B-1 | Sequence 1, Appli |
| 64 | 20 | 58.8 | 31 | 3 | US-08-904-760B-6 | Sequence 6, Appli |
| 65 | 20 | 58.8 | 31 | 3 | US-08-904-760B-14 | Sequence 14, Appl |
| 66 | 20 | 58.8 | 31 | 3 | US-08-904-760B-32 | Sequence 32, Appl |
| 67 | 20 | 58.8 | 31 | 4 | US-09-406-813-2 | Sequence 2, Appli |
| 68 | 20 | 58.8 | 31 | 4 | US-09-536-785A-1 | Sequence 1, Appli |

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| 69 | 20 | 58.8 | 31 | 4 | US-09-536-785A-6 | Sequence 6, Appli |
| 70 | 20 | 58.8 | 31 | 4 | US-09-536-785A-14 | Sequence 14, Appl |
| 71 | 20 | 58.8 | 31 | 4 | US-09-536-785A-32 | Sequence 32, Appl |
| 72 | 20 | 58.8 | 34 | 3 | US-09-044-536A-25 | Sequence 25, Appl |
| 73 | 19 | 55.9 | 30 | 1 | US-08-262-495C-5 | Sequence 5, Appli |
| 74 | 19 | 55.9 | 34 | 3 | US-08-903-497A-3 | Sequence 3, Appli |
| 75 | 19 | 55.9 | 34 | 4 | US-09-635-076-3 | Sequence 3, Appli |
| 76 | 18 | 52.9 | 34 | 1 | US-07-915-247A-2 | Sequence 2, Appli |
| 77 | 18 | 52.9 | 34 | 1 | US-08-443-863-2 | Sequence 2, Appli |
| 78 | 18 | 52.9 | 34 | 1 | US-08-448-070-2 | Sequence 2, Appli |
| 79 | 18 | 52.9 | 34 | 1 | US-08-488-105-2 | Sequence 2, Appli |
| 80 | 18 | 52.9 | 34 | 1 | US-08-488-105-8 | Sequence 8, Appli |
| 81 | 18 | 52.9 | 34 | 1 | US-08-449-500-2 | Sequence 2, Appli |
| 82 | 18 | 52.9 | 34 | 1 | US-08-449-317A-2 | Sequence 2, Appli |
| 83 | 18 | 52.9 | 34 | 2 | US-08-477-022-2 | Sequence 2, Appli |
| 84 | 18 | 52.9 | 34 | 2 | US-08-449-447-2 | Sequence 2, Appli |
| 85 | 18 | 52.9 | 34 | 2 | US-08-184-328-2 | Sequence 2, Appli |
| 86 | 18 | 52.9 | 34 | 2 | US-08-521-097-2 | Sequence 2, Appli |
| 87 | 18 | 52.9 | 34 | 3 | US-09-044-536A-18 | Sequence 18, Appl |
| 88 | 18 | 52.9 | 34 | 3 | US-09-044-536A-19 | Sequence 19, Appl |
| 89 | 17 | 50.0 | 28 | 4 | US-09-448-867-8 | Sequence 8, Appli |
| 90 | 17 | 50.0 | 28 | 4 | US-09-448-867-10 | Sequence 10, Appl |
| 91 | 17 | 50.0 | 28 | 4 | US-09-448-867-12 | Sequence 12, Appl |
| 92 | 17 | 50.0 | 34 | 1 | US-08-488-105-1 | Sequence 1, Appli |
| 93 | 17 | 50.0 | 34 | 1 | US-08-488-105-13 | Sequence 13, Appl |
| 94 | 17 | 50.0 | 34 | 1 | US-08-488-105-14 | Sequence 14, Appl |
| 95 | 17 | 50.0 | 34 | 3 | US-09-044-536A-16 | Sequence 16, Appl |
| 96 | 17 | 50.0 | 34 | 3 | US-09-044-536A-17 | Sequence 17, Appl |
| 97 | 16 | 47.1 | 34 | 1 | US-07-915-247A-3 | Sequence 3, Appli |
| 98 | 16 | 47.1 | 34 | 1 | US-08-443-863-3 | Sequence 3, Appli |
| 99 | 16 | 47.1 | 34 | 1 | US-08-448-070-3 | Sequence 3, Appli |
| 100 | 16 | 47.1 | 34 | 1 | US-08-449-500-3 | Sequence 3, Appli |
| 101 | 16 | 47.1 | 34 | 1 | US-08-449-317A-3 | Sequence 3, Appli |
| 102 | 16 | 47.1 | 34 | 2 | US-08-477-022-3 | Sequence 3, Appli |
| 103 | 16 | 47.1 | 34 | 2 | US-08-449-447-3 | Sequence 3, Appli |
| 104 | 16 | 47.1 | 34 | 2 | US-08-184-328-3 | Sequence 3, Appli |
| 105 | 16 | 47.1 | 34 | 2 | US-08-521-097-3 | Sequence 3, Appli |
| 106 | 15 | 44.1 | 28 | 4 | US-09-406-813-3 | Sequence 3, Appli |
| 107 | 15 | 44.1 | 29 | 4 | US-09-406-813-4 | Sequence 4, Appli |
| 108 | 15 | 44.1 | 30 | 1 | US-08-262-495C-6 | Sequence 6, Appli |
| 109 | 15 | 44.1 | 30 | 3 | US-08-904-760B-7 | Sequence 7, Appli |
| 110 | 15 | 44.1 | 30 | 4 | US-09-536-785A-7 | Sequence 7, Appli |
| 111 | 15 | 44.1 | 31 | 1 | US-08-262-495C-4 | Sequence 4, Appli |
| 112 | 15 | 44.1 | 31 | 2 | US-08-691-647C-2 | Sequence 2, Appli |
| 113 | 15 | 44.1 | 31 | 2 | US-08-691-647C-3 | Sequence 3, Appli |
| 114 | 15 | 44.1 | 31 | 2 | US-08-691-647C-4 | Sequence 4, Appli |
| 115 | 15 | 44.1 | 31 | 3 | US-08-904-760B-2 | Sequence 2, Appli |
| 116 | 15 | 44.1 | 31 | 3 | US-08-904-760B-3 | Sequence 3, Appli |
| 117 | 15 | 44.1 | 31 | 3 | US-08-904-760B-4 | Sequence 4, Appli |
| 118 | 15 | 44.1 | 31 | 3 | US-08-904-760B-5 | Sequence 5, Appli |
| 119 | 15 | 44.1 | 31 | 3 | US-08-904-760B-8 | Sequence 8, Appli |
| 120 | 15 | 44.1 | 31 | 3 | US-08-904-760B-11 | Sequence 11, Appl |
| 121 | 15 | 44.1 | 31 | 3 | US-08-904-760B-12 | Sequence 12, Appl |
| 122 | 15 | 44.1 | 31 | 3 | US-08-904-760B-15 | Sequence 15, Appl |
| 123 | 15 | 44.1 | 31 | 3 | US-08-904-760B-16 | Sequence 16, Appl |
| 124 | 15 | 44.1 | 31 | 3 | US-08-904-760B-17 | Sequence 17, Appl |
| 125 | 15 | 44.1 | 31 | 4 | US-09-536-785A-2 | Sequence 2, Appli |

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| 126 | 15 | 44.1 | 31 | 4 | US-09-536-785A-3 | Sequence 3, Appli |
| 127 | 15 | 44.1 | 31 | 4 | US-09-536-785A-4 | Sequence 4, Appli |
| 128 | 15 | 44.1 | 31 | 4 | US-09-536-785A-5 | Sequence 5, Appli |
| 129 | 15 | 44.1 | 31 | 4 | US-09-536-785A-8 | Sequence 8, Appli |
| 130 | 15 | 44.1 | 31 | 4 | US-09-536-785A-11 | Sequence 11, Appl |
| 131 | 15 | 44.1 | 31 | 4 | US-09-536-785A-12 | Sequence 12, Appl |
| 132 | 15 | 44.1 | 31 | 4 | US-09-536-785A-15 | Sequence 15, Appl |
| 133 | 15 | 44.1 | 31 | 4 | US-09-536-785A-16 | Sequence 16, Appl |
| 134 | 15 | 44.1 | 31 | 4 | US-09-536-785A-17 | Sequence 17, Appl |
| 135 | 15 | 44.1 | 34 | 1 | US-08-262-495C-2 | Sequence 2, Appli |
| 136 | 15 | 44.1 | 34 | 1 | US-08-488-105-4 | Sequence 4, Appli |
| 137 | 15 | 44.1 | 34 | 1 | US-08-488-105-6 | Sequence 6, Appli |
| 138 | 15 | 44.1 | 34 | 1 | US-08-488-105-10 | Sequence 10, Appl |
| 139 | 15 | 44.1 | 34 | 1 | US-08-488-105-11 | Sequence 11, Appl |
| 140 | 15 | 44.1 | 34 | 1 | US-08-488-105-16 | Sequence 16, Appl |
| 141 | 15 | 44.1 | 34 | 1 | US-08-488-105-18 | Sequence 18, Appl |
| 142 | 15 | 44.1 | 34 | 1 | US-08-449-500-79 | Sequence 79, Appl |
| 143 | 15 | 44.1 | 34 | 1 | US-08-449-317A-79 | Sequence 79, Appl |
| 144 | 15 | 44.1 | 34 | 2 | US-08-142-551B-3 | Sequence 3, Appli |
| 145 | 15 | 44.1 | 34 | 2 | US-08-477-022-79 | Sequence 79, Appl |
| 146 | 15 | 44.1 | 34 | 2 | US-08-449-447-79 | Sequence 79, Appl |
| 147 | 15 | 44.1 | 34 | 2 | US-08-184-328-79 | Sequence 79, Appl |
| 148 | 15 | 44.1 | 34 | 2 | US-08-521-097-79 | Sequence 79, Appl |
| 149 | 15 | 44.1 | 34 | 3 | US-09-044-536A-27 | Sequence 27, Appl |
| 150 | 15 | 44.1 | 34 | 3 | US-08-904-760B-9 | Sequence 9, Appli |
| 151 | 15 | 44.1 | 34 | 3 | US-08-904-760B-10 | Sequence 10, Appl |
| 152 | 15 | 44.1 | 34 | 3 | US-08-903-497A-4 | Sequence 4, Appli |
| 153 | 15 | 44.1 | 34 | 4 | US-09-635-076-4 | Sequence 4, Appli |
| 154 | 15 | 44.1 | 34 | 4 | US-09-536-785A-9 | Sequence 9, Appli |
| 155 | 15 | 44.1 | 34 | 4 | US-09-536-785A-10 | Sequence 10, Appl |
| 156 | 15 | 44.1 | 35 | 2 | US-08-142-551B-4 | Sequence 4, Appli |
| 157 | 15 | 44.1 | 35 | 2 | US-08-142-551B-5 | Sequence 5, Appli |
| 158 | 15 | 44.1 | 35 | 2 | US-08-142-551B-7 | Sequence 7, Appli |
| 159 | 15 | 44.1 | 35 | 2 | US-08-142-551B-11 | Sequence 11, Appl |
| 160 | 15 | 44.1 | 35 | 2 | US-08-142-551B-12 | Sequence 12, Appl |
| 161 | 15 | 44.1 | 35 | 2 | US-08-142-551B-13 | Sequence 13, Appl |
| 162 | 15 | 44.1 | 35 | 2 | US-08-142-551B-14 | Sequence 14, Appl |
| 163 | 15 | 44.1 | 35 | 2 | US-08-142-551B-15 | Sequence 15, Appl |
| 164 | 15 | 44.1 | 35 | 2 | US-08-142-551B-16 | Sequence 16, Appl |
| 165 | 15 | 44.1 | 35 | 2 | US-08-142-551B-17 | Sequence 17, Appl |
| 166 | 15 | 44.1 | 35 | 2 | US-08-142-551B-18 | Sequence 18, Appl |
| 167 | 15 | 44.1 | 35 | 2 | US-08-142-551B-19 | Sequence 19, Appl |
| 168 | 15 | 44.1 | 35 | 2 | US-08-142-551B-20 | Sequence 20, Appl |
| 169 | 15 | 44.1 | 35 | 2 | US-08-142-551B-21 | Sequence 21, Appl |
| 170 | 15 | 44.1 | 35 | 2 | US-08-142-551B-22 | Sequence 22, Appl |
| 171 | 15 | 44.1 | 35 | 2 | US-08-142-551B-23 | Sequence 23, Appl |
| 172 | 15 | 44.1 | 35 | 2 | US-08-142-551B-24 | Sequence 24, Appl |
| 173 | 15 | 44.1 | 35 | 2 | US-08-142-551B-25 | Sequence 25, Appl |
| 174 | 15 | 44.1 | 35 | 2 | US-08-142-551B-26 | Sequence 26, Appl |
| 175 | 15 | 44.1 | 35 | 2 | US-08-142-551B-27 | Sequence 27, Appl |
| 176 | 15 | 44.1 | 35 | 2 | US-08-142-551B-28 | Sequence 28, Appl |
| 177 | 15 | 44.1 | 35 | 2 | US-08-142-551B-29 | Sequence 29, Appl |
| 178 | 15 | 44.1 | 35 | 2 | US-08-142-551B-30 | Sequence 30, Appl |
| 179 | 15 | 44.1 | 35 | 2 | US-08-142-551B-31 | Sequence 31, Appl |
| 180 | 15 | 44.1 | 35 | 2 | US-08-142-551B-32 | Sequence 32, Appl |
| 181 | 15 | 44.1 | 35 | 2 | US-08-142-551B-33 | Sequence 33, Appl |
| 182 | 15 | 44.1 | 35 | 2 | US-08-142-551B-34 | Sequence 34, Appl |

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| 183 | 15 | 44.1 | 35 | 2 | US-08-142-551B-35 | Sequence 35, Appl |
| 184 | 15 | 44.1 | 35 | 2 | US-08-142-551B-36 | Sequence 36, Appl |
| 185 | 15 | 44.1 | 35 | 2 | US-08-142-551B-37 | Sequence 37, Appl |
| 186 | 15 | 44.1 | 35 | 2 | US-08-142-551B-38 | Sequence 38, Appl |
| 187 | 15 | 44.1 | 35 | 2 | US-08-142-551B-39 | Sequence 39, Appl |
| 188 | 15 | 44.1 | 35 | 2 | US-08-142-551B-40 | Sequence 40, Appl |
| 189 | 15 | 44.1 | 35 | 2 | US-08-142-551B-41 | Sequence 41, Appl |
| 190 | 15 | 44.1 | 35 | 2 | US-08-142-551B-42 | Sequence 42, Appl |
| 191 | 15 | 44.1 | 35 | 2 | US-08-142-551B-43 | Sequence 43, Appl |
| 192 | 15 | 44.1 | 35 | 2 | US-08-142-551B-44 | Sequence 44, Appl |
| 193 | 15 | 44.1 | 35 | 2 | US-08-142-551B-45 | Sequence 45, Appl |
| 194 | 15 | 44.1 | 35 | 2 | US-08-142-551B-46 | Sequence 46, Appl |
| 195 | 15 | 44.1 | 35 | 2 | US-08-142-551B-47 | Sequence 47, Appl |
| 196 | 15 | 44.1 | 35 | 2 | US-08-142-551B-48 | Sequence 48, Appl |
| 197 | 15 | 44.1 | 35 | 2 | US-08-142-551B-49 | Sequence 49, Appl |
| 198 | 15 | 44.1 | 35 | 2 | US-08-142-551B-50 | Sequence 50, Appl |
| 199 | 15 | 44.1 | 35 | 2 | US-08-142-551B-51 | Sequence 51, Appl |
| 200 | 15 | 44.1 | 35 | 2 | US-08-142-551B-52 | Sequence 52, Appl |
| 201 | 15 | 44.1 | 35 | 2 | US-08-142-551B-53 | Sequence 53, Appl |
| 202 | 15 | 44.1 | 35 | 2 | US-08-142-551B-54 | Sequence 54, Appl |
| 203 | 15 | 44.1 | 35 | 2 | US-08-142-551B-55 | Sequence 55, Appl |
| 204 | 15 | 44.1 | 35 | 2 | US-08-142-551B-56 | Sequence 56, Appl |
| 205 | 15 | 44.1 | 35 | 2 | US-08-142-551B-57 | Sequence 57, Appl |
| 206 | 15 | 44.1 | 35 | 2 | US-08-142-551B-58 | Sequence 58, Appl |
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| 208 | 15 | 44.1 | 35 | 2 | US-08-142-551B-60 | Sequence 60, Appl |
| 209 | 15 | 44.1 | 35 | 2 | US-08-142-551B-61 | Sequence 61, Appl |
| 210 | 15 | 44.1 | 35 | 2 | US-08-142-551B-62 | Sequence 62, Appl |
| 211 | 15 | 44.1 | 35 | 2 | US-08-142-551B-63 | Sequence 63, Appl |
| 212 | 15 | 44.1 | 35 | 2 | US-08-142-551B-64 | Sequence 64, Appl |
| 213 | 15 | 44.1 | 35 | 2 | US-08-142-551B-65 | Sequence 65, Appl |
| 214 | 15 | 44.1 | 35 | 2 | US-08-142-551B-66 | Sequence 66, Appl |
| 215 | 15 | 44.1 | 35 | 2 | US-08-142-551B-67 | Sequence 67, Appl |
| 216 | 15 | 44.1 | 35 | 2 | US-08-142-551B-68 | Sequence 68, Appl |
| 217 | 15 | 44.1 | 35 | 2 | US-08-142-551B-70 | Sequence 70, Appl |
| 218 | 15 | 44.1 | 35 | 2 | US-08-142-551B-73 | Sequence 73, Appl |
| 219 | 15 | 44.1 | 35 | 2 | US-08-142-551B-80 | Sequence 80, Appl |
| 220 | 15 | 44.1 | 35 | 2 | US-08-142-551B-90 | Sequence 90, Appl |
| 221 | 15 | 44.1 | 35 | 2 | US-08-142-551B-94 | Sequence 94, Appl |
| 222 | 14 | 41.2 | 31 | 3 | US-08-904-760B-21 | Sequence 21, Appl |
| 223 | 14 | 41.2 | 31 | 4 | US-09-536-785A-21 | Sequence 21, Appl |
| 224 | 14 | 41.2 | 34 | 3 | US-09-044-536A-29 | Sequence 29, Appl |
| 225 | 14 | 41.2 | 35 | 2 | US-08-142-551B-69 | Sequence 69, Appl |
| 226 | 14 | 41.2 | 35 | 2 | US-08-142-551B-71 | Sequence 71, Appl |
| 227 | 14 | 41.2 | 35 | 2 | US-08-142-551B-115 | Sequence 115, App |
| 228 | 14 | 41.2 | 35 | 2 | US-08-142-551B-116 | Sequence 116, App |
| 229 | 14 | 41.2 | 35 | 2 | US-08-142-551B-117 | Sequence 117, App |
| 230 | 14 | 41.2 | 35 | 2 | US-08-142-551B-118 | Sequence 118, App |
| 231 | 13 | 38.2 | 34 | 1 | US-07-773-098-5 | Sequence 5, Appli |
| 232 | 13 | 38.2 | 34 | 1 | US-07-773-098-6 | Sequence 6, Appli |
| 233 | 13 | 38.2 | 34 | 3 | US-09-044-536A-28 | Sequence 28, Appl |
| 234 | 13 | 38.2 | 35 | 2 | US-08-142-551B-72 | Sequence 72, Appl |
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| 236 | 13 | 38.2 | 35 | 2 | US-08-142-551B-75 | Sequence 75, Appl |
| 237 | 13 | 38.2 | 35 | 2 | US-08-142-551B-111 | Sequence 111, App |
| 238 | 13 | 38.2 | 35 | 2 | US-08-142-551B-112 | Sequence 112, App |
| 239 | 13 | 38.2 | 35 | 2 | US-08-142-551B-113 | Sequence 113, App |

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| 240 | 13 | 38.2 | 35 | 2 | US-08-142-551B-114 | Sequence 114, App |
| 241 | 12 | 35.3 | 34 | 1 | US-08-488-105-3 | Sequence 3, Appli |
| 242 | 12 | 35.3 | 34 | 1 | US-08-488-105-9 | Sequence 9, Appli |
| 243 | 12 | 35.3 | 34 | 1 | US-08-488-105-15 | Sequence 15, Appl |
| 244 | 12 | 35.3 | 34 | 3 | US-08-903-497A-5 | Sequence 5, Appli |
| 245 | 12 | 35.3 | 34 | 4 | US-09-635-076-5 | Sequence 5, Appli |
| 246 | 12 | 35.3 | 35 | 2 | US-08-142-551B-76 | Sequence 76, Appl |
| 247 | 12 | 35.3 | 35 | 2 | US-08-142-551B-77 | Sequence 77, Appl |
| 248 | 12 | 35.3 | 35 | 2 | US-08-142-551B-78 | Sequence 78, Appl |
| 249 | 12 | 35.3 | 35 | 2 | US-08-142-551B-107 | Sequence 107, App |
| 250 | 12 | 35.3 | 35 | 2 | US-08-142-551B-108 | Sequence 108, App |
| 251 | 12 | 35.3 | 35 | 2 | US-08-142-551B-109 | Sequence 109, App |
| 252 | 12 | 35.3 | 35 | 2 | US-08-142-551B-110 | Sequence 110, App |
| 253 | 11 | 32.4 | 34 | 1 | US-08-488-105-5 | Sequence 5, Appli |
| 254 | 11 | 32.4 | 34 | 1 | US-08-488-105-12 | Sequence 12, Appl |
| 255 | 11 | 32.4 | 34 | 1 | US-08-488-105-17 | Sequence 17, Appl |
| 256 | 11 | 32.4 | 34 | 1 | US-08-449-500-61 | Sequence 61, Appl |
| 257 | 11 | 32.4 | 34 | 1 | US-08-449-317A-61 | Sequence 61, Appl |
| 258 | 11 | 32.4 | 34 | 2 | US-08-477-022-61 | Sequence 61, Appl |
| 259 | 11 | 32.4 | 34 | 2 | US-08-449-447-61 | Sequence 61, Appl |
| 260 | 11 | 32.4 | 34 | 2 | US-08-184-328-61 | Sequence 61, Appl |
| 261 | 11 | 32.4 | 34 | 2 | US-08-521-097-61 | Sequence 61, Appl |
| 262 | 11 | 32.4 | 34 | 4 | US-09-449-632-22 | Sequence 22, Appl |
| 263 | 11 | 32.4 | 35 | 2 | US-08-142-551B-79 | Sequence 79, Appl |
| 264 | 11 | 32.4 | 35 | 2 | US-08-142-551B-81 | Sequence 81, Appl |
| 265 | 11 | 32.4 | 35 | 2 | US-08-142-551B-104 | Sequence 104, App |
| 266 | 11 | 32.4 | 35 | 2 | US-08-142-551B-105 | Sequence 105, App |
| 267 | 11 | 32.4 | 35 | 2 | US-08-142-551B-106 | Sequence 106, App |
| 268 | 11 | 32.4 | 35 | 2 | US-08-142-551B-121 | Sequence 121, App |
| 269 | 11 | 32.4 | 35 | 2 | US-08-142-551B-122 | Sequence 122, App |
| 270 | 11 | 32.4 | 35 | 2 | US-08-142-551B-123 | Sequence 123, App |
| 271 | 10 | 29.4 | 28 | 4 | US-09-406-813-6 | Sequence 6, Appli |
| 272 | 10 | 29.4 | 28 | 4 | US-09-448-867-6 | Sequence 6, Appli |
| 273 | 10 | 29.4 | 30 | 3 | US-08-904-760B-33 | Sequence 33, Appl |
| 274 | 10 | 29.4 | 30 | 3 | US-08-904-760B-34 | Sequence 34, Appl |
| 275 | 10 | 29.4 | 30 | 3 | US-08-904-760B-35 | Sequence 35, Appl |
| 276 | 10 | 29.4 | 30 | 4 | US-09-536-785A-33 | Sequence 33, Appl |
| 277 | 10 | 29.4 | 30 | 4 | US-09-536-785A-34 | Sequence 34, Appl |
| 278 | 10 | 29.4 | 30 | 4 | US-09-536-785A-35 | Sequence 35, Appl |
| 279 | 10 | 29.4 | 31 | 3 | US-08-904-760B-18 | Sequence 18, Appl |
| 280 | 10 | 29.4 | 31 | 3 | US-08-904-760B-19 | Sequence 19, Appl |
| 281 | 10 | 29.4 | 31 | 3 | US-08-904-760B-20 | Sequence 20, Appl |
| 282 | 10 | 29.4 | 31 | 4 | US-09-406-813-5 | Sequence 5, Appli |
| 283 | 10 | 29.4 | 31 | 4 | US-09-536-785A-18 | Sequence 18, Appl |
| 284 | 10 | 29.4 | 31 | 4 | US-09-536-785A-19 | Sequence 19, Appl |
| 285 | 10 | 29.4 | 31 | 4 | US-09-536-785A-20 | Sequence 20, Appl |
| 286 | 10 | 29.4 | 34 | 3 | US-09-044-536A-20 | Sequence 20, Appl |
| 287 | 10 | 29.4 | 34 | 3 | US-09-044-536A-21 | Sequence 21, Appl |
| 288 | 10 | 29.4 | 34 | 3 | US-09-044-536A-22 | Sequence 22, Appl |
| 289 | 10 | 29.4 | 34 | 3 | US-09-044-536A-24 | Sequence 24, Appl |
| 290 | 10 | 29.4 | 34 | 3 | US-08-903-497A-6 | Sequence 6, Appli |
| 291 | 10 | 29.4 | 34 | 3 | US-08-903-497A-7 | Sequence 7, Appli |
| 292 | 10 | 29.4 | 34 | 4 | US-08-952-980B-9 | Sequence 9, Appli |
| 293 | 10 | 29.4 | 34 | 4 | US-09-635-076-6 | Sequence 6, Appli |
| 294 | 10 | 29.4 | 34 | 4 | US-09-635-076-7 | Sequence 7, Appli |
| 295 | 10 | 29.4 | 35 | 2 | US-08-142-551B-82 | Sequence 82, Appl |
| 296 | 10 | 29.4 | 35 | 2 | US-08-142-551B-83 | Sequence 83, Appl |

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| 297 | 10 | 29.4 | 35 | 2 | US-08-142-551B-84 | Sequence 84, Appl |
| 298 | 10 | 29.4 | 35 | 2 | US-08-142-551B-101 | Sequence 101, App |
| 299 | 10 | 29.4 | 35 | 2 | US-08-142-551B-102 | Sequence 102, App |
| 300 | 10 | 29.4 | 35 | 2 | US-08-142-551B-103 | Sequence 103, App |
| 301 | 10 | 29.4 | 35 | 2 | US-08-142-551B-120 | Sequence 120, App |
| 302 | 9 | 26.5 | 28 | 4 | US-09-448-867-1 | Sequence 1, Appli |
| 303 | 9 | 26.5 | 28 | 4 | US-09-448-867-2 | Sequence 2, Appli |
| 304 | 9 | 26.5 | 28 | 4 | US-09-448-867-4 | Sequence 4, Appli |
| 305 | 9 | 26.5 | 34 | 3 | US-09-044-536A-2 | Sequence 2, Appli |
| 306 | 9 | 26.5 | 34 | 3 | US-09-044-536A-23 | Sequence 23, Appl |
| 307 | 9 | 26.5 | 35 | 2 | US-08-142-551B-85 | Sequence 85, Appl |
| 308 | 9 | 26.5 | 35 | 2 | US-08-142-551B-86 | Sequence 86, Appl |
| 309 | 9 | 26.5 | 35 | 2 | US-08-142-551B-87 | Sequence 87, Appl |
| 310 | 9 | 26.5 | 35 | 2 | US-08-142-551B-98 | Sequence 98, Appl |
| 311 | 9 | 26.5 | 35 | 2 | US-08-142-551B-99 | Sequence 99, Appl |
| 312 | 9 | 26.5 | 35 | 2 | US-08-142-551B-100 | Sequence 100, App |
| 313 | 9 | 26.5 | 35 | 3 | US-09-044-536A-30 | Sequence 30, Appl |
| 314 | 9 | 26.5 | 36 | 3 | US-09-044-536A-31 | Sequence 31, Appl |
| 315 | 9 | 26.5 | 37 | 3 | US-09-044-536A-32 | Sequence 32, Appl |
| 316 | 9 | 26.5 | 38 | 3 | US-09-044-536A-33 | Sequence 33, Appl |
| 317 | 9 | 26.5 | 39 | 3 | US-09-044-536A-34 | Sequence 34, Appl |
| 318 | 9 | 26.5 | 40 | 3 | US-09-044-536A-35 | Sequence 35, Appl |
| 319 | 8 | 23.5 | 31 | 3 | US-08-904-760B-13 | Sequence 13, Appl |
| 320 | 8 | 23.5 | 31 | 4 | US-09-228-990-50 | Sequence 50, Appl |
| 321 | 8 | 23.5 | 31 | 4 | US-09-228-990-51 | Sequence 51, Appl |
| 322 | 8 | 23.5 | 31 | 4 | US-09-228-990-66 | Sequence 66, Appl |
| 323 | 8 | 23.5 | 31 | 4 | US-09-228-990-67 | Sequence 67, Appl |
| 324 | 8 | 23.5 | 31 | 4 | US-09-228-990-76 | Sequence 76, Appl |
| 325 | 8 | 23.5 | 31 | 4 | US-09-536-785A-13 | Sequence 13, Appl |
| 326 | 8 | 23.5 | 34 | 1 | US-07-773-098-3 | Sequence 3, Appli |
| 327 | 8 | 23.5 | 34 | 1 | US-07-773-098-4 | Sequence 4, Appli |
| 328 | 8 | 23.5 | 34 | 1 | US-08-049-402-2 | Sequence 2, Appli |
| 329 | 8 | 23.5 | 34 | 1 | US-08-526-987-2 | Sequence 2, Appli |
| 330 | 8 | 23.5 | 35 | 2 | US-08-142-551B-88 | Sequence 88, Appl |
| 331 | 8 | 23.5 | 35 | 2 | US-08-142-551B-89 | Sequence 89, Appl |
| 332 | 8 | 23.5 | 35 | 2 | US-08-142-551B-95 | Sequence 95, Appl |
| 333 | 8 | 23.5 | 35 | 2 | US-08-142-551B-96 | Sequence 96, Appl |
| 334 | 8 | 23.5 | 35 | 2 | US-08-142-551B-97 | Sequence 97, Appl |
| 335 | 7 | 20.6 | 28 | 4 | US-09-228-990-65 | Sequence 65, Appl |
| 336 | 7 | 20.6 | 28 | 4 | US-09-228-990-78 | Sequence 78, Appl |
| 337 | 7 | 20.6 | 28 | 4 | US-09-228-990-79 | Sequence 79, Appl |
| 338 | 7 | 20.6 | 28 | 4 | US-09-442-989-22 | Sequence 22, Appl |
| 339 | 7 | 20.6 | 28 | 4 | US-09-442-989-24 | Sequence 24, Appl |
| 340 | 7 | 20.6 | 28 | 4 | US-09-442-989-25 | Sequence 25, Appl |
| 341 | 7 | 20.6 | 29 | 4 | US-09-406-813-8 | Sequence 8, Appli |
| 342 | 7 | 20.6 | 31 | 4 | US-09-406-813-9 | Sequence 9, Appli |
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| 344 | 7 | 20.6 | 32 | 1 | US-08-305-799A-2 | Sequence 2, Appli |
| 345 | 7 | 20.6 | 34 | 1 | US-08-033-099-2 | Sequence 2, Appli |
| 346 | 7 | 20.6 | 34 | 1 | US-08-468-275-7 | Sequence 7, Appli |
| 347 | 7 | 20.6 | 34 | 1 | US-08-468-275-8 | Sequence 8, Appli |
| 348 | 7 | 20.6 | 34 | 1 | US-08-449-500-37 | Sequence 37, Appl |
| 349 | 7 | 20.6 | 34 | 1 | US-08-449-317A-37 | Sequence 37, Appl |
| 350 | 7 | 20.6 | 34 | 2 | US-08-477-022-37 | Sequence 37, Appl |
| 351 | 7 | 20.6 | 34 | 2 | US-08-449-447-37 | Sequence 37, Appl |
| 352 | 7 | 20.6 | 34 | 2 | US-08-184-328-37 | Sequence 37, Appl |
| 353 | 7 | 20.6 | 34 | 2 | US-08-521-097-37 | Sequence 37, Appl |

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| 355 | 7 | 20.6 | 34 | 4 | US-09-007-466-8 | Sequence 8, Appli |
| 356 | 7 | 20.6 | 34 | 4 | US-09-228-990-46 | Sequence 46, Appl |
| 357 | 7 | 20.6 | 34 | 4 | US-09-228-990-75 | Sequence 75, Appl |
| 358 | 7 | 20.6 | 34 | 4 | US-09-442-989-18 | Sequence 18, Appl |
| 359 | 7 | 20.6 | 34 | 4 | US-09-442-989-19 | Sequence 19, Appl |
| 360 | 7 | 20.6 | 34 | 4 | US-09-442-989-46 | Sequence 46, Appl |
| 361 | 7 | 20.6 | 35 | 2 | US-08-142-551B-10 | Sequence 10, Appl |
| 362 | 7 | 20.6 | 35 | 2 | US-08-142-551B-91 | Sequence 91, Appl |
| 363 | 7 | 20.6 | 35 | 2 | US-08-142-551B-92 | Sequence 92, Appl |
| 364 | 7 | 20.6 | 35 | 2 | US-08-142-551B-93 | Sequence 93, Appl |
| 365 | 7 | 20.6 | 35 | 2 | US-08-142-551B-124 | Sequence 124, App |
| 366 | 7 | 20.6 | 35 | 4 | US-08-952-980B-7 | Sequence 7, Appli |
| 367 | 7 | 20.6 | 35 | 4 | US-08-952-980B-8 | Sequence 8, Appli |
| 368 | 6 | 17.6 | 28 | 4 | US-09-228-990-54 | Sequence 54, Appl |
| 369 | 6 | 17.6 | 28 | 4 | US-09-228-990-62 | Sequence 62, Appl |
| 370 | 6 | 17.6 | 29 | 4 | US-09-228-990-53 | Sequence 53, Appl |
| 371 | 6 | 17.6 | 29 | 4 | US-09-228-990-63 | Sequence 63, Appl |
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| 373 | 6 | 17.6 | 30 | 4 | US-09-228-990-64 | Sequence 64, Appl |
| 374 | 6 | 17.6 | 30 | 4 | US-09-536-785A-23 | Sequence 23, Appl |
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| 379 | 6 | 17.6 | 31 | 4 | US-09-228-990-5 | Sequence 5, Appli |
| 380 | 6 | 17.6 | 31 | 4 | US-09-228-990-6 | Sequence 6, Appli |
| 381 | 6 | 17.6 | 31 | 4 | US-09-228-990-7 | Sequence 7, Appli |
| 382 | 6 | 17.6 | 31 | 4 | US-09-228-990-8 | Sequence 8, Appli |
| 383 | 6 | 17.6 | 31 | 4 | US-09-228-990-9 | Sequence 9, Appli |
| 384 | 6 | 17.6 | 31 | 4 | US-09-228-990-10 | Sequence 10, Appl |
| 385 | 6 | 17.6 | 31 | 4 | US-09-228-990-11 | Sequence 11, Appl |
| 386 | 6 | 17.6 | 31 | 4 | US-09-228-990-12 | Sequence 12, Appl |
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| 389 | 6 | 17.6 | 31 | 4 | US-09-228-990-15 | Sequence 15, Appl |
| 390 | 6 | 17.6 | 31 | 4 | US-09-228-990-16 | Sequence 16, Appl |
| 391 | 6 | 17.6 | 31 | 4 | US-09-228-990-17 | Sequence 17, Appl |
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| 393 | 6 | 17.6 | 31 | 4 | US-09-228-990-19 | Sequence 19, Appl |
| 394 | 6 | 17.6 | 31 | 4 | US-09-228-990-20 | Sequence 20, Appl |
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| 396 | 6 | 17.6 | 31 | 4 | US-09-228-990-22 | Sequence 22, Appl |
| 397 | 6 | 17.6 | 31 | 4 | US-09-228-990-23 | Sequence 23, Appl |
| 398 | 6 | 17.6 | 31 | 4 | US-09-228-990-24 | Sequence 24, Appl |
| 399 | 6 | 17.6 | 31 | 4 | US-09-228-990-25 | Sequence 25, Appl |
| 400 | 6 | 17.6 | 31 | 4 | US-09-228-990-26 | Sequence 26, Appl |
| 401 | 6 | 17.6 | 31 | 4 | US-09-228-990-27 | Sequence 27, Appl |
| 402 | 6 | 17.6 | 31 | 4 | US-09-228-990-28 | Sequence 28, Appl |
| 403 | 6 | 17.6 | 31 | 4 | US-09-228-990-29 | Sequence 29, Appl |
| 404 | 6 | 17.6 | 31 | 4 | US-09-228-990-30 | Sequence 30, Appl |
| 405 | 6 | 17.6 | 31 | 4 | US-09-228-990-31 | Sequence 31, Appl |
| 406 | 6 | 17.6 | 31 | 4 | US-09-228-990-32 | Sequence 32, Appl |
| 407 | 6 | 17.6 | 31 | 4 | US-09-228-990-33 | Sequence 33, Appl |
| 408 | 6 | 17.6 | 31 | 4 | US-09-228-990-34 | Sequence 34, Appl |
| 409 | 6 | 17.6 | 31 | 4 | US-09-228-990-35 | Sequence 35, Appl |
| 410 | 6 | 17.6 | 31 | 4 | US-09-228-990-36 | Sequence 36, Appl |

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| 412 | 6 | 17.6 | 31 | 4 | US-09-228-990-38 | Sequence 38, Appl |
| 413 | 6 | 17.6 | 31 | 4 | US-09-228-990-39 | Sequence 39, Appl |
| 414 | 6 | 17.6 | 31 | 4 | US-09-228-990-40 | Sequence 40, Appl |
| 415 | 6 | 17.6 | 31 | 4 | US-09-228-990-41 | Sequence 41, Appl |
| 416 | 6 | 17.6 | 31 | 4 | US-09-228-990-42 | Sequence 42, Appl |
| 417 | 6 | 17.6 | 31 | 4 | US-09-228-990-43 | Sequence 43, Appl |
| 418 | 6 | 17.6 | 31 | 4 | US-09-228-990-44 | Sequence 44, Appl |
| 419 | 6 | 17.6 | 31 | 4 | US-09-228-990-45 | Sequence 45, Appl |
| 420 | 6 | 17.6 | 31 | 4 | US-09-228-990-47 | Sequence 47, Appl |
| 421 | 6 | 17.6 | 31 | 4 | US-09-228-990-48 | Sequence 48, Appl |
| 422 | 6 | 17.6 | 31 | 4 | US-09-228-990-49 | Sequence 49, Appl |
| 423 | 6 | 17.6 | 31 | 4 | US-09-228-990-68 | Sequence 68, Appl |
| 424 | 6 | 17.6 | 31 | 4 | US-09-228-990-69 | Sequence 69, Appl |
| 425 | 6 | 17.6 | 31 | 4 | US-09-228-990-70 | Sequence 70, Appl |
| 426 | 6 | 17.6 | 31 | 4 | US-09-228-990-73 | Sequence 73, Appl |
| 427 | 6 | 17.6 | 31 | 4 | US-09-228-990-74 | Sequence 74, Appl |
| 428 | 6 | 17.6 | 31 | 4 | US-09-228-990-80 | Sequence 80, Appl |
| 429 | 6 | 17.6 | 31 | 4 | US-09-228-990-81 | Sequence 81, Appl |
| 430 | 6 | 17.6 | 31 | 4 | US-09-228-990-82 | Sequence 82, Appl |
| 431 | 6 | 17.6 | 31 | 4 | US-09-228-990-83 | Sequence 83, Appl |
| 432 | 6 | 17.6 | 31 | 4 | US-09-228-990-84 | Sequence 84, Appl |
| 433 | 6 | 17.6 | 31 | 4 | US-09-228-990-85 | Sequence 85, Appl |
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| 435 | 6 | 17.6 | 31 | 4 | US-09-228-990-87 | Sequence 87, Appl |
| 436 | 6 | 17.6 | 31 | 4 | US-09-228-990-88 | Sequence 88, Appl |
| 437 | 6 | 17.6 | 31 | 4 | US-09-536-785A-36 | Sequence 36, Appl |
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| 440 | 6 | 17.6 | 31 | 4 | US-09-442-989-3 | Sequence 3, Appli |
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| 442 | 6 | 17.6 | 31 | 4 | US-09-442-989-5 | Sequence 5, Appli |
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| 444 | 6 | 17.6 | 31 | 4 | US-09-442-989-7 | Sequence 7, Appli |
| 445 | 6 | 17.6 | 31 | 4 | US-09-442-989-8 | Sequence 8, Appli |
| 446 | 6 | 17.6 | 31 | 4 | US-09-442-989-9 | Sequence 9, Appli |
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| 454 | 6 | 17.6 | 31 | 4 | US-09-442-989-17 | Sequence 17, Appl |
| 455 | 6 | 17.6 | 31 | 4 | US-09-442-989-32 | Sequence 32, Appl |
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| 457 | 6 | 17.6 | 33 | 4 | US-09-536-785A-38 | Sequence 38, Appl |
| 458 | 6 | 17.6 | 34 | 1 | US-07-765-373-2 | Sequence 2, Appli |
| 459 | 6 | 17.6 | 34 | 1 | US-08-049-402-1 | Sequence 1, Appli |
| 460 | 6 | 17.6 | 34 | 1 | US-08-526-987-1 | Sequence 1, Appli |
| 461 | 6 | 17.6 | 34 | 4 | US-09-536-785A-24 | Sequence 24, Appl |
| 462 | 6 | 17.6 | 35 | 4 | US-09-536-785A-25 | Sequence 25, Appl |
| 463 | 6 | 17.6 | 36 | 4 | US-09-536-785A-26 | Sequence 26, Appl |
| 464 | 6 | 17.6 | 37 | 4 | US-09-536-785A-27 | Sequence 27, Appl |
| 465 | 5 | 14.7 | 29 | 1 | US-07-778-926-6 | Sequence 6, Appli |
| 466 | 5 | 14.7 | 29 | 1 | US-08-188-582-33 | Sequence 33, Appl |
| 467 | 5 | 14.7 | 29 | 1 | US-08-646-715-33 | Sequence 33, Appl |

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| 481 | 5 | 14.7 | 34 | 1 | US-08-443-863-24 | Sequence 24, Appl |
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| 483 | 5 | 14.7 | 34 | 1 | US-08-448-070-24 | Sequence 24, Appl |
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| 485 | 5 | 14.7 | 34 | 1 | US-08-449-500-24 | Sequence 24, Appl |
| 486 | 5 | 14.7 | 34 | 1 | US-08-449-500-35 | Sequence 35, Appl |
| 487 | 5 | 14.7 | 34 | 1 | US-08-449-500-36 | Sequence 36, Appl |
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| 489 | 5 | 14.7 | 34 | 1 | US-08-449-317A-24 | Sequence 24, Appl |
| 490 | 5 | 14.7 | 34 | 1 | US-08-449-317A-35 | Sequence 35, Appl |
| 491 | 5 | 14.7 | 34 | 1 | US-08-449-317A-36 | Sequence 36, Appl |
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| 495 | 5 | 14.7 | 34 | 2 | US-08-477-022-36 | Sequence 36, Appl |
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| 498 | 5 | 14.7 | 34 | 2 | US-08-449-447-35 | Sequence 35, Appl |
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| 510 | 5 | 14.7 | 37 | 1 | US-07-778-926-8 | Sequence 8, Appli |
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| 517 | 4 | 11.8 | 28 | 2 | US-08-185-949B-76 | Sequence 76, Appl |
| 518 | 4 | 11.8 | 28 | 2 | US-08-620-151-126 | Sequence 126, App |
| 519 | 4 | 11.8 | 28 | 2 | US-08-818-253-22 | Sequence 22, Appl |
| 520 | 4 | 11.8 | 28 | 3 | US-08-641-873-8 | Sequence 8, Appli |
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| 522 | 4 | 11.8 | 28 | 4 | US-08-842-322-16 | Sequence 16, Appl |
| 523 | 4 | 11.8 | 28 | 4 | US-09-316-919-38 | Sequence 38, Appl |
| 524 | 4 | 11.8 | 28 | 4 | US-09-323-867A-153 | Sequence 153, App |

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| 531 | 4 | 11.8 | 30 | 4 | US-09-205-258-821 | Sequence 821, App |
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| 537 | 4 | 11.8 | 31 | 1 | US-08-323-531-62 | Sequence 62, Appl |
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| 540 | 4 | 11.8 | 31 | 1 | US-08-198-094-62 | Sequence 62, Appl |
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| 545 | 4 | 11.8 | 31 | 2 | US-08-288-065A-32 | Sequence 32, Appl |
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| 547 | 4 | 11.8 | 31 | 3 | US-08-107-794A-44 | Sequence 44, Appl |
| 548 | 4 | 11.8 | 31 | 3 | US-08-107-794A-50 | Sequence 50, Appl |
| 549 | 4 | 11.8 | 31 | 3 | US-08-107-794A-62 | Sequence 62, Appl |
| 550 | 4 | 11.8 | 31 | 4 | US-09-205-258-1001 | Sequence 1001, Ap |
| 551 | 4 | 11.8 | 31 | 5 | PCT-US93-00909-3 | Sequence 3, Appli |
| 552 | 4 | 11.8 | 31 | 5 | PCT-US93-07424-44 | Sequence 44, Appl |
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| 554 | 4 | 11.8 | 31 | 5 | PCT-US93-07424-62 | Sequence 62, Appl |
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| 557 | 4 | 11.8 | 31 | 5 | PCT-US95-02087-62 | Sequence 62, Appl |
| 558 | 4 | 11.8 | 31 | 5 | PCT-US95-10245-32 | Sequence 32, Appl |
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| 562 | 4 | 11.8 | 32 | 1 | US-08-190-802A-183 | Sequence 183, App |
| 563 | 4 | 11.8 | 32 | 1 | US-08-190-802A-216 | Sequence 216, App |
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| 565 | 4 | 11.8 | 32 | 3 | US-08-477-346-114 | Sequence 114, App |
| 566 | 4 | 11.8 | 32 | 3 | US-08-477-346-183 | Sequence 183, App |
| 567 | 4 | 11.8 | 32 | 3 | US-08-477-346-216 | Sequence 216, App |
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| 570 | 4 | 11.8 | 32 | 4 | US-08-473-089-183 | Sequence 183, App |
| 571 | 4 | 11.8 | 32 | 4 | US-08-473-089-216 | Sequence 216, App |
| 572 | 4 | 11.8 | 32 | 4 | US-09-149-476-442 | Sequence 442, App |
| 573 | 4 | 11.8 | 32 | 4 | US-08-487-072A-110 | Sequence 110, App |
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| 575 | 4 | 11.8 | 32 | 4 | US-08-487-072A-183 | Sequence 183, App |
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| 588 | 4 | 11.8 | 34 | 4 | US-09-433-043B-7 | Sequence 7, Appli |
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| 590 | 4 | 11.8 | 35 | 4 | US-09-690-454-138 | Sequence 138, App |
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| 598 | 4 | 11.8 | 37 | 3 | US-08-689-489C-45 | Sequence 45, Appl |
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| 601 | 4 | 11.8 | 37 | 3 | US-09-232-802A-45 | Sequence 45, Appl |
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| 604 | 4 | 11.8 | 37 | 4 | US-09-758-318-16 | Sequence 16, Appl |
| 605 | 4 | 11.8 | 37 | 5 | PCT-US95-04718-45 | Sequence 45, Appl |
| 606 | 4 | 11.8 | 37 | 5 | PCT-US95-09338-50 | Sequence 50, Appl |
| 607 | 4 | 11.8 | 37 | 5 | PCT-US95-09339-50 | Sequence 50, Appl |
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| 616 | 3 | 8.8 | 28 | 1 | US-07-690-300B-24 | Sequence 24, Appl |
| 617 | 3 | 8.8 | 28 | 1 | US-07-690-300B-25 | Sequence 25, Appl |
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| 620 | 3 | 8.8 | 28 | 1 | US-07-690-300B-28 | Sequence 28, Appl |
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| 622 | 3 | 8.8 | 28 | 1 | US-07-690-300B-30 | Sequence 30, Appl |
| 623 | 3 | 8.8 | 28 | 1 | US-07-690-300B-31 | Sequence 31, Appl |
| 624 | 3 | 8.8 | 28 | 1 | US-07-690-300B-32 | Sequence 32, Appl |
| 625 | 3 | 8.8 | 28 | 1 | US-07-690-300B-33 | Sequence 33, Appl |
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| 629 | 3 | 8.8 | 28 | 1 | US-07-690-300B-37 | Sequence 37, Appl |
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| 631 | 3 | 8.8 | 28 | 1 | US-07-690-300B-39 | Sequence 39, Appl |
| 632 | 3 | 8.8 | 28 | 1 | US-07-690-300B-40 | Sequence 40, Appl |
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| 634 | 3 | 8.8 | 28 | 1 | US-07-690-300B-42 | Sequence 42, Appl |
| 635 | 3 | 8.8 | 28 | 1 | US-07-690-300B-43 | Sequence 43, Appl |
| 636 | 3 | 8.8 | 28 | 1 | US-07-690-300B-44 | Sequence 44, Appl |
| 637 | 3 | 8.8 | 28 | 1 | US-07-690-300B-45 | Sequence 45, Appl |
| 638 | 3 | 8.8 | 28 | 1 | US-07-690-300B-46 | Sequence 46, Appl |

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| 641 | 3 | 8.8 | 28 | 1 | US-07-690-300B-49 | Sequence 49, Appl |
| 642 | 3 | 8.8 | 28 | 1 | US-07-690-300B-50 | Sequence 50, Appl |
| 643 | 3 | 8.8 | 28 | 1 | US-07-690-300B-51 | Sequence 51, Appl |
| 644 | 3 | 8.8 | 28 | 1 | US-07-690-300B-52 | Sequence 52, Appl |
| 645 | 3 | 8.8 | 28 | 1 | US-07-690-300B-53 | Sequence 53, Appl |
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| 648 | 3 | 8.8 | 28 | 1 | US-07-690-300B-56 | Sequence 56, Appl |
| 649 | 3 | 8.8 | 28 | 1 | US-07-690-300B-63 | Sequence 63, Appl |
| 650 | 3 | 8.8 | 28 | 1 | US-07-690-300B-64 | Sequence 64, Appl |
| 651 | 3 | 8.8 | 28 | 1 | US-07-690-300B-68 | Sequence 68, Appl |
| 652 | 3 | 8.8 | 28 | 1 | US-07-690-300B-71 | Sequence 71, Appl |
| 653 | 3 | 8.8 | 28 | 1 | US-07-690-300B-78 | Sequence 78, Appl |
| 654 | 3 | 8.8 | 28 | 1 | US-07-690-300B-79 | Sequence 79, Appl |
| 655 | 3 | 8.8 | 28 | 1 | US-07-690-300B-82 | Sequence 82, Appl |
| 656 | 3 | 8.8 | 28 | 1 | US-07-690-300B-88 | Sequence 88, Appl |
| 657 | 3 | 8.8 | 28 | 1 | US-07-690-300B-91 | Sequence 91, Appl |
| 658 | 3 | 8.8 | 28 | 1 | US-07-690-300B-93 | Sequence 93, Appl |
| 659 | 3 | 8.8 | 28 | 1 | US-07-663-413-29 | Sequence 29, Appl |
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| 681 | 3 | 8.8 | 28 | 1 | US-08-311-611A-194 | Sequence 194, App |
| 682 | 3 | 8.8 | 28 | 1 | US-08-311-611A-195 | Sequence 195, App |
| 683 | 3 | 8.8 | 28 | 1 | US-08-311-611A-196 | Sequence 196, App |
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| 692 | 3 | 8.8 | 28 | 1 | US-08-372-783-194 | Sequence 194, App |
| 693 | 3 | 8.8 | 28 | 1 | US-08-372-783-195 | Sequence 195, App |
| 694 | 3 | 8.8 | 28 | 1 | US-08-372-783-196 | Sequence 196, App |
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| 751 | 3 | 8.8 | 28 | 1 | US-08-308-729-39 | Sequence 39, Appl |
| 752 | 3 | 8.8 | 28 | 1 | US-08-308-729-40 | Sequence 40, Appl |

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| 818 | 3 | 8.8 | 28 | 2 | US-08-485-445A-194 | Sequence 194, App |
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| 834 | 3 | 8.8 | 28 | 2 | US-08-620-151-129 | Sequence 129, App |
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| 861 | 3 | 8.8 | 28 | 3 | US-08-484-223B-136 | Sequence 136, App |
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| 881 | 3 | 8.8 | 28 | 3 | US-08-952-568-13 | Sequence 13, Appl |
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| 883 | 3 | 8.8 | 28 | 3 | US-08-919-597-84 | Sequence 84, Appl |
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| 898 | 3 | 8.8 | 28 | 3 | US-08-471-913A-136 | Sequence 136, App |
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| 934 | 3 | 8.8 | 28 | 3 | US-08-985-499-39 | Sequence 39, Appl |
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| 936 | 3 | 8.8 | 28 | 3 | US-08-363-558-1 | Sequence 1, Appli |
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| 985 | 3 | 8.8 | 28 | 4 | US-09-406-781-11 | Sequence 11, Appl |
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| 995 | 3 | 8.8 | 28 | 4 | US-09-315-304B-62 | Sequence 62, Appl |
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| 998 | 3 | 8.8 | 28 | 4 | US-09-315-304B-1280 | Sequence 1280, Ap |
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ALIGNMENTS

RESULT 1

US-09-044-536A-8

; Sequence 8, Application US/09044536A

; Patent No. 6025467

; GENERAL INFORMATION:

; APPLICANT: FUKUDA, Tsunehiko

; APPLICANT: NAKAGAWA, Shizue

; APPLICANT: HABASHITA, Junko

; APPLICANT: TAKETOMI, Shigehisa

; TITLE OF INVENTION: PARATHYROID HORMONE DERIVATIVES AND THEIR USE

; NUMBER OF SEQUENCES: 36

; CORRESPONDENCE ADDRESS:

; ADDRESSEE: DIKE, BRONSTEIN, ROBERTS & CUSHMAN

; STREET: 130 Water Street

; CITY: Boston

; STATE: Massachusetts

; COUNTRY: US

; ZIP: 02109

; COMPUTER READABLE FORM:

; MEDIUM TYPE: Floppy disk

; COMPUTER: IBM PC compatible

; OPERATING SYSTEM: PC-DOS/MS-DOS

; SOFTWARE: PatentIn Release #1.0, Version #1.30

; CURRENT APPLICATION DATA:

; APPLICATION NUMBER: US/09/044,536A

; FILING DATE: 19-MAR-1998

; PRIOR APPLICATION DATA:

; APPLICATION NUMBER: 08/662,871

; FILING DATE: 12-JUN-1996

; ATTORNEY/AGENT INFORMATION:

; NAME: CONLIN, David G

; REGISTRATION NUMBER: 27,026

; REFERENCE/DOCKET NUMBER: 46509-DIV
 ; TELECOMMUNICATION INFORMATION:
 ; TELEPHONE: (617)523-3400
 ; TELEFAX: (617)523-6440
 ; INFORMATION FOR SEQ ID NO: 8:
 ; SEQUENCE CHARACTERISTICS:
 ; LENGTH: 34 amino acids
 ; TYPE: amino acid
 ; STRANDEDNESS:
 ; TOPOLOGY: linear
 ; MOLECULE TYPE: peptide
 ; FEATURE:
 ; NAME/KEY: partial peptide
 ; LOCATION: 1..34
 US-09-044-536A-8

Query Match 70.6%; Score 24; DB 3; Length 34;
 Best Local Similarity 100.0%; Pred. No. 3.5e-17;
 Matches 24; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 11 KGKHLNSMERVEWLRKKLQDVHNF 34
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 Db 11 KGKHLNSMERVEWLRKKLQDVHNF 34

RESULT 2

US-08-256-363-1

; Sequence 1, Application US/08256363
 ; Patent No. 5783558
 ; GENERAL INFORMATION:
 ; APPLICANT: DUVOS, CHRISTIAN
 ; APPLICANT: MAYER, HUBERT
 ; APPLICANT: MUELLER-BECKMANN, BERND
 ; APPLICANT: STREIN, KLAUS
 ; APPLICANT: WINGENDER, EDGAR
 ; TITLE OF INVENTION: PARATHYROID HORMONE FRAGMENTS, THEIR
 ; TITLE OF INVENTION: PREPARATION AND MEDICAMENTS CONTAINING THE SAME
 ; NUMBER OF SEQUENCES: 4
 ; CORRESPONDENCE ADDRESS:
 ; ADDRESSEE: NIKAIDO, MARMELESTEIN, MURRAY, AND ORAM
 ; STREET: 655 15th ST. N.W. SUITE 330- G ST. LOBBY
 ; CITY: WASHINGTON
 ; STATE: D.C.
 ; COUNTRY: U.S.A.
 ; ZIP: 2005 5701
 ; COMPUTER READABLE FORM:
 ; MEDIUM TYPE: Floppy disk
 ; COMPUTER: IBM PC compatible
 ; OPERATING SYSTEM: PC-DOS/MS-DOS
 ; SOFTWARE: PatentIn Release #1.0, Version #1.25
 ; CURRENT APPLICATION DATA:
 ; APPLICATION NUMBER: US/08/256,363
 ; FILING DATE:
 ; CLASSIFICATION: 514
 ; PRIOR APPLICATION DATA:
 ; APPLICATION NUMBER: DE P 42 03 040.4
 ; FILING DATE: 04-FEB-1992

; PRIOR APPLICATION DATA:
 ; APPLICATION NUMBER: PCT/EP93/00259
 ; FILING DATE: 04-FEB-1993
 ; ATTORNEY/AGENT INFORMATION:
 ; NAME: KLESNER, SHARON N.
 ; REGISTRATION NUMBER: 36,335
 ; REFERENCE/DOCKET NUMBER: P1614-4025
 ; TELECOMMUNICATION INFORMATION:
 ; TELEPHONE: (202) 638-5000
 ; TELEFAX: (202) 638-4810
 ; INFORMATION FOR SEQ ID NO: 1:
 ; SEQUENCE CHARACTERISTICS:
 ; LENGTH: 33 amino acids
 ; TYPE: amino acid
 ; STRANDEDNESS: single
 ; TOPOLOGY: linear
 ; MOLECULE TYPE: peptide
 US-08-256-363-1

Query Match 67.6%; Score 23; DB 1; Length 33;
 Best Local Similarity 100.0%; Pred. No. 3.3e-16;
 Matches 23; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 12 GKHLNSMERVEWLRKKLQDVHNF 34
 |||||
 Db 10 GKHLNSMERVEWLRKKLQDVHNF 32

RESULT 3

US-07-765-373-1

; Sequence 1, Application US/07765373
 ; Patent No. 5393869
 ; GENERAL INFORMATION:
 ; APPLICANT: NAKAGAWA, Shizue
 ; APPLICANT: FUKUDA, Tsunehiko
 ; APPLICANT: KAWASE, Masahiro
 ; APPLICANT: YAMAZAKI, Iwao
 ; TITLE OF INVENTION: PARATHYROID HORMONE DERIVATIVES
 ; NUMBER OF SEQUENCES: 2
 ; CORRESPONDENCE ADDRESS:
 ; ADDRESSEE: DAVID G. CONLIN; DIKE, BRONSTEIN, ROBERTS &
 ; ADDRESSEE: CUSHMAN
 ; STREET: 130 Water Street
 ; CITY: Boston
 ; STATE: Massachusetts
 ; COUNTRY: US
 ; ZIP: 02109
 ; COMPUTER READABLE FORM:
 ; MEDIUM TYPE: Floppy disk
 ; COMPUTER: IBM PC compatible
 ; OPERATING SYSTEM: PC-DOS/MS-DOS
 ; SOFTWARE: PatentIn Release #1.0, Version #1.25
 ; CURRENT APPLICATION DATA:
 ; APPLICATION NUMBER: US/07/765,373
 ; FILING DATE: 19910925
 ; CLASSIFICATION: 530
 ; ATTORNEY/AGENT INFORMATION:

; NAME: WILLIAMS, Gregory D.
; REGISTRATION NUMBER: 30901
; REFERENCE/DOCKET NUMBER: 41289
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (617)523-3400
; TELEFAX: (617)523-6440
; TELEX: 20091 STRE UR
; INFORMATION FOR SEQ ID NO: 1:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 34 amino acids
; TYPE: AMINO ACID
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
; FRAGMENT TYPE: N-terminal
US-07-765-373-1

Query Match 67.6%; Score 23; DB 1; Length 34;
Best Local Similarity 100.0%; Pred. No. 3.4e-16;
Matches 23; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 12 GKHLNSMERVEWLRKKLQDVHNF 34
|||
Db 12 GKHLNSMERVEWLRKKLQDVHNF 34

RESULT 4

US-08-033-099-1

; Sequence 1, Application US/08033099
; Patent No. 5434246
; GENERAL INFORMATION:
; APPLICANT: FUKUDA, Tsunehiko
; APPLICANT: NAKAGAWA, Shizue
; APPLICANT: TAKETOMI, Shigehisa
; TITLE OF INVENTION: PARATHYROID HORMONE DERIVATIVES
; NUMBER OF SEQUENCES: 2
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: DAVID G.CONLIN; DIKE, BRONSTEIN, ROBERTS &
; ADDRESSEE: CUSHMAN
; STREET: 130 Water Street
; CITY: Boston
; STATE: Massachusetts
; COUNTRY: US
; ZIP: 02109
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/033,099
; FILING DATE: 19930316
; CLASSIFICATION: 530
; ATTORNEY/AGENT INFORMATION:
; NAME: WILLIAMS, Gregory D
; REGISTRATION NUMBER: 30901
; REFERENCE/DOCKET NUMBER: 42528
; TELECOMMUNICATION INFORMATION:

```

; TELEPHONE: (617) 523-3400
; TELEFAX: (613) 523-6440
; TELEX: 200291 STRE UR
; INFORMATION FOR SEQ ID NO: 1:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 34 amino acids
; TYPE: AMINO ACID
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; FRAGMENT TYPE: N-terminal
US-08-033-099-1

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Query Match 67.6%; Score 23; DB 1; Length 34;
Best Local Similarity 100.0%; Pred. No. 3.4e-16;
Matches 23; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 12 GKHLNSMERVEWLRKKLQDVHNF 34
 |||||
 Db 12 GKHLNSMERVEWLRKKLQDVHNF 34

RESULT 5

US-08-262-495C-1

; Sequence 1, Application US/08262495C

; Patent No. 5556940

GENERAL INFORMATION:

APPLICANT: WILLICK, Gordon E.

APPLICANT: WHITFIELD, James F.

APPLICANT: SUREWICZ, Witold

; APPLICANT: SUNG, Wing L.

APPLICANT: NEUGENBAUER, Witold

TITLE OF INVENTION: PARATHYROID HORMONE ANALOGUES

10; TITLE OF INVENTION: FOR THE TREATMENT OF OSTEOPOROSIS

; NUMBER OF SEQUENCES: 6

CORRESPONDENCE ADDRESS:

ADDRESSEE: Kirby, Eades, Gale, Baker

STREET: 112 Kent Street, Suite 770,

; CITY: Ottawa

COUNTRY: Canada

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk

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;      COMPUTER:  IBM PC Compatible

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OPERATING SYSTEM: PC-DOS/MS-DOS

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; SOFTWARE: Wordperfect 5.1

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; CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/08/262,495C

FILING DATE:

CLASSIFICATION: 530

PRIOR APPLICATION DATA:

APPLICATION NUMBER:

FILING DATE:

CLASSIFICATION: 530

ATTORNEY/AGENT INFORMATION:

NAME: EADES, No. 5556940ris M

REGISTRATION NUMBER: 5.263

REFERENCE/DOCKET NUMBER: 36210

US-08-262-495C-1

Matches 23; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Db 12 GKHLNSMERVEWLRKKLODVHNF 34

RESULT 6

US-07-915-247A-1

; Sequence 1, Application US/07915247A

; Patent No. 5589452

: GENERAL INFORMATION:

APPLICANT: Krstenansky, John L.

APPLICANT: Nestor Jr., John J.

APPLICANT: Ho, Teresa H.

APPLICANT: Vickery, Brian H.

APPLICANT: Bach, Chinh T.

7. TITLE OF INVENTION: ANALOGS OF PARATHYROID HORMONE AND

; TITLE OF INVENTION: PARATHYROID HORMONE RELATED PEPTIDE: SYNTHESIS AND USE

TITLE OF INVENTION: FOR THE TREATMENT OF OSTEOPOROSIS

NUMBER OF SEQUENCES: 34

CORRESPONDENCE ADDRESS:

ADDRESSEE: Patent Dept., Syntex (U.S.A.), Inc.

STREET: 3401 Hillview Ave.

CITY: Palo Alto

; STATE: CA

; COUNTRY: USA

: ZTP. 94303

; COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk

COMPUTER: IBM PC compatible

OPERATING SYSTEM: PC-DOS/MS-DOS

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; SOFTWARE: PatentIn Release #1.0, Version #1.25

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; CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/07/915,247A

FILING DATE: 19920714

CLASSIFICATION: 435

ATTORNEY/AGENT INFORMATION:

NAME: Schmonsees, William

REGISTRATION NUMBER: 31,796

REFERENCE/DOCKET NUMBER: 27610

TELECOMMUNICATION INFORMATION:

TELEPHONE: 415-855-6593

TELEFAX: 415-496-3529

INFORMATION FOR SEO ID NO: 1:

; LENGTH: 34 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
; HYPOTHETICAL: NO
; FRAGMENT TYPE: N-terminal

US-08-443-863-1

Query Match 67.6%; Score 23; DB 1; Length 34;
Best Local Similarity 100.0%; Pred. No. 3.4e-16;
Matches 23; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 12 GKHLNSMERVEWLRKKLQDVHNF 34
|||
Db 12 GKHLNSMERVEWLRKKLQDVHNF 34

RESULT 8

US-08-448-070-1

; Sequence 1, Application US/08448070

; Patent No. 5695955

; GENERAL INFORMATION:

; APPLICANT: Krstenansky, John L.

; APPLICANT: Nestor Jr., John J.

; APPLICANT: Ho, Teresa H.

; APPLICANT: Vickery, Brian H.

; APPLICANT: Bach, Chinh T.

; TITLE OF INVENTION: ANALOGS OF PARATHYROID HORMONE AND

; TITLE OF INVENTION: PARATHYROID HORMONE RELATED PEPTIDE: SYNTHESIS AND USE

; TITLE OF INVENTION: FOR THE TREATMENT OF OSTEOPOROSIS

; NUMBER OF SEQUENCES: 34

; CORRESPONDENCE ADDRESS:

; ADDRESSEE: Patent Dept., Syntex (U.S.A.), Inc.

; STREET: 3401 Hillview Ave.

; CITY: Palo Alto

; STATE: CA

; COUNTRY: USA

; ZIP: 94303

; COMPUTER READABLE FORM:

; MEDIUM TYPE: Floppy disk

; COMPUTER: IBM PC compatible

; OPERATING SYSTEM: PC-DOS/MS-DOS

; SOFTWARE: PatentIn Release #1.0, Version #1.25

; CURRENT APPLICATION DATA:

; APPLICATION NUMBER: US/08/448,070

; FILING DATE: 14-JUL-1992

; CLASSIFICATION: 435

; ATTORNEY/AGENT INFORMATION:

; NAME: Schmonsees, William

; REGISTRATION NUMBER: 31,796

; REFERENCE/DOCKET NUMBER: 27610

; TELECOMMUNICATION INFORMATION:

; TELEPHONE: 415-855-6593

; TELEFAX: 415-496-3529

; INFORMATION FOR SEQ ID NO: 1:

; SEQUENCE CHARACTERISTICS:

; LENGTH: 34 amino acids

; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
; HYPOTHETICAL: NO
; FRAGMENT TYPE: N-terminal
US-08-448-070-1

Query Match 67.6%; Score 23; DB 1; Length 34;
Best Local Similarity 100.0%; Pred. No. 3.4e-16;
Matches 23; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 12 GKHLNSMERVEWLRKKLQDVHNF 34
|||
Db 12 GKHLNSMERVEWLRKKLQDVHNF 34

RESULT 9

US-08-488-105-7

; Sequence 7, Application US/08488105

; Patent No. 5717062

; GENERAL INFORMATION:

; APPLICANT: Chorev, Michael

; APPLICANT: Rosenblatt, Michael

; TITLE OF INVENTION: CYCLIC ANALOGS OF PTH AND PTHrP

; NUMBER OF SEQUENCES: 22

; CORRESPONDENCE ADDRESS:

; ADDRESSEE: Fish & Richardson P.C.

; STREET: 225 Franklin Street

; CITY: Boston

; STATE: MA

; COUNTRY: USA

; ZIP: 02110-2804

; COMPUTER READABLE FORM:

; MEDIUM TYPE: Floppy disk

; COMPUTER: IBM PC compatible

; OPERATING SYSTEM: PC-DOS/MS-DOS

; SOFTWARE: PatentIn Release #1.0, Version #1.30

; CURRENT APPLICATION DATA:

; APPLICATION NUMBER: US/08/488,105

; FILING DATE: 07-JUN-1995

; CLASSIFICATION: 530

; ATTORNEY/AGENT INFORMATION:

; NAME: Tsao, Y. Rocky

; REGISTRATION NUMBER: 34,053

; REFERENCE/DOCKET NUMBER: 00537/112001

; TELECOMMUNICATION INFORMATION:

; TELEPHONE: 617/542-5070

; TELEFAX: 617/542-8906

; TELEX: 200154

; INFORMATION FOR SEQ ID NO: 7:

; SEQUENCE CHARACTERISTICS:

; LENGTH: 34 amino acids

; TYPE: amino acid

; STRANDEDNESS: not relevant

; TOPOLOGY: linear

; MOLECULE TYPE: protein

; FEATURE:

; OTHER INFORMATION: The side chains of Lys at
; OTHER INFORMATION: position 26 and Asp at position 30 are linked by an
amide bond,
; OTHER INFORMATION: and this sequence has an amide C-terminus (i.e.,
CONH2), rather
; OTHER INFORMATION: than a carboxy C-terminus (i.e., COOH).
US-08-488-105-7

Query Match 67.6%; Score 23; DB 1; Length 34;
Best Local Similarity 100.0%; Pred. No. 3.4e-16;
Matches 23; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 12 GKHLNSMERVEWLRKKLQDVHNF 34
|||
Db 12 GKHLNSMERVEWLRKKLQDVHNF 34

RESULT 10

US-08-468-275-6

; Sequence 6, Application US/08468275

; Patent No. 5747453

; GENERAL INFORMATION:

; APPLICANT: HOLLADAY, LESLIE A.

; APPLICANT: OLDENBURG, KEVIN R.

; TITLE OF INVENTION: METHOD FOR INCREASING THE

; TITLE OF INVENTION: ELECTROTRANSPORT FLUX OF POLYPEPTIDES

; NUMBER OF SEQUENCES: 10

; CORRESPONDENCE ADDRESS:

; ADDRESSEE: ALZA CORPORATION

; STREET: 950 PAGE MILL ROAD

; CITY: PALO ALTO

; STATE: CALIFORNIA

; COUNTRY: USA

; ZIP: 94303-0802

; COMPUTER READABLE FORM:

; MEDIUM TYPE: Floppy disk

; COMPUTER: IBM PC compatible

; OPERATING SYSTEM: PC-DOS/MS-DOS

; SOFTWARE: PatentIn Release #1.0, Version #1.30

; CURRENT APPLICATION DATA:

; APPLICATION NUMBER: US/08/468,275

; FILING DATE: 06-JUN-1995

; CLASSIFICATION: 514

; ATTORNEY/AGENT INFORMATION:

; NAME: MILLER, D. BYRON

; REGISTRATION NUMBER: 30,661

; REFERENCE/DOCKET NUMBER: 0360-0002; ARC-2349

; TELECOMMUNICATION INFORMATION:

; TELEPHONE: (415) 496-8150

; TELEFAX: (415) 496-8048

; INFORMATION FOR SEQ ID NO: 6:

; SEQUENCE CHARACTERISTICS:

; LENGTH: 34 amino acids

; TYPE: amino acid

; STRANDEDNESS: single

; TOPOLOGY: linear

; MOLECULE TYPE: protein

US-08-468-275-6

Query Match 67.6%; Score 23; DB 1; Length 34;
Best Local Similarity 100.0%; Pred. No. 3.4e-16;
Matches 23; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 12 GKHLNSMERVEWLRKKLQDVHNF 34
|||
Db 12 GKHLNSMERVEWLRKKLQDVHNF 34

RESULT 11

US-08-256-363-2

; Sequence 2, Application US/08256363

; Patent No. 5783558

; GENERAL INFORMATION:

; APPLICANT: DUVOS, CHRISTIAN

; APPLICANT: MAYER, HUBERT

; APPLICANT: MUELLER-BECKMANN, BERND

; APPLICANT: STREIN, KLAUS

; APPLICANT: WINGENDER, EDGAR

; TITLE OF INVENTION: PARATHYROID HORMONE FRAGMENTS, THEIR

; TITLE OF INVENTION: PREPARATION AND MEDICAMENTS CONTAINING THE SAME

; NUMBER OF SEQUENCES: 4

; CORRESPONDENCE ADDRESS:

; ADDRESSEE: NIKAI DO, MARME LSTEIN, MURRAY, AND ORAM

; STREET: 655 15th ST. N.W. SUITE 330- G ST. LOBBY

; CITY: WASHINGTON

; STATE: D.C.

; COUNTRY: U.S.A.

; ZIP: 2005 5701

; COMPUTER READABLE FORM:

; MEDIUM TYPE: Floppy disk

; COMPUTER: IBM PC compatible

; OPERATING SYSTEM: PC-DOS/MS-DOS

; SOFTWARE: PatentIn Release #1.0, Version #1.25

; CURRENT APPLICATION DATA:

; APPLICATION NUMBER: US/08/256,363

; FILING DATE:

; CLASSIFICATION: 514

; PRIOR APPLICATION DATA:

; APPLICATION NUMBER: DE P 42 03 040.4

; FILING DATE: 04-FEB-1992

; PRIOR APPLICATION DATA:

; APPLICATION NUMBER: PCT/EP93/00259

; FILING DATE: 04-FEB-1993

; ATTORNEY/AGENT INFORMATION:

; NAME: KLESNER, SHARON N.

; REGISTRATION NUMBER: 36,335

; REFERENCE/DOCKET NUMBER: P1614-4025

; TELECOMMUNICATION INFORMATION:

; TELEPHONE: (202) 638-5000

; TELEFAX: (202) 638-4810

; INFORMATION FOR SEQ ID NO: 2:

; SEQUENCE CHARACTERISTICS:

; LENGTH: 34 amino acids

; TYPE: amino acid

; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
US-08-256-363-2

Query Match 67.6%; Score 23; DB 1; Length 34;
Best Local Similarity 100.0%; Pred. No. 3.4e-16;
Matches 23; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 12 GKHLNSMERVEWLRKKLQDVHNF 34
|||
Db 10 GKHLNSMERVEWLRKKLQDVHNF 32

RESULT 12

US-08-449-500-1

; Sequence 1, Application US/08449500
; Patent No. 5798225

; GENERAL INFORMATION:

; APPLICANT: Krstenansky, John L.
; APPLICANT: Nestor Jr., John J.
; APPLICANT: Ho, Teresa H.
; APPLICANT: Vickery, Brian H.
; APPLICANT: Bach, Chinh T.

; TITLE OF INVENTION: ANALOGS OF PARATHYROID HORMONE AND
; TITLE OF INVENTION: PARATHYROID HORMONE RELATED PEPTIDE: SYNTHESIS AND USE
; TITLE OF INVENTION: FOR THE TREATMENT OF OSTEOPOROSIS
; NUMBER OF SEQUENCES: 86

; CORRESPONDENCE ADDRESS:

; ADDRESSEE: Patent Dept., Syntex (U.S.A.), Inc.
; STREET: 3401 Hillview Ave.
; CITY: Palo Alto
; STATE: CA
; COUNTRY: USA
; ZIP: 94303

; COMPUTER READABLE FORM:

; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25

; CURRENT APPLICATION DATA:

; APPLICATION NUMBER: US/08/449,500
; FILING DATE: 18-JAN-1994
; CLASSIFICATION: 435

; ATTORNEY/AGENT INFORMATION:

; NAME: Schmonsees, William
; REGISTRATION NUMBER: 31,796
; REFERENCE/DOCKET NUMBER: 27610-P1

; TELECOMMUNICATION INFORMATION:

; TELEPHONE: 415-855-6593
; TELEFAX: 415-496-3529

; INFORMATION FOR SEQ ID NO: 1:

; SEQUENCE CHARACTERISTICS:

; LENGTH: 34 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: peptide

; HYPOTHETICAL: NO
; FRAGMENT TYPE: N-terminal
US-08-449-500-1

Query Match 67.6%; Score 23; DB 1; Length 34;
Best Local Similarity 100.0%; Pred. No. 3.4e-16;
Matches 23; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 12 GKHLNSMERVEWLRKKLQDVHNF 34
|||
Db 12 GKHLNSMERVEWLRKKLQDVHNF 34

RESULT 13

US-08-449-317A-1

; Sequence 1, Application US/08449317A
; Patent No. 5807823
; GENERAL INFORMATION:
; APPLICANT: Vickery, Brian H.
; TITLE OF INVENTION: METHOD FOR TREATMENT OF CORTICOSTEROID
; TITLE OF INVENTION: INDUCED OSTEOPENIA
; NUMBER OF SEQUENCES: 86
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Patent Dept., Syntex (U.S.A.), Inc.
; STREET: 3401 Hillview Ave.
; CITY: Palo Alto
; STATE: CA
; COUNTRY: USA
; ZIP: 94303
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/449,317A
; FILING DATE: 07-JUN-1995
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: Schmonsees, William
; REGISTRATION NUMBER: 31,796
; REFERENCE/DOCKET NUMBER: 27610-P2
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 415-855-6593
; TELEFAX: 415-496-3529
; INFORMATION FOR SEQ ID NO: 1:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 34 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
; HYPOTHETICAL: NO
; FRAGMENT TYPE: N-terminal
US-08-449-317A-1

Query Match 67.6%; Score 23; DB 1; Length 34;
Best Local Similarity 100.0%; Pred. No. 3.4e-16;

Matches 23; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 12 GKHLNSMERVEWLRKKLQDVHNF 34
| | | | | | | | | | | | | | | | | |
Db 12 GKHLNSMERVEWLRKKLQDVHNF 34

RESULT 14

US-08-142-551B-2

; Sequence 2, Application US/08142551B

; Patent No. 5814603

; GENERAL INFORMATION:

; APPLICANT: Oldenburg, Kevin R.

; APPLICANT: Selick, Harold E.

; TITLE OF INVENTION: COMPOUNDS WITH PTH ACTIVITY AND

; TITLE OF INVENTION: RECOMBINANT DNA VECTORS ENCODING SAME

; NUMBER OF SEQUENCES: 132

; CORRESPONDENCE ADDRESS:

; ADDRESSEE: Burns, Doane, Swecker & Mathis

; STREET: 699 Prince Street

; CITY: Alexandria

; STATE: Virginia

; COUNTRY: US

; ZIP: 22313

; COMPUTER READABLE FORM:

; MEDIUM TYPE: Floppy disk

; COMPUTER: IBM PC compatible

; OPERATING SYSTEM: PC-DOS/MS-DOS

; SOFTWARE: PatentIn Release #1.0, Version #1.25

; CURRENT APPLICATION DATA:

; APPLICATION NUMBER: US/08/142,551B

; FILING DATE: 25-OCT-1993

; CLASSIFICATION: 435

; PRIOR APPLICATION DATA:

; APPLICATION NUMBER: US 08/077,296

; FILING DATE: 14-JUN-1993

; PRIOR APPLICATION DATA:

; APPLICATION NUMBER: US 07/898,219

; FILING DATE: 12-JUN-1992

; PRIOR APPLICATION DATA:

; APPLICATION NUMBER: US 07/965,677

; FILING DATE: 22-OCT-1992

; ATTORNEY/AGENT INFORMATION:

; NAME: Swiss, Gerald F.

; REGISTRATION NUMBER: 30,113

; REFERENCE/DOCKET NUMBER: 000324-010

; TELECOMMUNICATION INFORMATION:

; TELEPHONE: (415) 854-7400

; TELEFAX: (415) 854-8275

; INFORMATION FOR SEQ ID NO: 2:

; SEQUENCE CHARACTERISTICS:

; LENGTH: 34 amino acids

; TYPE: amino acid

; TOPOLOGY: unknown

; MOLECULE TYPE: protein

; FEATURE:

; NAME/KEY: Peptide

; LOCATION: 1..34
; OTHER INFORMATION: /note= "The sequence of the 34
; OTHER INFORMATION: amino acid truncated human PTH peptide,
; OTHER INFORMATION: designated: Human PTH."
US-08-142-551B-2

Query Match 67.6%; Score 23; DB 2; Length 34;
Best Local Similarity 100.0%; Pred. No. 3.4e-16;
Matches 23; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 12 GKHLNSMERVEWLRKKLQDVHNF 34
| | | | | | | | | | | | | | | | | |
Db 12 GKHLNSMERVEWLRKKLQDVHNF 34

RESULT 15

US-08-477-022-1

; Sequence 1, Application US/08477022
; Patent No. 5821225

; GENERAL INFORMATION:

; APPLICANT: Vickery, Brian H.
; TITLE OF INVENTION: METHOD FOR TREATMENT OF CORTICOSTEROID
; TITLE OF INVENTION: INDUCED OSTEOPENIA
; NUMBER OF SEQUENCES: 86
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Patent Dept., Syntex (U.S.A.), Inc.
; STREET: 3401 Hillview Ave.
; CITY: Palo Alto
; STATE: CA
; COUNTRY: USA
; ZIP: 94303

; COMPUTER READABLE FORM:

; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25

; CURRENT APPLICATION DATA:

; APPLICATION NUMBER: US/08/477,022
; FILING DATE: 07-JUN-1995
; CLASSIFICATION: 435

; ATTORNEY/AGENT INFORMATION:

; NAME: Schmonsees, William
; REGISTRATION NUMBER: 31,796
; REFERENCE/DOCKET NUMBER: 27610-P2

; TELECOMMUNICATION INFORMATION:

; TELEPHONE: 415-855-6593
; TELEFAX: 415-496-3529

; INFORMATION FOR SEQ ID NO: 1:

; SEQUENCE CHARACTERISTICS:

; LENGTH: 34 amino acids
; TYPE: amino acid
; TOPOLOGY: linear

; MOLECULE TYPE: peptide

; HYPOTHETICAL: NO

; FRAGMENT TYPE: N-terminal

US-08-477-022-1

Query Match 67.6%; Score 23; DB 2; Length 34;
Best Local Similarity 100.0%; Pred. No. 3.4e-16;
Matches 23; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 12 GKHLNSMERVEWLRKKLQDVHNF 34
| | | | | | | | | | | | | | | | | |
Db 12 GKHLNSMERVEWLRKKLQDVHNF 34

RESULT 16

US-08-449-447-1

; Sequence 1, Application US/08449447

; Patent No. 5840837

; GENERAL INFORMATION:

; APPLICANT: Krstenansky, John L.

; APPLICANT: Nestor Jr., John J.

; APPLICANT: Ho, Teresa H.

; APPLICANT: Vickery, Brian H.

; APPLICANT: Bach, Chinh T.

; TITLE OF INVENTION: ANALOGS OF PARATHYROID HORMONE AND

; TITLE OF INVENTION: PARATHYROID HORMONE RELATED PEPTIDE: SYNTHESIS AND USE

; TITLE OF INVENTION: FOR THE TREATMENT OF OSTEOPOROSIS

; NUMBER OF SEQUENCES: 86

; CORRESPONDENCE ADDRESS:

; ADDRESSEE: Patent Dept., Syntex (U.S.A.), Inc.

; STREET: 3401 Hillview Ave.

; CITY: Palo Alto

; STATE: CA

; COUNTRY: USA

; ZIP: 94303

; COMPUTER READABLE FORM:

; MEDIUM TYPE: Floppy disk

; COMPUTER: IBM PC compatible

; OPERATING SYSTEM: PC-DOS/MS-DOS

; SOFTWARE: PatentIn Release #1.0, Version #1.25

; CURRENT APPLICATION DATA:

; APPLICATION NUMBER: US/08/449,447

; FILING DATE: 18-JAN-1994

; CLASSIFICATION: 530

; ATTORNEY/AGENT INFORMATION:

; NAME: Schmonsees, William

; REGISTRATION NUMBER: 31,796

; REFERENCE/DOCKET NUMBER: 27610-P1

; TELECOMMUNICATION INFORMATION:

; TELEPHONE: 415-855-6593

; TELEFAX: 415-496-3529

; INFORMATION FOR SEQ ID NO: 1:

; SEQUENCE CHARACTERISTICS:

; LENGTH: 34 amino acids

; TYPE: amino acid

; TOPOLOGY: linear

; MOLECULE TYPE: peptide

; HYPOTHETICAL: NO

; FRAGMENT TYPE: N-terminal

US-08-449-447-1

Query Match 67.6%; Score 23; DB 2; Length 34;

Best Local Similarity 100.0%; Pred. No. 3.4e-16;
Matches 23; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 12 GKHLNSMERVEWLRKKLQDVHNF 34
 |||||
Db 12 GKHLNSMERVEWLRKKLQDVHNF 34

RESULT 17

US-08-835-231-13

; Sequence 13, Application US/08835231

; Patent No. 5861284

; GENERAL INFORMATION:

; APPLICANT: NISHIMURA, Osamu

; APPLICANT: KURIYAMA, Masato

; APPLICANT: KOYAMA, No. 5861284uyuki

; APPLICANT: FUKUDA, Tsunehiko

; TITLE OF INVENTION: METHOD FOR PRODUCING A BIOLOGICALLY

; TITLE OF INVENTION: ACTIVE RECOMBINANT CYSTEINE-FREE

; NUMBER OF SEQUENCES: 37

; CORRESPONDENCE ADDRESS:

; ADDRESSEE: DIKE, BRONSTEIN, ROBERTS & CUSHMAN, LLP

; STREET: 130 WATER STREET

; CITY: BOSTON

; STATE: MA

; COUNTRY: USA

; ZIP: 02109

; COMPUTER READABLE FORM:

; MEDIUM TYPE: Diskette

; COMPUTER: IBM Compatible

; OPERATING SYSTEM: DOS

; SOFTWARE: FastSEQ Version 1.5

; CURRENT APPLICATION DATA:

; APPLICATION NUMBER: US/08/835,231

; FILING DATE:

; CLASSIFICATION: 435

; PRIOR APPLICATION DATA:

; APPLICATION NUMBER: 08/350,709

; FILING DATE: 07-DEC-1994

; APPLICATION NUMBER: 07/838,857

; FILING DATE: 18-FEB-1992

; APPLICATION NUMBER: JP 024841

; FILING DATE: 19-FEB-1991

; APPLICATION NUMBER: JP 0271438

; FILING DATE: 18-OCT-1991

; ATTORNEY/AGENT INFORMATION:

; NAME: DAVID, RESNICK S

; REGISTRATION NUMBER: 34,235

; REFERENCE/DOCKET NUMBER: 41614-FWC

; TELECOMMUNICATION INFORMATION:

; TELEPHONE: 617-523-3400

; TELEFAX: 617-523-6440

; TELEX: 200291 STRE

; INFORMATION FOR SEQ ID NO: 13:

; SEQUENCE CHARACTERISTICS:

; LENGTH: 34 amino acids

; TYPE: amino acid

; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
; HYPOTHETICAL: NO
; ANTI-SENSE: NO
; FRAGMENT TYPE: N-terminal
; ORIGINAL SOURCE:
US-08-835-231-13

Query Match 67.6%; Score 23; DB 2; Length 34;
Best Local Similarity 100.0%; Pred. No. 3.4e-16;
Matches 23; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 12 GKHLNSMERVEWLRKKLQDVHNF 34
| | | | | | | | | | | | | | | | | | | | | |
Db 12 GKHLNSMERVEWLRKKLQDVHNF 34

RESULT 18

US-08-184-328-1

; Sequence 1, Application US/08184328

; Patent No. 5874086

; GENERAL INFORMATION:

; APPLICANT: Krstenansky, John L.

; APPLICANT: Nestor Jr., John J.

; APPLICANT: Ho, Teresa H.

; APPLICANT: Vickery, Brian H.

; APPLICANT: Bach, Chinh T.

; TITLE OF INVENTION: ANALOGS OF PARATHYROID HORMONE AND

; TITLE OF INVENTION: PARATHYROID HORMONE RELATED PEPTIDE: SYNTHESIS AND USE

; TITLE OF INVENTION: FOR THE TREATMENT OF OSTEOPOROSIS

; NUMBER OF SEQUENCES: 86

; CORRESPONDENCE ADDRESS:

; ADDRESSEE: Patent Dept., Syntex (U.S.A.), Inc.

; STREET: 3401 Hillview Ave.

; CITY: Palo Alto

; STATE: CA

; COUNTRY: USA

; ZIP: 94303

; COMPUTER READABLE FORM:

; MEDIUM TYPE: Floppy disk

; COMPUTER: IBM PC compatible

; OPERATING SYSTEM: PC-DOS/MS-DOS

; SOFTWARE: PatentIn Release #1.0, Version #1.25

; CURRENT APPLICATION DATA:

; APPLICATION NUMBER: US/08/184,328

; FILING DATE: 18-JAN-1994

; CLASSIFICATION: 435

; ATTORNEY/AGENT INFORMATION:

; NAME: Schmonsees, William

; REGISTRATION NUMBER: 31,796

; REFERENCE/DOCKET NUMBER: 27610-P1

; TELECOMMUNICATION INFORMATION:

; TELEPHONE: 415-855-6593

; TELEFAX: 415-496-3529

; INFORMATION FOR SEQ ID NO: 1:

; SEQUENCE CHARACTERISTICS:

; LENGTH: 34 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
; HYPOTHETICAL: NO
; FRAGMENT TYPE: N-terminal
US-08-184-328-1

Query Match 67.6%; Score 23; DB 2; Length 34;
Best Local Similarity 100.0%; Pred. No. 3.4e-16;
Matches 23; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 12 GKHLNSMERVEWLRKKLQDVHNF 34
|||
Db 12 GKHLNSMERVEWLRKKLQDVHNF 34

RESULT 19

US-08-411-726-2

; Sequence 2, Application US/08411726

; Patent No. 5880093

; GENERAL INFORMATION:

; APPLICANT: BAGNOLI, Franco

; TITLE OF INVENTION: Use of Parathormone, Its Biologically

; TITLE OF INVENTION: Active Fragments and Correlated Peptides, for The
Preparation of

; TITLE OF INVENTION: Pharmaceutical Compositions Useful for The Treatment
of Pregnanc

; NUMBER OF SEQUENCES: 5

; CORRESPONDENCE ADDRESS:

; ADDRESSEE: Kenyon & Kenyon

; STREET: 1 Broadway

; CITY: New York

; STATE: NY

; COUNTRY: US

; ZIP: 10004

; COMPUTER READABLE FORM:

; MEDIUM TYPE: 3.5 Floppy disk

; COMPUTER: IBM PC compatible

; OPERATING SYSTEM: PC-DOS/MS-DOS 6.2

; SOFTWARE: WordPerfect 6.1 for Windows

; CURRENT APPLICATION DATA:

; APPLICATION NUMBER: US/08/411,726

; FILING DATE: 05-APR-1995

; CLASSIFICATION: 514

; PRIOR APPLICATION DATA:

; APPLICATION NUMBER: PCT/EP93/02755

; FILING DATE: 08-OCT-1993

; APPLICATION NUMBER: MI-92A002331

; FILING DATE: 09-OCT-1992

; ATTORNEY/AGENT INFORMATION:

; NAME: PALMESE, Maria Luisa

; REGISTRATION NUMBER: 34,402

; REFERENCE/DOCKET NUMBER: 2111/1300

; TELECOMMUNICATION INFORMATION:

; TELEPHONE: 212-425-7200

; TELEFAX: 212-425-5288


```

; INFORMATION FOR SEQ ID NO: 2:
;   SEQUENCE CHARACTERISTICS:
;     LENGTH: 34 amino acids
;     TYPE: amino acid
;     STRANDEDNESS: single
;     TOPOLOGY: linear
;     MOLECULE TYPE: protein
US-08-411-726-2

```

Query Match 67.6%; Score 23; DB 2; Length 34;
Best Local Similarity 100.0%; Pred. No. 3.4e-16;
Matches 23; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 12 GKHLNSMERVEWLRKKLQDVHNF 34
 |||||
 Db 12 GKHLNSMERVEWLRKKLODVHNF 34

RESULT 20

US-08-691-647C-5

; Sequence 5, Application US/08691647C

; Patent No. 5955425

; GENERAL INFORMATION:

; APPLICANT: Barbier, Jean-Rene

; APPLICANT: Morley, Paul

; APPLICANT: Neugebauer, Witold

; APPLICANT: Ross, Virginia

; APPLICANT: Whitfield, James

; APPLICANT: Willick, Gordon E.

; TITLE OF INVENTION: CYCLIC PARATHYROID HORMONE ANALOGUES

; TITLE OF INVENTION: FOR THE TREATMENT OF OSTEOPOROSIS

```
; NUMBER OF SEQUENCES: 6
```

; CORRESPONDENCE ADDRESS:

ADDRESSEE: NIXON & VANDERHYE, P.C.

STREET: 1100 New York Avenue; 8th Floor

; CITY: Arlington

; STATE: Virginia

; COUNTRY: U.S.A.

ZIP: 22201-4714

; COMPUTER READABLE FORM:

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; MEDIUM TYPE: Floppy disk
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;      COMPUTER:  IBM PC compatible
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```
;      OPERATING SYSTEM:  PC-DOS/MS-DOS
```

```
; SOFTWARE:  ASCII Text
```

; CURRENT APPLICATION DATA:

; APPLICATION NUMBER: US/08/691,647C

FILING DATE: August 2, 1996

CLASSIFICATION: 514

; ATTORNEY/AGENT INFORMATION:

NAME: Crawford, Arthur R.

REGISTRATION NUMBER: 25.327

REFERENCE/DOCKET NUMBER: 1339-5

; TELECOMMUNICATION INFORMATION:

TELEPHONE: (703) 816-4005

; TELEFAX: (703) 816-4100

TELEX: N/A

; INFORMATION FOR SEQ ID NO: 5:

; SEQUENCE CHARACTERISTICS:
; LENGTH: 34 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
US-08-691-647C-5

Query Match 67.6%; Score 23; DB 2; Length 34;
Best Local Similarity 100.0%; Pred. No. 3.4e-16;
Matches 23; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 12 GKHLNSMERVEWLRKKLQDVHNF 34
|||
Db 12 GKHLNSMERVEWLRKKLQDVHNF 34

RESULT 21

US-08-521-097-1

; Sequence 1, Application US/08521097

; Patent No. 5977070

; GENERAL INFORMATION:

; APPLICANT: Krstenansky, John L.

; APPLICANT: Nestor Jr., John J.

; APPLICANT: Ho, Teresa H.

; APPLICANT: Vickery, Brian H.

; APPLICANT: Bach, Chinh T.

; TITLE OF INVENTION: ANALOGS OF PARATHYROID HORMONE AND

; TITLE OF INVENTION: PARATHYROID HORMONE RELATED PEPTIDE: SYNTHESIS AND USE

; TITLE OF INVENTION: FOR THE TREATMENT OF OSTEOPOROSIS

; NUMBER OF SEQUENCES: 86

; CORRESPONDENCE ADDRESS:

; ADDRESSEE: Patent Dept., Syntex (U.S.A.), Inc.

; STREET: 3401 Hillview Ave.

; CITY: Palo Alto

; STATE: CA

; COUNTRY: USA

; ZIP: 94303

; COMPUTER READABLE FORM:

; MEDIUM TYPE: Floppy disk

; COMPUTER: IBM PC compatible

; OPERATING SYSTEM: PC-DOS/MS-DOS

; SOFTWARE: PatentIn Release #1.0, Version #1.25

; CURRENT APPLICATION DATA:

; APPLICATION NUMBER: US/08/521,097

; FILING DATE: 29-AUG-1995

; CLASSIFICATION: 514

; PRIOR APPLICATION DATA:

; APPLICATION NUMBER: 08/184,328

; FILING DATE: 18-JAN-1994

; ATTORNEY/AGENT INFORMATION:

; NAME: Schmonsees, William

; REGISTRATION NUMBER: 31,796

; REFERENCE/DOCKET NUMBER: 27610-P1

; TELECOMMUNICATION INFORMATION:

; TELEPHONE: 415-855-6593

; TELEFAX: 415-496-3529

; INFORMATION FOR SEQ ID NO: 1:

```

; SEQUENCE CHARACTERISTICS:
;   LENGTH: 34 amino acids
;   TYPE: amino acid
;   TOPOLOGY: linear
; MOLECULE TYPE: peptide
; HYPOTHETICAL: NO
; FRAGMENT TYPE: N-terminal
US-08-521-097-1

```

Query Match 67.6%; Score 23; DB 2; Length 34;
Best Local Similarity 100.0%; Pred. No. 3.4e-16;
Matches 23; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 12 GKHLNSMERVEWLRKKLQDVHNF 34
 |||||
 Db 12 GKHLNSMERVEWLRKKLODVHNF 34

RESULT 22

US-09-044-536A-1

; Sequence 1, Application US/09044536A

; Patent No. 6025467

; GENERAL INFORMATION:

; APPLICANT: FUKUDA, Tsunehiko

APPLICANT: NAKAGAWA, Shizue

; APPLICANT: HABASHITA, Junko

; APPLICANT: TAKETOMI, Shigehisa

10 TITLE OF INVENTION: PARATHYROID HORMONE DERIVATIVES AND THEIR USE

; NUMBER OF SEQUENCES: 36

; CORRESPONDENCE ADDRESS:

ADDRESSEE: DIKE, BRONSTEIN, ROBERTS & CUSHMAN

; STREET: 130 Water Street

; CITY: Boston

```
; STATE: Massachusetts
```

; COUNTRY: US

; ZIP: 02109

COMPUTER READABLE FORM:

```
; MEDIUM TYPE: Floppy disk
```

```
;      COMPUTER:  IBM PC compatible
```

; OPERATING SYSTEM: PC-DOS/MS-DOS

```
; SOFTWARE: PatentIn Release #1.0, Version #1.30
```

```
; CURRENT APPLICATION DATA:
```

APPLICATION NUMBER: US/09/044,536A

FILING DATE: 19-MAR-1998

; PRIOR APPLICATION DATA:

APPLICATION NUMBER: 08/662,871

; FILING DATE: 12-JUN-1996

; ATTORNEY/AGENT INFORMATION:

; NAME: CONLIN, David G

REGISTRATION NUMBER: 27,026

REFERENCE/DOCKET NUMBER: 46509-DIV

; TELECOMMUNICATION INFORMATION:

TELEPHONE: (617) 523-3400

TELEFAX: (617) 523-6440

; INFORMATION FOR SEQ ID NO: 1:

SEQUENCE CHARACTERISTICS:

; LENGTH: 34 amino acids

; TYPE: amino acid
; STRANDEDNESS:
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
; FEATURE:
; NAME/KEY: partial peptide
; LOCATION: 1..34
US-09-044-536A-1

Query Match 67.6%; Score 23; DB 3; Length 34;
Best Local Similarity 100.0%; Pred. No. 3.4e-16;
Matches 23; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 12 GKHLNSMERVEWLRKKLQDVHNF 34
|||
Db 12 GKHLNSMERVEWLRKKLQDVHNF 34

RESULT 23

US-09-044-536A-9

; Sequence 9, Application US/09044536A
; Patent No. 6025467
; GENERAL INFORMATION:
; APPLICANT: FUKUDA, Tsunehiko
; APPLICANT: NAKAGAWA, Shizue
; APPLICANT: HABASHITA, Junko
; APPLICANT: TAKETOMI, Shigehisa
; TITLE OF INVENTION: PARATHYROID HORMONE DERIVATIVES AND THEIR USE
; NUMBER OF SEQUENCES: 36
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: DIKE, BRONSTEIN, ROBERTS & CUSHMAN
; STREET: 130 Water Street
; CITY: Boston
; STATE: Massachusetts
; COUNTRY: US
; ZIP: 02109
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/044,536A
; FILING DATE: 19-MAR-1998
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/662,871
; FILING DATE: 12-JUN-1996
; ATTORNEY/AGENT INFORMATION:
; NAME: CONLIN, David G
; REGISTRATION NUMBER: 27,026
; REFERENCE/DOCKET NUMBER: 46509-DIV
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (617)523-3400
; TELEFAX: (617)523-6440
; INFORMATION FOR SEQ ID NO: 9:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 34 amino acids

; TYPE: amino acid
; STRANDEDNESS:
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
; FEATURE:
; NAME/KEY: partial peptide
; LOCATION: 1..34
US-09-044-536A-9

Query Match 67.6%; Score 23; DB 3; Length 34;
Best Local Similarity 100.0%; Pred. No. 3.4e-16;
Matches 23; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 12 GKHLNSMERVEWLRKKLQDVHNF 34
|||
Db 12 GKHLNSMERVEWLRKKLQDVHNF 34

RESULT 24

US-09-044-536A-10

; Sequence 10, Application US/09044536A

; Patent No. 6025467

; GENERAL INFORMATION:

; APPLICANT: FUKUDA, Tsunehiko

; APPLICANT: NAKAGAWA, Shizue

; APPLICANT: HABASHITA, Junko

; APPLICANT: TAKETOMI, Shigehisa

; TITLE OF INVENTION: PARATHYROID HORMONE DERIVATIVES AND THEIR USE

; NUMBER OF SEQUENCES: 36

; CORRESPONDENCE ADDRESS:

; ADDRESSEE: DIKE, BRONSTEIN, ROBERTS & CUSHMAN

; STREET: 130 Water Street

; CITY: Boston

; STATE: Massachusetts

; COUNTRY: US

; ZIP: 02109

; COMPUTER READABLE FORM:

; MEDIUM TYPE: Floppy disk

; COMPUTER: IBM PC compatible

; OPERATING SYSTEM: PC-DOS/MS-DOS

; SOFTWARE: PatentIn Release #1.0, Version #1.30

; CURRENT APPLICATION DATA:

; APPLICATION NUMBER: US/09/044,536A

; FILING DATE: 19-MAR-1998

; PRIOR APPLICATION DATA:

; APPLICATION NUMBER: 08/662,871

; FILING DATE: 12-JUN-1996

; ATTORNEY/AGENT INFORMATION:

; NAME: CONLIN, David G

; REGISTRATION NUMBER: 27,026

; REFERENCE/DOCKET NUMBER: 46509-DIV

; TELECOMMUNICATION INFORMATION:

; TELEPHONE: (617)523-3400

; TELEFAX: (617)523-6440

; INFORMATION FOR SEQ ID NO: 10:

; SEQUENCE CHARACTERISTICS:

; LENGTH: 34 amino acids

; TYPE: amino acid
; STRANDEDNESS:
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
; FEATURE:
; NAME/KEY: partial peptide
; LOCATION: 1..34
US-09-044-536A-10

Query Match 67.6%; Score 23; DB 3; Length 34;
Best Local Similarity 100.0%; Pred. No. 3.4e-16;
Matches 23; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 12 GKHLNSMERVEWLRKKLQDVHNF 34
|||
Db 12 GKHLNSMERVEWLRKKLQDVHNF 34

RESULT 25

US-09-044-536A-11

; Sequence 11, Application US/09044536A
; Patent No. 6025467
; GENERAL INFORMATION:
; APPLICANT: FUKUDA, Tsunehiko
; APPLICANT: NAKAGAWA, Shizue
; APPLICANT: HABASHITA, Junko
; APPLICANT: TAKETOMI, Shigehisa
; TITLE OF INVENTION: PARATHYROID HORMONE DERIVATIVES AND THEIR USE
; NUMBER OF SEQUENCES: 36
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: DIKE, BRONSTEIN, ROBERTS & CUSHMAN
; STREET: 130 Water Street
; CITY: Boston
; STATE: Massachusetts
; COUNTRY: US
; ZIP: 02109
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/044,536A
; FILING DATE: 19-MAR-1998
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/662,871
; FILING DATE: 12-JUN-1996
; ATTORNEY/AGENT INFORMATION:
; NAME: CONLIN, David G
; REGISTRATION NUMBER: 27,026
; REFERENCE/DOCKET NUMBER: 46509-DIV
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (617)523-3400
; TELEFAX: (617)523-6440
; INFORMATION FOR SEQ ID NO: 11:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 34 amino acids

; TYPE: amino acid
; STRANDEDNESS:
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
; FEATURE:
; NAME/KEY: partial peptide
; LOCATION: 1..34
US-09-044-536A-11

Query Match 67.6%; Score 23; DB 3; Length 34;
Best Local Similarity 100.0%; Pred. No. 3.4e-16;
Matches 23; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 12 GKHLNSMERVEWLRKKLQDVHNF 34
|||
Db 12 GKHLNSMERVEWLRKKLQDVHNF 34

RESULT 26

US-09-044-536A-12

; Sequence 12, Application US/09044536A
; Patent No. 6025467
; GENERAL INFORMATION:
; APPLICANT: FUKUDA, Tsunehiko
; APPLICANT: NAKAGAWA, Shizue
; APPLICANT: HABASHITA, Junko
; APPLICANT: TAKETOMI, Shigehisa
; TITLE OF INVENTION: PARATHYROID HORMONE DERIVATIVES AND THEIR USE
; NUMBER OF SEQUENCES: 36
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: DIKE, BRONSTEIN, ROBERTS & CUSHMAN
; STREET: 130 Water Street
; CITY: Boston
; STATE: Massachusetts
; COUNTRY: US
; ZIP: 02109
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/044,536A
; FILING DATE: 19-MAR-1998
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/662,871
; FILING DATE: 12-JUN-1996
; ATTORNEY/AGENT INFORMATION:
; NAME: CONLIN, David G
; REGISTRATION NUMBER: 27,026
; REFERENCE/DOCKET NUMBER: 46509-DIV
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (617)523-3400
; TELEFAX: (617)523-6440
; INFORMATION FOR SEQ ID NO: 12:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 34 amino acids

```

;     TYPE:  amino acid
;     STRANDEDNESS:
;     TOPOLOGY:  linear
;     MOLECULE TYPE:  peptide
;     FEATURE:
;     NAME/KEY:  partial peptide
;     LOCATION:  1..34
;     FEATURE:
;     NAME/KEY:  Modified-site
;     LOCATION:  11
;     OTHER INFORMATION:  /product= "Xaa=Ala(2-Naph)"
US-09-044-536A-12

```

```

Query Match          67.6%;  Score 23;  DB 3;  Length 34;
Best Local Similarity 100.0%;  Pred. No. 3.4e-16;
Matches    23;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

```

```

Qy      12 GKHLNSMERVEWLRKKLQDVHNF 34
        ||||||||||||||||||||
Db      12 GKHLNSMERVEWLRKKLQDVHNF 34

```

RESULT 27

US-09-044-536A-13

; Sequence 13, Application US/09044536A

; Patent No. 6025467

; GENERAL INFORMATION:

; APPLICANT: FUKUDA, Tsunehiko

; APPLICANT: NAKAGAWA, Shizue

; APPLICANT: HABASHITA, Junko

; APPLICANT: TAKETOMI, Shigehisa

; TITLE OF INVENTION: PARATHYROID HORMONE DERIVATIVES AND THEIR USE

; NUMBER OF SEQUENCES: 36

; CORRESPONDENCE ADDRESS:

; ADDRESSEE: DIKE, BRONSTEIN, ROBERTS & CUSHMAN

; STREET: 130 Water Street

; CITY: Boston

; STATE: Massachusetts

; COUNTRY: US

; ZIP: 02109

; COMPUTER READABLE FORM:

; MEDIUM TYPE: Floppy disk

; COMPUTER: IBM PC compatible

; OPERATING SYSTEM: PC-DOS/MS-DOS

; SOFTWARE: PatentIn Release #1.0, Version #1.30

; CURRENT APPLICATION DATA:

; APPLICATION NUMBER: US/09/044,536A

; FILING DATE: 19-MAR-1998

; PRIOR APPLICATION DATA:

; APPLICATION NUMBER: 08/662,871

; FILING DATE: 12-JUN-1996

; ATTORNEY/AGENT INFORMATION:

; NAME: CONLIN, David G

; REGISTRATION NUMBER: 27,026

; REFERENCE/DOCKET NUMBER: 46509-DIV

; TELECOMMUNICATION INFORMATION:

; TELEPHONE: (617) 523-3400

; TELEFAX: (617)523-6440
 ; INFORMATION FOR SEQ ID NO: 13:
 ; SEQUENCE CHARACTERISTICS:
 ; LENGTH: 34 amino acids
 ; TYPE: amino acid
 ; STRANDEDNESS:
 ; TOPOLOGY: linear
 ; MOLECULE TYPE: peptide
 ; FEATURE:
 ; NAME/KEY: partial peptide
 ; LOCATION: 1..34
 ; FEATURE:
 ; NAME/KEY: Modified-site
 ; LOCATION: 10
 ; OTHER INFORMATION: /product= "Xaa=4-carboxyglutamic
 ; OTHER INFORMATION: acid"
 US-09-044-536A-13

Query Match 67.6%; Score 23; DB 3; Length 34;
 Best Local Similarity 100.0%; Pred. No. 3.4e-16;
 Matches 23; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 12 GKHLNSMERVEWLRKKLQDVHNF 34
 ||||||||||||||||||
 Db 12 GKHLNSMERVEWLRKKLQDVHNF 34

RESULT 28

US-09-044-536A-14

; Sequence 14, Application US/09044536A
 ; Patent No. 6025467
 ; GENERAL INFORMATION:
 ; APPLICANT: FUKUDA, Tsunehiko
 ; APPLICANT: NAKAGAWA, Shizue
 ; APPLICANT: HABASHITA, Junko
 ; APPLICANT: TAKETOMI, Shigehisa
 ; TITLE OF INVENTION: PARATHYROID HORMONE DERIVATIVES AND THEIR USE
 ; NUMBER OF SEQUENCES: 36
 ; CORRESPONDENCE ADDRESS:
 ; ADDRESSEE: DIKE, BRONSTEIN, ROBERTS & CUSHMAN
 ; STREET: 130 Water Street
 ; CITY: Boston
 ; STATE: Massachusetts
 ; COUNTRY: US
 ; ZIP: 02109
 ; COMPUTER READABLE FORM:
 ; MEDIUM TYPE: Floppy disk
 ; COMPUTER: IBM PC compatible
 ; OPERATING SYSTEM: PC-DOS/MS-DOS
 ; SOFTWARE: PatentIn Release #1.0, Version #1.30
 ; CURRENT APPLICATION DATA:
 ; APPLICATION NUMBER: US/09/044,536A
 ; FILING DATE: 19-MAR-1998
 ; PRIOR APPLICATION DATA:
 ; APPLICATION NUMBER: 08/662,871
 ; FILING DATE: 12-JUN-1996
 ; ATTORNEY/AGENT INFORMATION:

```

; NAME: CONLIN, David G
; REGISTRATION NUMBER: 27,026
; REFERENCE/DOCKET NUMBER: 46509-DIV
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (617)523-3400
; TELEFAX: (617)523-6440
; INFORMATION FOR SEQ ID NO: 14:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 34 amino acids
; TYPE: amino acid
; STRANDEDNESS:
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
; FEATURE:
; NAME/KEY: partial peptide
; LOCATION: 1..34
; FEATURE:
; NAME/KEY: Modified-site
; LOCATION: 10
; OTHER INFORMATION: /product= "Xaa=2-aminosuberic acid"
US-09-044-536A-14

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Query Match          67.6%; Score 23; DB 3; Length 34;
Best Local Similarity 100.0%; Pred. No. 3.4e-16;
Matches 23; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Qy      12 GKHLNSMERVEWLRKKLQDVHNF 34
        ||||||||||||||||||||
Db      12 GKHLNSMERVEWLRKKLQDVHNF 34

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RESULT 29

US-09-044-536A-15

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; Sequence 15, Application US/09044536A
; Patent No. 6025467
; GENERAL INFORMATION:
; APPLICANT: FUKUDA, Tsunehiko
; APPLICANT: NAKAGAWA, Shizue
; APPLICANT: HABASHITA, Junko
; APPLICANT: TAKETOMI, Shigehisa
; TITLE OF INVENTION: PARATHYROID HORMONE DERIVATIVES AND THEIR USE
; NUMBER OF SEQUENCES: 36
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: DIKE, BRONSTEIN, ROBERTS & CUSHMAN
; STREET: 130 Water Street
; CITY: Boston
; STATE: Massachusetts
; COUNTRY: US
; ZIP: 02109
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/044,536A
; FILING DATE: 19-MAR-1998

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```

; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/662,871
; FILING DATE: 12-JUN-1996
; ATTORNEY/AGENT INFORMATION:
; NAME: CONLIN, David G
; REGISTRATION NUMBER: 27,026
; REFERENCE/DOCKET NUMBER: 46509-DIV
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (617)523-3400
; TELEFAX: (617)523-6440
; INFORMATION FOR SEQ ID NO: 15:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 34 amino acids
; TYPE: amino acid
; STRANDEDNESS:
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
; FEATURE:
; NAME/KEY: partial peptide
; LOCATION: 1..34
; FEATURE:
; NAME/KEY: Modified-site
; LOCATION: 10
; OTHER INFORMATION: /product= "2-aminoadipic acid"
US-09-044-536A-15

```

```

Query Match          67.6%; Score 23; DB 3; Length 34;
Best Local Similarity 100.0%; Pred. No. 3.4e-16;
Matches 23; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Qy      12 GKHLNSMERVEWLRKKLQDVHNF 34
        ||||||||||||||||||||
Db      12 GKHLNSMERVEWLRKKLQDVHNF 34

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RESULT 30

US-08-904-760B-22

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; Sequence 22, Application US/08904760B
; Patent No. 6110892
; GENERAL INFORMATION:
; APPLICANT: Jean-Rene, Barbier
; APPLICANT: Neugebauer, Witold
; APPLICANT: Ross, Virginia
; APPLICANT: Whitfield, James
; APPLICANT: Willick, Gordon E.
; TITLE OF INVENTION: PARATHYROID HORMONE ANALOGUES FOR THE
; TITLE OF INVENTION: TREATMENT OF OSTEOPOROSIS
; NUMBER OF SEQUENCES: 35
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: NIXON & VANDERHYE P.C.
; STREET: 1100 No. 6110892th Glebe Rd. 8th floor
; CITY: Arlington
; STATE: VA
; COUNTRY: USA
; ZIP: 22201-4741
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk

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;     COMPUTER:  IBM PC compatible
;     OPERATING SYSTEM:  PC-DOS/MS-DOS
;     SOFTWARE:  PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
;     APPLICATION NUMBER:  US/08/904,760B
;     FILING DATE:  01-AUG-1997
;     CLASSIFICATION:  514
; PRIOR APPLICATION DATA:
;     APPLICATION NUMBER:  08/691,647
;     FILING DATE:  02-AUG-1996
; ATTORNEY/AGENT INFORMATION:
;     NAME:  Crawford, Arthur R.
;     REGISTRATION NUMBER:  25,327
;     REFERENCE/DOCKET NUMBER:  1339-6
; TELECOMMUNICATION INFORMATION:
;     TELEPHONE:  703-816-4000
;     TELEFAX:  703-816-4100
; INFORMATION FOR SEQ ID NO:  22:
;     SEQUENCE CHARACTERISTICS:
;     LENGTH:  34 amino acids
;     TYPE:  amino acid
;     STRANDEDNESS:
;     TOPOLOGY:  linear
;     MOLECULE TYPE:  protein
US-08-904-760B-22

```

```

Query Match          67.6%;  Score 23;  DB 3;  Length 34;
Best Local Similarity 100.0%;  Pred. No. 3.4e-16;
Matches   23;  Conservative   0;  Mismatches   0;  Indels   0;  Gaps   0;

```

```

QY      12 GKHLNSMERVEWLRKKLQDVHNF 34
        ||||||||||||||||||||
Db      12 GKHLNSMERVEWLRKKLQDVHNF 34

```

RESULT 31

US-09-108-661-13

; Sequence 13, Application US/09108661

; Patent No. 6287806

; GENERAL INFORMATION:

; APPLICANT: NISHIMURA, Osamu

; APPLICANT: KURIYAMA, Masato

; APPLICANT: KOYAMA, No. 6287806uyuki

; APPLICANT: FUKUDA, Tsunehiko

; TITLE OF INVENTION: METHOD FOR PRODUCING A BIOLOGICALLY

; TITLE OF INVENTION: ACTIVE RECOMBINANT CYSTEINE-FREE

; NUMBER OF SEQUENCES: 37

; CORRESPONDENCE ADDRESS:

; ADDRESSEE: DIKE, BRONSTEIN, ROBERTS & CUSHMAN, LLP

; STREET: 130 WATER STREET

; CITY: BOSTON

; STATE: MA

; COUNTRY: USA

; ZIP: 02109

; COMPUTER READABLE FORM:

; MEDIUM TYPE: Diskette

; COMPUTER: IBM Compatible

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;   OPERATING SYSTEM:  DOS
;   SOFTWARE:  FastSEQ Version 1.5
;   CURRENT APPLICATION DATA:
;   APPLICATION NUMBER:  US/09/108,661
;   FILING DATE:
;   CLASSIFICATION:  435
;   PRIOR APPLICATION DATA:
;   APPLICATION NUMBER:  08/350,709
;   FILING DATE:  07-DEC-1994
;   APPLICATION NUMBER:  07/838,857
;   FILING DATE:  18-FEB-1992
;   APPLICATION NUMBER:  JP 024841
;   FILING DATE:  19-FEB-1991
;   APPLICATION NUMBER:  JP 0271438
;   FILING DATE:  18-OCT-1991
;   ATTORNEY/AGENT INFORMATION:
;   NAME:  DAVID, RESNICK S
;   REGISTRATION NUMBER:  34,235
;   REFERENCE/DOCKET NUMBER:  41614-FWC
;   TELECOMMUNICATION INFORMATION:
;   TELEPHONE:  617-523-3400
;   TELEFAX:  617-523-6440
;   TELEX:  200291 STRE
;   INFORMATION FOR SEQ ID NO:  13:
;   SEQUENCE CHARACTERISTICS:
;   LENGTH:  34 amino acids
;   TYPE:  amino acid
;   STRANDEDNESS:  single
;   TOPOLOGY:  linear
;   MOLECULE TYPE:  peptide
;   HYPOTHETICAL:  NO
;   ANTI-SENSE:  NO
;   FRAGMENT TYPE:  N-terminal
;   ORIGINAL SOURCE:
US-09-108-661-13

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Query Match          67.6%;  Score 23;  DB 3;  Length 34;
Best Local Similarity 100.0%;  Pred. No. 3.4e-16;
Matches 23;  Conservative 0;  Mismatches 0;  Indels 0;  Gaps 0;

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QY      12 GKHLNSMERVEWLRKKLQDVHNF 34
        ||||||||||||||||||||
Db      12 GKHLNSMERVEWLRKKLQDVHNF 34

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RESULT 32

US-09-007-466-6

```

; Sequence 6, Application US/09007466
; Patent No. 6313092
; GENERAL INFORMATION:
;   APPLICANT:  HOLLADAY, LESLIE A.
;   APPLICANT:  OLDENBURG, KEVIN R.
;   TITLE OF INVENTION:  METHOD FOR INCREASING THE
;   TITLE OF INVENTION:  ELECTROTRANSPORT FLUX OF POLYPEPTIDES
;   NUMBER OF SEQUENCES:  10
;   CORRESPONDENCE ADDRESS:
;   ADDRESSEE:  ALZA CORPORATION

```

; STREET: 950 PAGE MILL ROAD
 ; CITY: PALO ALTO
 ; STATE: CALIFORNIA
 ; COUNTRY: USA
 ; ZIP: 94303-0802
 ; COMPUTER READABLE FORM:
 ; MEDIUM TYPE: Floppy disk
 ; COMPUTER: IBM PC compatible
 ; OPERATING SYSTEM: PC-DOS/MS-DOS
 ; SOFTWARE: PatentIn Release #1.0, Version #1.30
 ; CURRENT APPLICATION DATA:
 ; APPLICATION NUMBER: US/09/007,466
 ; FILING DATE:
 ; CLASSIFICATION:
 ; PRIOR APPLICATION DATA:
 ; APPLICATION NUMBER: US 08/468,275
 ; FILING DATE: 06-JUN-1995
 ; ATTORNEY/AGENT INFORMATION:
 ; NAME: MILLER, D. BYRON
 ; REGISTRATION NUMBER: 30,661
 ; REFERENCE/DOCKET NUMBER: 0360-0002; ARC-2349
 ; TELECOMMUNICATION INFORMATION:
 ; TELEPHONE: (415) 496-8150
 ; TELEFAX: (415) 496-8048
 ; INFORMATION FOR SEQ ID NO: 6:
 ; SEQUENCE CHARACTERISTICS:
 ; LENGTH: 34 amino acids
 ; TYPE: amino acid
 ; STRANDEDNESS: single
 ; TOPOLOGY: linear
 ; MOLECULE TYPE: protein
 US-09-007-466-6

Query Match 67.6%; Score 23; DB 4; Length 34;
 Best Local Similarity 100.0%; Pred. No. 3.4e-16;
 Matches 23; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 12 GKHLNSMERVEWLRKKLQDVHNF 34
 |||||
 Db 12 GKHLNSMERVEWLRKKLQDVHNF 34

RESULT 33

US-09-406-813-1

; Sequence 1, Application US/09406813
 ; Patent No. 6316410
 ; GENERAL INFORMATION:
 ; APPLICANT: Barbier, Jean-Rene
 ; APPLICANT: Morley, Paul
 ; APPLICANT: Whitfield, James
 ; APPLICANT: Willick, Gordon E.
 ; TITLE OF INVENTION: PARATHYROID HORMONE ANALOGUES FOR THE TREATMENT OF
 ; TITLE OF INVENTION: OSTEOPOROSIS
 ; FILE REFERENCE: 10688-1B
 ; CURRENT APPLICATION NUMBER: US/09/406,813
 ; CURRENT FILING DATE: 1999-09-22
 ; PRIOR APPLICATION NUMBER: 08/904,760

; PRIOR FILING DATE: 1997-08-01
; NUMBER OF SEQ ID NOS: 9
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 1
; LENGTH: 34
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-406-813-1

Query Match 67.6%; Score 23; DB 4; Length 34;
Best Local Similarity 100.0%; Pred. No. 3.4e-16;
Matches 23; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 12 GKHLNSMERVEWLRKKLQDVHNF 34
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Db 12 GKHLNSMERVEWLRKKLQDVHNF 34

RESULT 34

US-08-952-980B-6

; Sequence 6, Application US/08952980B

; Patent No. 6333189

; GENERAL INFORMATION:

; APPLICANT: HOLLADAY, LESLIE A.

; APPLICANT: OLDENBURG, KEVIN R.

; TITLE OF INVENTION: METHOD FOR INCREASING THE

; TITLE OF INVENTION: ELECTROTRANSPORT FLUX OF POLYPEPTIDES

; NUMBER OF SEQUENCES: 12

; CORRESPONDENCE ADDRESS:

; ADDRESSEE: ALZA CORPORATION

; STREET: 950 PAGE MILL ROAD

; CITY: PALO ALTO

; STATE: CALIFORNIA

; COUNTRY: USA

; ZIP: 94303-0802

; COMPUTER READABLE FORM:

; MEDIUM TYPE: Floppy disk

; COMPUTER: IBM PC compatible

; OPERATING SYSTEM: PC-DOS/MS-DOS

; SOFTWARE: PatentIn Release #1.0, Version #1.30

; CURRENT APPLICATION DATA:

; APPLICATION NUMBER: US/08/952,980B

; FILING DATE: 20-NOV-1997

; CLASSIFICATION: 530

; ATTORNEY/AGENT INFORMATION:

; NAME: MILLER, D. BYRON

; REGISTRATION NUMBER: 30,661

; REFERENCE/DOCKET NUMBER: 2349 CIP 1

; TELECOMMUNICATION INFORMATION:

; TELEPHONE: (650) 496-8150

; TELEFAX: (650) 496-8048

; INFORMATION FOR SEQ ID NO: 6:

; SEQUENCE CHARACTERISTICS:

; LENGTH: 34 amino acids

; TYPE: amino acid

; STRANDEDNESS: single

; TOPOLOGY: linear

; MOLECULE TYPE: protein
US-08-952-980B-6

Query Match 67.6%; Score 23; DB 4; Length 34;
Best Local Similarity 100.0%; Pred. No. 3.4e-16;
Matches 23; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 12 GKHLNSMERVEWLRKKLQDVHNF 34
| | | | | | | | | | | | | | | | | |
Db 12 GKHLNSMERVEWLRKKLQDVHNF 34

RESULT 35

US-09-228-990-1

; Sequence 1, Application US/09228990
; Patent No. 6472505

; GENERAL INFORMATION:

; APPLICANT: Condon, Stephen M.
; APPLICANT: Morize, Isabelle
; TITLE OF INVENTION: PEPTIDE PARATHYROID HORMONE ANALOGS
; NUMBER OF SEQUENCES: 88
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Rhone-Poulenc Rorer Inc.
; STREET: 500 Arcola Road, Mailstop 3C43
; CITY: Collegeville
; STATE: PA
; COUNTRY: USA
; ZIP: 19426

; COMPUTER READABLE FORM:

; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30

; CURRENT APPLICATION DATA:

; APPLICATION NUMBER: US/09/228,990
; FILING DATE:
; CLASSIFICATION:

; PRIOR APPLICATION DATA:

; APPLICATION NUMBER: US 60/046,472
; FILING DATE: 14-MAY-1997

; ATTORNEY/AGENT INFORMATION:

; NAME: Martin Esq., Michael B.
; REGISTRATION NUMBER: 37,521
; REFERENCE/DOCKET NUMBER: A2678B-WO

; TELECOMMUNICATION INFORMATION:

; TELEPHONE: (610) 454-2793
; TELEFAX: (610) 454-3808

; INFORMATION FOR SEQ ID NO: 1:

; SEQUENCE CHARACTERISTICS:

; LENGTH: 34 amino acids
; TYPE: amino acid
; STRANDEDNESS:

; TOPOLOGY: not relevant

; MOLECULE TYPE: peptide

; FRAGMENT TYPE: N-terminal

US-09-228-990-1

Query Match 67.6%; Score 23; DB 4; Length 34;
Best Local Similarity 100.0%; Pred. No. 3.4e-16;
Matches 23; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 12 GKHLNSMERVEWLRKKLQDVHNF 34
| | | | | | | | | | | | | | | | | |
Db 12 GKHLNSMERVEWLRKKLQDVHNF 34

RESULT 36

US-09-447-800-1
; Sequence 1, Application US/09447800
; Patent No. 6537965
; GENERAL INFORMATION:
; APPLICANT: BRINGHURST, F. RICHARD
; APPLICANT: TAKASU, HISASHI
; APPLICANT: GARDELLA, THOMAS J.
; TITLE OF INVENTION: AMINO-TERMINAL MODIFIED PARATHYROID HORMONE (PTH)
; TITLE OF INVENTION: ANALOGS
; FILE REFERENCE: 0609.4630001
; CURRENT APPLICATION NUMBER: US/09/447,800
; CURRENT FILING DATE: 1999-11-23
; EARLIER APPLICATION NUMBER: 60/110,152
; EARLIER FILING DATE: 1998-11-25
; NUMBER OF SEQ ID NOS: 10
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 1
; LENGTH: 34
; TYPE: PRT
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: UNSURE
; LOCATION: (1)
; OTHER INFORMATION: Can be desamino Ser, desamino Ala, or desamino Gly
US-09-447-800-1

Query Match 67.6%; Score 23; DB 4; Length 34;
Best Local Similarity 100.0%; Pred. No. 3.4e-16;
Matches 23; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 12 GKHLNSMERVEWLRKKLQDVHNF 34
| | | | | | | | | | | | | | | | | |
Db 12 GKHLNSMERVEWLRKKLQDVHNF 34

RESULT 37

US-09-447-800-2
; Sequence 2, Application US/09447800
; Patent No. 6537965
; GENERAL INFORMATION:
; APPLICANT: BRINGHURST, F. RICHARD
; APPLICANT: TAKASU, HISASHI
; APPLICANT: GARDELLA, THOMAS J.
; TITLE OF INVENTION: AMINO-TERMINAL MODIFIED PARATHYROID HORMONE (PTH)
; TITLE OF INVENTION: ANALOGS
; FILE REFERENCE: 0609.4630001
; CURRENT APPLICATION NUMBER: US/09/447,800

; CURRENT FILING DATE: 1999-11-23
; EARLIER APPLICATION NUMBER: 60/110,152
; EARLIER FILING DATE: 1998-11-25
; NUMBER OF SEQ ID NOS: 10
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 2
; LENGTH: 34
; TYPE: PRT
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: MOD_RES
; LOCATION: (1)
; OTHER INFORMATION: Desamino Gly
US-09-447-800-2

Query Match 67.6%; Score 23; DB 4; Length 34;
Best Local Similarity 100.0%; Pred. No. 3.4e-16;
Matches 23; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 12 GKHLNSMERVEWLRKKLQDVHNF 34
| | | | | | | | | | | | | | | | | |
Db 12 GKHLNSMERVEWLRKKLQDVHNF 34

RESULT 38

US-09-447-800-5

; Sequence 5, Application US/09447800
; Patent No. 6537965
; GENERAL INFORMATION:
; APPLICANT: BRINGHURST, F. RICHARD
; APPLICANT: TAKASU, HISASHI
; APPLICANT: GARDELLA, THOMAS J.
; TITLE OF INVENTION: AMINO-TERMINAL MODIFIED PARATHYROID HORMONE (PTH)
; TITLE OF INVENTION: ANALOGS
; FILE REFERENCE: 0609.4630001
; CURRENT APPLICATION NUMBER: US/09/447,800
; CURRENT FILING DATE: 1999-11-23
; EARLIER APPLICATION NUMBER: 60/110,152
; EARLIER FILING DATE: 1998-11-25
; NUMBER OF SEQ ID NOS: 10
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 5
; LENGTH: 34
; TYPE: PRT
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: MOD_RES
; LOCATION: (1)
; OTHER INFORMATION: Desamino Ala
US-09-447-800-5

Query Match 67.6%; Score 23; DB 4; Length 34;
Best Local Similarity 100.0%; Pred. No. 3.4e-16;
Matches 23; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 12 GKHLNSMERVEWLRKKLQDVHNF 34
| | | | | | | | | | | | | | | | | |

Db 12 GKHLNSMERVEWLRKKLQDVHNF 34

RESULT 39

US-09-447-800-8

; Sequence 8, Application US/09447800
; Patent No. 6537965
; GENERAL INFORMATION:
; APPLICANT: BRINGHURST, F. RICHARD
; APPLICANT: TAKASU, HISASHI
; APPLICANT: GARDELLA, THOMAS J.
; TITLE OF INVENTION: AMINO-TERMINAL MODIFIED PARATHYROID HORMONE (PTH)
; TITLE OF INVENTION: ANALOGS
; FILE REFERENCE: 0609.4630001
; CURRENT APPLICATION NUMBER: US/09/447,800
; CURRENT FILING DATE: 1999-11-23
; EARLIER APPLICATION NUMBER: 60/110,152
; EARLIER FILING DATE: 1998-11-25
; NUMBER OF SEQ ID NOS: 10
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 8
; LENGTH: 34
; TYPE: PRT
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: MOD_RES
; LOCATION: (1)
; OTHER INFORMATION: Desamino Ser
US-09-447-800-8

Query Match 67.6%; Score 23; DB 4; Length 34;
Best Local Similarity 100.0%; Pred. No. 3.4e-16;
Matches 23; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 12 GKHLNSMERVEWLRKKLQDVHNF 34
| | | | | | | | | | | | | | | | | | | | | |
Db 12 GKHLNSMERVEWLRKKLQDVHNF 34

RESULT 40

US-09-536-785A-22

; Sequence 22, Application US/09536785A
; Patent No. 6541450
; GENERAL INFORMATION:
; APPLICANT: BARBIER, JEAN-RENE
; APPLICANT: MORLEY, PAUL
; APPLICANT: NEUGEBAUER, WITOLD
; APPLICANT: ROSS, VIRGINIA J.S.
; APPLICANT: WHITFIELD, JAMES F.
; APPLICANT: WILLICK, GORDON E.
; TITLE OF INVENTION: PARATHYROID HORMONE ANALOGUES FOR THE TREATMENT OF
; TITLE OF INVENTION: OSTEOPOROSIS
; FILE REFERENCE: 1339-9
; CURRENT APPLICATION NUMBER: US/09/536,785A
; CURRENT FILING DATE: 2000-03-28
; PRIOR APPLICATION NUMBER: 08/904,760
; PRIOR FILING DATE: 1997-08-01

; PRIOR APPLICATION NUMBER: 08/691,647
; PRIOR FILING DATE: 1996-08-02
; PRIOR APPLICATION NUMBER: 08/262,495
; PRIOR FILING DATE: 1994-06-20
; PRIOR APPLICATION NUMBER: 60/040,560
; PRIOR FILING DATE: 1997-03-14
; NUMBER OF SEQ ID NOS: 39
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 22
; LENGTH: 34
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-536-785A-22

Query Match 67.6%; Score 23; DB 4; Length 34;
Best Local Similarity 100.0%; Pred. No. 3.4e-16;
Matches 23; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 12 GKHLNSMERVEWLRKKLQDVHNF 34
| | | | | | | | | | | | | | | | | |
Db 12 GKHLNSMERVEWLRKKLQDVHNF 34

Search completed: January 14, 2004, 10:43:31
Job time : 13.5452 secs

GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: January 14, 2004, 10:28:19 ; Search time 10.0623 Seconds
(without alignments)
324.949 Million cell updates/sec

Title: US-09-843-221A-163
Perfect score: 34
Sequence: 1 SVSEIQLMHNKGKHLNSMERVEWLRKKLQDVHNF 34

Scoring table: OLIGO
Gapop 60.0 , Gapext 60.0

Searched: 283308 seqs, 96168682 residues

Word size : 0

Total number of hits satisfying chosen parameters: 3709

Minimum DB seq length: 28

Maximum DB seq length: 40

Post-processing: Listing first 1000 summaries

Database : PIR_76:*
1: pir1:*
2: pir2:*
3: pir3:*
4: pir4:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

| Result No. | Score | % Query Match | Length | DB | ID | Description |
|------------|-------|------------------|--------|----|--------|--------------------|
| 1 | 5 | 14.7 | 34 | 2 | A84241 | hypothetical prote |
| 2 | 5 | 14.7 | 34 | 2 | B97032 | transcription regu |
| 3 | 5 | 14.7 | 35 | 2 | E95098 | hypothetical prote |
| 4 | 4 | 11.8 | 28 | 2 | T09594 | gene LFY protein - |
| 5 | 4 | 11.8 | 29 | 1 | A55527 | pyrroloquinoline q |
| 6 | 4 | 11.8 | 29 | 2 | S01614 | dystrophin - rat (|
| 7 | 4 | 11.8 | 29 | 2 | I78537 | copper transportin |
| 8 | 4 | 11.8 | 29 | 2 | S78412 | ribosomal protein |
| 9 | 4 | 11.8 | 30 | 2 | S63531 | hypothetical prote |
| 10 | 4 | 11.8 | 31 | 2 | S44471 | glucagon G1 - Nort |
| 11 | 4 | 11.8 | 31 | 2 | S44472 | glucagon G2 - Nort |
| 12 | 4 | 11.8 | 31 | 2 | D70236 | hypothetical prote |
| 13 | 4 | 11.8 | 32 | 2 | F23454 | ovalbumin phosphos |

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|----|---|------|----|---|--------|--------------------|
| 14 | 4 | 11.8 | 32 | 2 | D31461 | T-cell receptor de |
| 15 | 4 | 11.8 | 32 | 2 | G84161 | hypothetical prote |
| 16 | 4 | 11.8 | 33 | 2 | E81714 | hypothetical prote |
| 17 | 4 | 11.8 | 35 | 2 | D23454 | ovalbumin phosphos |
| 18 | 4 | 11.8 | 35 | 2 | G23454 | ovalbumin phosphos |
| 19 | 4 | 11.8 | 35 | 2 | D82125 | hypothetical prote |
| 20 | 4 | 11.8 | 36 | 2 | S70806 | hypothetical prote |
| 21 | 4 | 11.8 | 36 | 2 | F95057 | hypothetical prote |
| 22 | 4 | 11.8 | 36 | 2 | A84774 | hypothetical prote |
| 23 | 4 | 11.8 | 36 | 2 | S46227 | hypothetical prote |
| 24 | 4 | 11.8 | 37 | 2 | S71912 | hemoglobin, extrac |
| 25 | 4 | 11.8 | 37 | 2 | T12635 | homeotic protein H |
| 26 | 4 | 11.8 | 37 | 2 | A43933 | antigen 5 epitope |
| 27 | 4 | 11.8 | 39 | 1 | CKFHCS | sarcotoxin IC - fl |
| 28 | 4 | 11.8 | 39 | 2 | S71913 | hemoglobin, extrac |
| 29 | 4 | 11.8 | 39 | 2 | S77164 | ycf32 protein - Sy |
| 30 | 3 | 8.8 | 28 | 2 | A42272 | brain-type creatin |
| 31 | 3 | 8.8 | 28 | 2 | C32416 | phospholipase A2 (|
| 32 | 3 | 8.8 | 28 | 2 | B60071 | vasoactive intesti |
| 33 | 3 | 8.8 | 28 | 2 | A60304 | vasoactive intesti |
| 34 | 3 | 8.8 | 28 | 2 | S58386 | T-cell receptor be |
| 35 | 3 | 8.8 | 28 | 2 | S10052 | ribosomal protein |
| 36 | 3 | 8.8 | 28 | 2 | A60752 | outer membrane pro |
| 37 | 3 | 8.8 | 28 | 2 | S56121 | type I DNA methylt |
| 38 | 3 | 8.8 | 28 | 2 | S70894 | hypothetical prote |
| 39 | 3 | 8.8 | 28 | 2 | S22469 | hypothetical prote |
| 40 | 3 | 8.8 | 28 | 2 | C60683 | malate dehydrogena |
| 41 | 3 | 8.8 | 28 | 2 | S06668 | toxin-like protein |
| 42 | 3 | 8.8 | 28 | 2 | S26254 | rel protein - chic |
| 43 | 3 | 8.8 | 28 | 2 | I59477 | antigen, T-cell re |
| 44 | 3 | 8.8 | 28 | 2 | F46522 | T-cell receptor et |
| 45 | 3 | 8.8 | 28 | 2 | H85908 | hypothetical prote |
| 46 | 3 | 8.8 | 29 | 1 | GCCB | glucagon - Chinch |
| 47 | 3 | 8.8 | 29 | 2 | S39968 | probable hydro-lya |
| 48 | 3 | 8.8 | 29 | 2 | S17147 | galanin - chicken |
| 49 | 3 | 8.8 | 29 | 2 | JH0699 | omega-conotoxin MV |
| 50 | 3 | 8.8 | 29 | 2 | T44245 | ribosomal protein |
| 51 | 3 | 8.8 | 29 | 2 | A05272 | gelsolin, cytosoli |
| 52 | 3 | 8.8 | 29 | 2 | B44101 | calmodulin, vasoac |
| 53 | 3 | 8.8 | 29 | 2 | S42642 | probable rhicadhes |
| 54 | 3 | 8.8 | 29 | 2 | A00774 | 3-oxoadipate enol- |
| 55 | 3 | 8.8 | 29 | 2 | I84189 | cyclic AMP recepto |
| 56 | 3 | 8.8 | 29 | 2 | S65747 | CDP-paratose synth |
| 57 | 3 | 8.8 | 29 | 2 | S65748 | CDP-paratose synth |
| 58 | 3 | 8.8 | 29 | 2 | B41476 | probable antigen 2 |
| 59 | 3 | 8.8 | 29 | 2 | T31443 | cytochrome bc chai |
| 60 | 3 | 8.8 | 29 | 2 | F85570 | hypothetical prote |
| 61 | 3 | 8.8 | 29 | 2 | I49732 | NADH2 dehydrogenas |
| 62 | 3 | 8.8 | 30 | 2 | S40309 | tyrosine 3-monooxy |
| 63 | 3 | 8.8 | 30 | 2 | C21897 | ornithine carbamoy |
| 64 | 3 | 8.8 | 30 | 2 | A05315 | pancreatic ribonuc |
| 65 | 3 | 8.8 | 30 | 2 | A61333 | trypsin (EC 3.4.21 |
| 66 | 3 | 8.8 | 30 | 2 | S21815 | H+-exporting ATPas |
| 67 | 3 | 8.8 | 30 | 2 | A44912 | cysteine proteinas |
| 68 | 3 | 8.8 | 30 | 2 | B61125 | glucagon-like pept |
| 69 | 3 | 8.8 | 30 | 2 | C61125 | glucagon-like pept |
| 70 | 3 | 8.8 | 30 | 2 | F32502 | T-cell receptor de |

| | | | | | | |
|-----|---|-----|----|---|--------|--------------------|
| 71 | 3 | 8.8 | 30 | 2 | PD0013 | cAMP response elem |
| 72 | 3 | 8.8 | 30 | 2 | S11617 | ribosomal protein |
| 73 | 3 | 8.8 | 30 | 2 | S21195 | spectrin beta chai |
| 74 | 3 | 8.8 | 30 | 2 | PC4172 | profilin - rat (fr |
| 75 | 3 | 8.8 | 30 | 2 | A34461 | heat shock protein |
| 76 | 3 | 8.8 | 30 | 2 | A22977 | delta-endotoxin - |
| 77 | 3 | 8.8 | 30 | 2 | S08565 | ribulose-bisphosph |
| 78 | 3 | 8.8 | 30 | 2 | S30333 | N-carbamoyl-D-amin |
| 79 | 3 | 8.8 | 30 | 2 | PQ0444 | hypothetical prote |
| 80 | 3 | 8.8 | 30 | 2 | B95020 | hypothetical prote |
| 81 | 3 | 8.8 | 30 | 2 | H95021 | hypothetical prote |
| 82 | 3 | 8.8 | 30 | 2 | D72276 | hypothetical prote |
| 83 | 3 | 8.8 | 30 | 2 | D70253 | conserved hypothet |
| 84 | 3 | 8.8 | 30 | 2 | B70165 | hypothetical prote |
| 85 | 3 | 8.8 | 30 | 2 | C81791 | hypothetical prote |
| 86 | 3 | 8.8 | 30 | 2 | E82294 | hypothetical prote |
| 87 | 3 | 8.8 | 30 | 2 | D82251 | hypothetical prote |
| 88 | 3 | 8.8 | 30 | 2 | F82209 | hypothetical prote |
| 89 | 3 | 8.8 | 30 | 2 | S72626 | small-cell-variant |
| 90 | 3 | 8.8 | 30 | 2 | A35687 | probable 39K inorg |
| 91 | 3 | 8.8 | 30 | 2 | A32946 | trypsin-like serin |
| 92 | 3 | 8.8 | 30 | 2 | S65519 | carcinoembryonic a |
| 93 | 3 | 8.8 | 30 | 2 | S34765 | 4-hydroxybutyryl-C |
| 94 | 3 | 8.8 | 30 | 2 | D81532 | hypothetical prote |
| 95 | 3 | 8.8 | 30 | 2 | A48923 | retrovirus-related |
| 96 | 3 | 8.8 | 30 | 2 | B56586 | storage hexamer 2 |
| 97 | 3 | 8.8 | 30 | 2 | F81360 | very hypothetical |
| 98 | 3 | 8.8 | 30 | 2 | S15650 | NADH2 dehydrogenas |
| 99 | 3 | 8.8 | 30 | 2 | H97596 | hypothetical prote |
| 100 | 3 | 8.8 | 30 | 4 | I52605 | hypothetical MLL/E |
| 101 | 3 | 8.8 | 31 | 2 | T44925 | hypothetical prote |
| 102 | 3 | 8.8 | 31 | 2 | S39019 | glucagon-like pept |
| 103 | 3 | 8.8 | 31 | 2 | A58793 | relaxin chain B - |
| 104 | 3 | 8.8 | 31 | 2 | A58586 | conotoxin MrVIA - |
| 105 | 3 | 8.8 | 31 | 2 | F30608 | Ig kappa chain V-I |
| 106 | 3 | 8.8 | 31 | 2 | D30608 | Ig kappa chain V-I |
| 107 | 3 | 8.8 | 31 | 2 | F31461 | T-cell receptor de |
| 108 | 3 | 8.8 | 31 | 2 | S03295 | Ig alpha chain C r |
| 109 | 3 | 8.8 | 31 | 2 | S03297 | Ig alpha chain C r |
| 110 | 3 | 8.8 | 31 | 2 | I52232 | tau protein - huma |
| 111 | 3 | 8.8 | 31 | 2 | A36162 | neutrophil-activat |
| 112 | 3 | 8.8 | 31 | 2 | S04980 | ferritin heavy cha |
| 113 | 3 | 8.8 | 31 | 2 | S32610 | antiviral protein |
| 114 | 3 | 8.8 | 31 | 2 | S38881 | inner membrane pro |
| 115 | 3 | 8.8 | 31 | 2 | G95018 | hypothetical prote |
| 116 | 3 | 8.8 | 31 | 2 | G95022 | hypothetical prote |
| 117 | 3 | 8.8 | 31 | 2 | A95085 | hypothetical prote |
| 118 | 3 | 8.8 | 31 | 2 | H95093 | hypothetical prote |
| 119 | 3 | 8.8 | 31 | 2 | E95151 | hypothetical prote |
| 120 | 3 | 8.8 | 31 | 2 | E70202 | hypothetical prote |
| 121 | 3 | 8.8 | 31 | 2 | E70223 | hypothetical prote |
| 122 | 3 | 8.8 | 31 | 2 | H70225 | hypothetical prote |
| 123 | 3 | 8.8 | 31 | 2 | C70240 | hypothetical prote |
| 124 | 3 | 8.8 | 31 | 2 | H70252 | hypothetical prote |
| 125 | 3 | 8.8 | 31 | 2 | S49191 | hypothetical prote |
| 126 | 3 | 8.8 | 31 | 2 | H82353 | hypothetical prote |
| 127 | 3 | 8.8 | 31 | 2 | B82151 | hypothetical prote |

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|-----|---|-----|----|---|--------|--------------------|
| 128 | 3 | 8.8 | 31 | 2 | A05051 | hypothetical prote |
| 129 | 3 | 8.8 | 31 | 2 | B23605 | histone H1.3 - whe |
| 130 | 3 | 8.8 | 31 | 2 | S78738 | protein YOL038c-a |
| 131 | 3 | 8.8 | 31 | 2 | A36221 | cecropin P1 - pig |
| 132 | 3 | 8.8 | 31 | 2 | S27112 | sarcolipin - rabbi |
| 133 | 3 | 8.8 | 31 | 2 | C84082 | hypothetical prote |
| 134 | 3 | 8.8 | 31 | 2 | D81591 | hypothetical prote |
| 135 | 3 | 8.8 | 31 | 2 | G81558 | hypothetical prote |
| 136 | 3 | 8.8 | 31 | 2 | G82816 | hypothetical prote |
| 137 | 3 | 8.8 | 31 | 2 | F82565 | hypothetical prote |
| 138 | 3 | 8.8 | 31 | 2 | C97398 | hypothetical prote |
| 139 | 3 | 8.8 | 32 | 1 | TCEE | calcitonin - Japan |
| 140 | 3 | 8.8 | 32 | 1 | TCON2 | calcitonin 2 - soc |
| 141 | 3 | 8.8 | 32 | 1 | TCON2C | calcitonin 2 - chu |
| 142 | 3 | 8.8 | 32 | 1 | TCON2P | calcitonin 2 - pin |
| 143 | 3 | 8.8 | 32 | 1 | TCON3 | calcitonin 3 - coh |
| 144 | 3 | 8.8 | 32 | 2 | S20719 | alcohol dehydrogen |
| 145 | 3 | 8.8 | 32 | 2 | A61143 | trypsin (EC 3.4.21 |
| 146 | 3 | 8.8 | 32 | 2 | D32502 | T-cell receptor de |
| 147 | 3 | 8.8 | 32 | 2 | A32502 | T-cell receptor de |
| 148 | 3 | 8.8 | 32 | 2 | B40186 | ubiquitin / riboso |
| 149 | 3 | 8.8 | 32 | 2 | S57780 | histone H3 - rice |
| 150 | 3 | 8.8 | 32 | 2 | A02687 | DNA-binding protei |
| 151 | 3 | 8.8 | 32 | 2 | S51524 | anchorin CII - bov |
| 152 | 3 | 8.8 | 32 | 2 | S36809 | GTP-binding regula |
| 153 | 3 | 8.8 | 32 | 2 | A29743 | translation initia |
| 154 | 3 | 8.8 | 32 | 2 | A03367 | lectin - Macrotylo |
| 155 | 3 | 8.8 | 32 | 2 | A44900 | fimbrin, SEF 21 - |
| 156 | 3 | 8.8 | 32 | 2 | S14300 | zona pellucida-bin |
| 157 | 3 | 8.8 | 32 | 2 | S03273 | photosystem II oxy |
| 158 | 3 | 8.8 | 32 | 2 | S08482 | regulatory protein |
| 159 | 3 | 8.8 | 32 | 2 | E87694 | hypothetical prote |
| 160 | 3 | 8.8 | 32 | 2 | D70222 | hypothetical prote |
| 161 | 3 | 8.8 | 32 | 2 | E70225 | hypothetical prote |
| 162 | 3 | 8.8 | 32 | 2 | B70241 | hypothetical prote |
| 163 | 3 | 8.8 | 32 | 2 | B70257 | hypothetical prote |
| 164 | 3 | 8.8 | 32 | 2 | D82353 | hypothetical prote |
| 165 | 3 | 8.8 | 32 | 2 | E82279 | hypothetical prote |
| 166 | 3 | 8.8 | 32 | 2 | E82089 | hypothetical prote |
| 167 | 3 | 8.8 | 32 | 2 | H82416 | hypothetical prote |
| 168 | 3 | 8.8 | 32 | 2 | T17394 | vrlN protein - Dic |
| 169 | 3 | 8.8 | 32 | 2 | S23476 | hypothetical prote |
| 170 | 3 | 8.8 | 32 | 2 | S22304 | hypothetical prote |
| 171 | 3 | 8.8 | 32 | 2 | S78323 | photosystem II pro |
| 172 | 3 | 8.8 | 32 | 2 | I38619 | zinc finger protei |
| 173 | 3 | 8.8 | 32 | 2 | S28398 | t-complex protein |
| 174 | 3 | 8.8 | 32 | 2 | T14569 | hypothetical prote |
| 175 | 3 | 8.8 | 32 | 2 | H84081 | hypothetical prote |
| 176 | 3 | 8.8 | 32 | 2 | F82833 | hypothetical prote |
| 177 | 3 | 8.8 | 32 | 2 | JC5802 | ovulation stimulat |
| 178 | 3 | 8.8 | 32 | 2 | E85588 | hypothetical prote |
| 179 | 3 | 8.8 | 33 | 2 | S43312 | 2',3'-cyclic-nucle |
| 180 | 3 | 8.8 | 33 | 2 | S26859 | chitinase (EC 3.2. |
| 181 | 3 | 8.8 | 33 | 2 | I52219 | c-ras-Ki-2 protein |
| 182 | 3 | 8.8 | 33 | 2 | I53221 | K-ras protein - hu |
| 183 | 3 | 8.8 | 33 | 2 | E32502 | T-cell receptor de |
| 184 | 3 | 8.8 | 33 | 2 | A31461 | T-cell receptor de |

| | | | | | | |
|-----|---|-----|----|---|--------|--------------------|
| 185 | 3 | 8.8 | 33 | 2 | B31461 | T-cell receptor de |
| 186 | 3 | 8.8 | 33 | 2 | S22604 | ribosomal protein |
| 187 | 3 | 8.8 | 33 | 2 | A03150 | retinoic acid-bind |
| 188 | 3 | 8.8 | 33 | 2 | C46027 | neurotransmitter t |
| 189 | 3 | 8.8 | 33 | 2 | PQ0150 | dnaK-type molecula |
| 190 | 3 | 8.8 | 33 | 2 | B44906 | L1 protein - human |
| 191 | 3 | 8.8 | 33 | 2 | PQ0418 | matrix protein M1 |
| 192 | 3 | 8.8 | 33 | 2 | S34505 | hypothetical prote |
| 193 | 3 | 8.8 | 33 | 2 | G95006 | hypothetical prote |
| 194 | 3 | 8.8 | 33 | 2 | C95200 | hypothetical prote |
| 195 | 3 | 8.8 | 33 | 2 | F84163 | hypothetical prote |
| 196 | 3 | 8.8 | 33 | 2 | H82475 | hypothetical prote |
| 197 | 3 | 8.8 | 33 | 2 | S68096 | lactate dehydrogen |
| 198 | 3 | 8.8 | 33 | 2 | E82526 | hypothetical prote |
| 199 | 3 | 8.8 | 33 | 2 | G85600 | hypothetical prote |
| 200 | 3 | 8.8 | 33 | 2 | H85651 | hypothetical prote |
| 201 | 3 | 8.8 | 33 | 2 | AC1012 | hypothetical prote |
| 202 | 3 | 8.8 | 33 | 2 | C97406 | hypothetical prote |
| 203 | 3 | 8.8 | 34 | 2 | S57282 | phospholipase A2 (|
| 204 | 3 | 8.8 | 34 | 2 | A40298 | dermaseptin - Sauv |
| 205 | 3 | 8.8 | 34 | 2 | JS0426 | big gastrin - goat |
| 206 | 3 | 8.8 | 34 | 2 | I48887 | cryptdin-4 - mouse |
| 207 | 3 | 8.8 | 34 | 2 | I32502 | T-cell receptor de |
| 208 | 3 | 8.8 | 34 | 2 | H31461 | T-cell receptor de |
| 209 | 3 | 8.8 | 34 | 2 | A19197 | class II histocomp |
| 210 | 3 | 8.8 | 34 | 2 | D48147 | troponin I (altern |
| 211 | 3 | 8.8 | 34 | 2 | A43564 | neurogenic protein |
| 212 | 3 | 8.8 | 34 | 2 | H95047 | hypothetical prote |
| 213 | 3 | 8.8 | 34 | 2 | D95189 | hypothetical prote |
| 214 | 3 | 8.8 | 34 | 2 | C90973 | hypothetical prote |
| 215 | 3 | 8.8 | 34 | 2 | F70242 | hypothetical prote |
| 216 | 3 | 8.8 | 34 | 2 | B70252 | hypothetical prote |
| 217 | 3 | 8.8 | 34 | 2 | F81919 | hypothetical prote |
| 218 | 3 | 8.8 | 34 | 2 | F81044 | hypothetical prote |
| 219 | 3 | 8.8 | 34 | 2 | F82163 | hypothetical prote |
| 220 | 3 | 8.8 | 34 | 2 | E82100 | hypothetical prote |
| 221 | 3 | 8.8 | 34 | 2 | B82449 | hypothetical prote |
| 222 | 3 | 8.8 | 34 | 2 | S13662 | cellulase (EC 3.2. |
| 223 | 3 | 8.8 | 34 | 2 | A60110 | repetitive protein |
| 224 | 3 | 8.8 | 34 | 2 | S44828 | F54F2.3 protein - |
| 225 | 3 | 8.8 | 34 | 2 | S40662 | P-cadherin - mouse |
| 226 | 3 | 8.8 | 34 | 2 | F84079 | hypothetical prote |
| 227 | 3 | 8.8 | 34 | 2 | H81600 | hypothetical prote |
| 228 | 3 | 8.8 | 34 | 2 | H82820 | hypothetical prote |
| 229 | 3 | 8.8 | 34 | 2 | C82819 | hypothetical prote |
| 230 | 3 | 8.8 | 34 | 2 | C82764 | hypothetical prote |
| 231 | 3 | 8.8 | 34 | 2 | B82679 | hypothetical prote |
| 232 | 3 | 8.8 | 34 | 2 | G85820 | unknown protein en |
| 233 | 3 | 8.8 | 34 | 2 | S12554 | hydroxymethylgluta |
| 234 | 3 | 8.8 | 35 | 2 | JH0639 | GTP-binding protei |
| 235 | 3 | 8.8 | 35 | 2 | S06667 | toxin-like protein |
| 236 | 3 | 8.8 | 35 | 2 | E38601 | Ig kappa chain V r |
| 237 | 3 | 8.8 | 35 | 2 | A05302 | hemoglobin beta ch |
| 238 | 3 | 8.8 | 35 | 2 | S27154 | ribosomal protein |
| 239 | 3 | 8.8 | 35 | 2 | S13435 | lectin III - furze |
| 240 | 3 | 8.8 | 35 | 2 | S18224 | filamentous hemagg |
| 241 | 3 | 8.8 | 35 | 2 | S18226 | opacity protein op |

| | | | | | | |
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| 242 | 3 | 8.8 | 35 | 2 | T07870 | major latex protei |
| 243 | 3 | 8.8 | 35 | 2 | B33770 | hypothetical prote |
| 244 | 3 | 8.8 | 35 | 2 | PS0439 | potassium channel |
| 245 | 3 | 8.8 | 35 | 2 | I48925 | homeobox protein - |
| 246 | 3 | 8.8 | 35 | 2 | G95014 | hypothetical prote |
| 247 | 3 | 8.8 | 35 | 2 | F87622 | hypothetical prote |
| 248 | 3 | 8.8 | 35 | 2 | C96619 | protein T30E16.7 [|
| 249 | 3 | 8.8 | 35 | 2 | B84674 | hypothetical prote |
| 250 | 3 | 8.8 | 35 | 2 | F84395 | hypothetical prote |
| 251 | 3 | 8.8 | 35 | 2 | B82012 | hypothetical prote |
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| 253 | 3 | 8.8 | 35 | 2 | A82151 | hypothetical prote |
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| 259 | 3 | 8.8 | 35 | 2 | S65772 | early nodulin 40 - |
| 260 | 3 | 8.8 | 35 | 2 | G60529 | hemocyanin M3' - c |
| 261 | 3 | 8.8 | 35 | 2 | S49309 | oncofetal protein |
| 262 | 3 | 8.8 | 35 | 2 | C81560 | hypothetical prote |
| 263 | 3 | 8.8 | 35 | 2 | B85708 | unknown protein en |
| 264 | 3 | 8.8 | 36 | 2 | H32502 | T-cell receptor de |
| 265 | 3 | 8.8 | 36 | 2 | C32502 | T-cell receptor de |
| 266 | 3 | 8.8 | 36 | 2 | S08552 | ribosomal protein |
| 267 | 3 | 8.8 | 36 | 2 | S72299 | ribosomal protein |
| 268 | 3 | 8.8 | 36 | 2 | I46593 | myosin - pig (frag |
| 269 | 3 | 8.8 | 36 | 2 | B31872 | retinoic acid-bind |
| 270 | 3 | 8.8 | 36 | 2 | S35572 | zona pellucida pro |
| 271 | 3 | 8.8 | 36 | 2 | B41481 | virulence-associat |
| 272 | 3 | 8.8 | 36 | 2 | A38659 | methanol dehydroge |
| 273 | 3 | 8.8 | 36 | 2 | E84416 | hypothetical prote |
| 274 | 3 | 8.8 | 36 | 2 | S17834 | acetyl-CoA carboxy |
| 275 | 3 | 8.8 | 36 | 2 | E70220 | hypothetical prote |
| 276 | 3 | 8.8 | 36 | 2 | F70237 | hypothetical prote |
| 277 | 3 | 8.8 | 36 | 2 | E70238 | hypothetical prote |
| 278 | 3 | 8.8 | 36 | 2 | F64604 | hypothetical prote |
| 279 | 3 | 8.8 | 36 | 2 | G81853 | hypothetical prote |
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| 281 | 3 | 8.8 | 36 | 2 | G82281 | hypothetical prote |
| 282 | 3 | 8.8 | 36 | 2 | A82163 | hypothetical prote |
| 283 | 3 | 8.8 | 36 | 2 | C82111 | hypothetical prote |
| 284 | 3 | 8.8 | 36 | 2 | A82092 | hypothetical prote |
| 285 | 3 | 8.8 | 36 | 2 | B82093 | hypothetical prote |
| 286 | 3 | 8.8 | 36 | 2 | A82437 | hypothetical prote |
| 287 | 3 | 8.8 | 36 | 2 | A69326 | hypothetical prote |
| 288 | 3 | 8.8 | 36 | 2 | S67795 | probable membrane |
| 289 | 3 | 8.8 | 36 | 2 | T22263 | hypothetical prote |
| 290 | 3 | 8.8 | 36 | 2 | A57443 | guanylate cyclase |
| 291 | 3 | 8.8 | 36 | 2 | D83682 | hypothetical prote |
| 292 | 3 | 8.8 | 36 | 2 | F84074 | hypothetical prote |
| 293 | 3 | 8.8 | 36 | 2 | A56634 | neuropeptide F - A |
| 294 | 3 | 8.8 | 36 | 2 | S77071 | probable plastiqui |
| 295 | 3 | 8.8 | 36 | 2 | AF1015 | hypothetical prote |
| 296 | 3 | 8.8 | 36 | 2 | AI1841 | hypothetical prote |
| 297 | 3 | 8.8 | 37 | 1 | S32792 | iberiotoxin - east |
| 298 | 3 | 8.8 | 37 | 1 | HSWT93 | histone H2A.3 - wh |

| | | | | | | |
|-----|---|-----|----|---|--------|---------------------|
| 299 | 3 | 8.8 | 37 | 1 | ZJBPF4 | gene J protein - p |
| 300 | 3 | 8.8 | 37 | 2 | S48656 | fusicoccin recepto |
| 301 | 3 | 8.8 | 37 | 2 | S03570 | trypsin (EC 3.4.21 |
| 302 | 3 | 8.8 | 37 | 2 | S39367 | proteinase omega - |
| 303 | 3 | 8.8 | 37 | 2 | S06217 | transforming prote |
| 304 | 3 | 8.8 | 37 | 2 | JH0735 | Ig heavy chain V r |
| 305 | 3 | 8.8 | 37 | 2 | A30607 | Ig kappa chain V-I |
| 306 | 3 | 8.8 | 37 | 2 | I48405 | histone H2a - mous |
| 307 | 3 | 8.8 | 37 | 2 | B32307 | ribosomal protein |
| 308 | 3 | 8.8 | 37 | 2 | S78257 | ribosomal protein |
| 309 | 3 | 8.8 | 37 | 2 | AH1776 | ribosomal protein |
| 310 | 3 | 8.8 | 37 | 2 | AI1400 | ribosomal protein |
| 311 | 3 | 8.8 | 37 | 2 | E97282 | ribosomal protein |
| 312 | 3 | 8.8 | 37 | 2 | F90019 | 50S ribosomal prot |
| 313 | 3 | 8.8 | 37 | 2 | PC1121 | antifungal 25K pro |
| 314 | 3 | 8.8 | 37 | 2 | G01887 | MEK kinase - human |
| 315 | 3 | 8.8 | 37 | 2 | S41509 | probable antimutat |
| 316 | 3 | 8.8 | 37 | 2 | S07517 | gene 6.3 protein - |
| 317 | 3 | 8.8 | 37 | 2 | E70241 | hypothetical prote |
| 318 | 3 | 8.8 | 37 | 2 | D83199 | hypothetical prote |
| 319 | 3 | 8.8 | 37 | 2 | H82304 | hypothetical prote |
| 320 | 3 | 8.8 | 37 | 2 | S21132 | photosystem II cyt |
| 321 | 3 | 8.8 | 37 | 2 | F59103 | hypothetical prote |
| 322 | 3 | 8.8 | 37 | 2 | T36662 | small hypothetical |
| 323 | 3 | 8.8 | 37 | 2 | T11815 | hypothetical prote |
| 324 | 3 | 8.8 | 37 | 2 | A57127 | diuretic hormone 1 |
| 325 | 3 | 8.8 | 37 | 2 | C32112 | R15 gamma peptide |
| 326 | 3 | 8.8 | 37 | 2 | G49050 | T-cell surface gly |
| 327 | 3 | 8.8 | 37 | 2 | S68261 | hypothetical prote |
| 328 | 3 | 8.8 | 37 | 2 | S49982 | Tcell receptor alp |
| 329 | 3 | 8.8 | 37 | 2 | B39030 | androgen-binding p |
| 330 | 3 | 8.8 | 37 | 2 | PN0550 | metabotropic gluta |
| 331 | 3 | 8.8 | 37 | 2 | S70931 | histone-like prote |
| 332 | 3 | 8.8 | 37 | 2 | F81403 | hypothetical prote |
| 333 | 3 | 8.8 | 38 | 1 | R5EC36 | ribosomal protein |
| 334 | 3 | 8.8 | 38 | 2 | C34047 | stylar glycoprotei |
| 335 | 3 | 8.8 | 38 | 2 | T11763 | acetyl-CoA carboxy |
| 336 | 3 | 8.8 | 38 | 2 | S39034 | lipid transfer pro |
| 337 | 3 | 8.8 | 38 | 2 | PS0129 | H-2 class I histoc |
| 338 | 3 | 8.8 | 38 | 2 | S50764 | ribosomal protein |
| 339 | 3 | 8.8 | 38 | 2 | E72247 | ribosomal protein |
| 340 | 3 | 8.8 | 38 | 2 | H83113 | 50S ribosomal prot |
| 341 | 3 | 8.8 | 38 | 2 | AG0028 | 50S ribosomal prot |
| 342 | 3 | 8.8 | 38 | 2 | D91149 | 50S ribosomal subu |
| 343 | 3 | 8.8 | 38 | 2 | AF1008 | 50S ribosomal chai |
| 344 | 3 | 8.8 | 38 | 2 | PH1920 | annexin-like 40K p |
| 345 | 3 | 8.8 | 38 | 2 | S72344 | pileE protein - Nei |
| 346 | 3 | 8.8 | 38 | 2 | JS0456 | gene J protein - p |
| 347 | 3 | 8.8 | 38 | 2 | A60216 | hyperglycemic horm |
| 348 | 3 | 8.8 | 38 | 2 | S65416 | pyruvate synthase |
| 349 | 3 | 8.8 | 38 | 2 | H91111 | hypothetical prote |
| 350 | 3 | 8.8 | 38 | 2 | D90631 | hypothetical prote |
| 351 | 3 | 8.8 | 38 | 2 | E72306 | hypothetical prote |
| 352 | 3 | 8.8 | 38 | 2 | E81873 | hypothetical prote |
| 353 | 3 | 8.8 | 38 | 2 | T14885 | hypothetical prote |
| 354 | 3 | 8.8 | 38 | 2 | A82478 | hypothetical prote |
| 355 | 3 | 8.8 | 38 | 2 | E82463 | hypothetical prote |

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|-----|---|-----|----|---|--------|--------------------|
| 356 | 3 | 8.8 | 38 | 2 | A82450 | hypothetical prote |
| 357 | 3 | 8.8 | 38 | 2 | G64001 | hypothetical prote |
| 358 | 3 | 8.8 | 38 | 2 | D37842 | hypothetical prote |
| 359 | 3 | 8.8 | 38 | 2 | B69492 | hypothetical prote |
| 360 | 3 | 8.8 | 38 | 2 | S23173 | photosystem I chai |
| 361 | 3 | 8.8 | 38 | 2 | S58601 | hypothetical prote |
| 362 | 3 | 8.8 | 38 | 2 | T01741 | hypothetical prote |
| 363 | 3 | 8.8 | 38 | 2 | B39888 | synapsin I - bovin |
| 364 | 3 | 8.8 | 38 | 2 | B49012 | orf 5' of megl - m |
| 365 | 3 | 8.8 | 38 | 2 | A83863 | hypothetical prote |
| 366 | 3 | 8.8 | 38 | 2 | H81603 | hypothetical prote |
| 367 | 3 | 8.8 | 38 | 2 | H81579 | hypothetical prote |
| 368 | 3 | 8.8 | 38 | 2 | E82858 | hypothetical prote |
| 369 | 3 | 8.8 | 38 | 2 | S71381 | lebetin 2 isoform |
| 370 | 3 | 8.8 | 38 | 2 | G71305 | probable ribosomal |
| 371 | 3 | 8.8 | 38 | 2 | B97327 | hypothetical prote |
| 372 | 3 | 8.8 | 38 | 2 | H85994 | 50S ribosomal subu |
| 373 | 3 | 8.8 | 38 | 2 | T08652 | hypothetical prote |
| 374 | 3 | 8.8 | 38 | 2 | T14226 | NADH2 dehydrogenas |
| 375 | 3 | 8.8 | 38 | 2 | AH0774 | hypothetical prote |
| 376 | 3 | 8.8 | 39 | 1 | CTDFAS | corticotropin - sp |
| 377 | 3 | 8.8 | 39 | 1 | HWGH3Z | exendin-3 - Mexica |
| 378 | 3 | 8.8 | 39 | 1 | HWGH4G | exendin-4 - Gila m |
| 379 | 3 | 8.8 | 39 | 2 | B45946 | gamma-glutamyltran |
| 380 | 3 | 8.8 | 39 | 2 | S09645 | hygromycin-B kinas |
| 381 | 3 | 8.8 | 39 | 2 | A01458 | corticotropin - fi |
| 382 | 3 | 8.8 | 39 | 2 | PN0127 | corticotropin - se |
| 383 | 3 | 8.8 | 39 | 2 | A61127 | adrenocorticotropi |
| 384 | 3 | 8.8 | 39 | 2 | A01459 | corticotropin - os |
| 385 | 3 | 8.8 | 39 | 2 | A01457 | corticotropin - ra |
| 386 | 3 | 8.8 | 39 | 2 | C55995 | prostaglandin E2 r |
| 387 | 3 | 8.8 | 39 | 2 | PH0878 | Ig kappa chain V r |
| 388 | 3 | 8.8 | 39 | 2 | S72459 | ribosomal protein |
| 389 | 3 | 8.8 | 39 | 2 | PQ0011 | tubulin beta chain |
| 390 | 3 | 8.8 | 39 | 2 | S63482 | tubulin beta chain |
| 391 | 3 | 8.8 | 39 | 2 | A45793 | actin - nematode (|
| 392 | 3 | 8.8 | 39 | 2 | AH2286 | photosystem II pro |
| 393 | 3 | 8.8 | 39 | 2 | G64944 | yebJ protein - Esc |
| 394 | 3 | 8.8 | 39 | 2 | A85795 | hypothetical prote |
| 395 | 3 | 8.8 | 39 | 2 | S78008 | fucosyltransferase |
| 396 | 3 | 8.8 | 39 | 2 | H95146 | hypothetical prote |
| 397 | 3 | 8.8 | 39 | 2 | D70239 | hypothetical prote |
| 398 | 3 | 8.8 | 39 | 2 | C70254 | hypothetical prote |
| 399 | 3 | 8.8 | 39 | 2 | G81899 | hypothetical prote |
| 400 | 3 | 8.8 | 39 | 2 | B81912 | hypothetical prote |
| 401 | 3 | 8.8 | 39 | 2 | B81954 | very hypothetical |
| 402 | 3 | 8.8 | 39 | 2 | F82329 | hypothetical prote |
| 403 | 3 | 8.8 | 39 | 2 | A44918 | lactococcin G pept |
| 404 | 3 | 8.8 | 39 | 2 | S73118 | photosystem II pro |
| 405 | 3 | 8.8 | 39 | 2 | PC4294 | high mobility grou |
| 406 | 3 | 8.8 | 39 | 2 | T15158 | hypothetical prote |
| 407 | 3 | 8.8 | 39 | 2 | I46466 | luteinizing hormon |
| 408 | 3 | 8.8 | 39 | 2 | B40984 | finger protein zfe |
| 409 | 3 | 8.8 | 39 | 2 | T03365 | gene e2 protein - |
| 410 | 3 | 8.8 | 39 | 2 | F81587 | hypothetical prote |
| 411 | 3 | 8.8 | 39 | 2 | E81540 | hypothetical prote |
| 412 | 3 | 8.8 | 39 | 2 | C81745 | hypothetical prote |

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|-----|---|-----|----|---|--------|--------------------|
| 413 | 3 | 8.8 | 39 | 2 | T12905 | hypothetical prote |
| 414 | 3 | 8.8 | 39 | 2 | D85739 | hypothetical prote |
| 415 | 3 | 8.8 | 39 | 2 | AD0162 | hypothetical prote |
| 416 | 3 | 8.8 | 39 | 2 | AE3109 | hypothetical prote |
| 417 | 3 | 8.8 | 40 | 1 | SWFGS | sauvagine - Sauvag |
| 418 | 3 | 8.8 | 40 | 2 | B61320 | plastocyanin - Aqu |
| 419 | 3 | 8.8 | 40 | 2 | S52343 | hypothetical prote |
| 420 | 3 | 8.8 | 40 | 2 | S00264 | creatine kinase (E |
| 421 | 3 | 8.8 | 40 | 2 | S34407 | adenylate kinase (|
| 422 | 3 | 8.8 | 40 | 2 | S03688 | type II site-speci |
| 423 | 3 | 8.8 | 40 | 2 | PQ0202 | endo-1,4-beta-xyla |
| 424 | 3 | 8.8 | 40 | 2 | S50021 | trypsin-like prote |
| 425 | 3 | 8.8 | 40 | 2 | B60908 | beta-lactamase (EC |
| 426 | 3 | 8.8 | 40 | 2 | B41440 | protein disulfide- |
| 427 | 3 | 8.8 | 40 | 2 | A19940 | antithrombin III - |
| 428 | 3 | 8.8 | 40 | 2 | B59005 | thymosin beta - sc |
| 429 | 3 | 8.8 | 40 | 2 | A59005 | thymosin beta - se |
| 430 | 3 | 8.8 | 40 | 2 | B31791 | sarcotoxin ID - fl |
| 431 | 3 | 8.8 | 40 | 2 | S07969 | T-cell receptor al |
| 432 | 3 | 8.8 | 40 | 2 | I50012 | MHC class I protei |
| 433 | 3 | 8.8 | 40 | 2 | I50013 | MHC class I protei |
| 434 | 3 | 8.8 | 40 | 2 | S61539 | ribosomal protein |
| 435 | 3 | 8.8 | 40 | 2 | A60171 | proteoglycan core |
| 436 | 3 | 8.8 | 40 | 2 | A60645 | tubulin beta chain |
| 437 | 3 | 8.8 | 40 | 2 | A29184 | vitellogenin - tur |
| 438 | 3 | 8.8 | 40 | 2 | S65907 | conglutin gamma - |
| 439 | 3 | 8.8 | 40 | 2 | S08656 | protein VI - human |
| 440 | 3 | 8.8 | 40 | 2 | A53708 | indolepyruvate syn |
| 441 | 3 | 8.8 | 40 | 2 | T08107 | nonenzymatic prote |
| 442 | 3 | 8.8 | 40 | 2 | S71917 | hemoglobin, extrac |
| 443 | 3 | 8.8 | 40 | 2 | S58853 | homeotic protein u |
| 444 | 3 | 8.8 | 40 | 2 | H95063 | hypothetical prote |
| 445 | 3 | 8.8 | 40 | 2 | H91281 | hypothetical prote |
| 446 | 3 | 8.8 | 40 | 2 | A87642 | hypothetical prote |
| 447 | 3 | 8.8 | 40 | 2 | F87419 | hypothetical prote |
| 448 | 3 | 8.8 | 40 | 2 | C32338 | hypothetical 4K pr |
| 449 | 3 | 8.8 | 40 | 2 | C72398 | hypothetical prote |
| 450 | 3 | 8.8 | 40 | 2 | S44935 | hypothetical prote |
| 451 | 3 | 8.8 | 40 | 2 | PC4218 | hypothetical 40 pr |
| 452 | 3 | 8.8 | 40 | 2 | A82203 | hypothetical prote |
| 453 | 3 | 8.8 | 40 | 2 | G82484 | hypothetical prote |
| 454 | 3 | 8.8 | 40 | 2 | A82382 | hypothetical prote |
| 455 | 3 | 8.8 | 40 | 2 | I39944 | regulatory extrace |
| 456 | 3 | 8.8 | 40 | 2 | F69677 | phosphatase (RapK) |
| 457 | 3 | 8.8 | 40 | 2 | I41476 | probable antigen 9 |
| 458 | 3 | 8.8 | 40 | 2 | S27709 | hypothetical prote |
| 459 | 3 | 8.8 | 40 | 2 | T11811 | hypothetical prote |
| 460 | 3 | 8.8 | 40 | 2 | T07472 | hypothetical prote |
| 461 | 3 | 8.8 | 40 | 2 | T07516 | hypothetical prote |
| 462 | 3 | 8.8 | 40 | 2 | T07523 | hypothetical prote |
| 463 | 3 | 8.8 | 40 | 2 | T07560 | hypothetical prote |
| 464 | 3 | 8.8 | 40 | 2 | T48629 | hypothetical prote |
| 465 | 3 | 8.8 | 40 | 2 | S53001 | mitotic-specific c |
| 466 | 3 | 8.8 | 40 | 2 | T03831 | hypothetical prote |
| 467 | 3 | 8.8 | 40 | 2 | S56768 | capsid protein - L |
| 468 | 3 | 8.8 | 40 | 2 | T07206 | hypothetical prote |
| 469 | 3 | 8.8 | 40 | 2 | H81592 | hypothetical prote |

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|-----|---|-----|----|---|--------|--------------------|
| 470 | 3 | 8.8 | 40 | 2 | F81511 | hypothetical prote |
| 471 | 3 | 8.8 | 40 | 2 | G82620 | hypothetical prote |
| 472 | 3 | 8.8 | 40 | 2 | A82590 | hypothetical prote |
| 473 | 3 | 8.8 | 40 | 2 | A86123 | hypothetical prote |
| 474 | 3 | 8.8 | 40 | 2 | B97413 | hypothetical prote |
| 475 | 2 | 5.9 | 28 | 1 | LFSEW | trp operon leader |
| 476 | 2 | 5.9 | 28 | 1 | LFEBLT | leu operon leader |
| 477 | 2 | 5.9 | 28 | 1 | LFECL | leu operon leader |
| 478 | 2 | 5.9 | 28 | 1 | G9BPSV | gene 9 protein - s |
| 479 | 2 | 5.9 | 28 | 2 | S41774 | ubiquinol-cytochro |
| 480 | 2 | 5.9 | 28 | 2 | S71598 | cytochrome P450 HP |
| 481 | 2 | 5.9 | 28 | 2 | S04341 | cytochrome P450 PB |
| 482 | 2 | 5.9 | 28 | 2 | PX0033 | cytochrome P450 te |
| 483 | 2 | 5.9 | 28 | 2 | S66436 | allophycocyanin al |
| 484 | 2 | 5.9 | 28 | 2 | S47624 | D-aspartate oxidas |
| 485 | 2 | 5.9 | 28 | 2 | T14210 | NADH2 dehydrogenas |
| 486 | 2 | 5.9 | 28 | 2 | T14213 | NADH2 dehydrogenas |
| 487 | 2 | 5.9 | 28 | 2 | T12301 | NADH2 dehydrogenas |
| 488 | 2 | 5.9 | 28 | 2 | PC1162 | cytochrome-c oxida |
| 489 | 2 | 5.9 | 28 | 2 | S21278 | glutathione transf |
| 490 | 2 | 5.9 | 28 | 2 | C33948 | glutathione transf |
| 491 | 2 | 5.9 | 28 | 2 | A34244 | hexokinase (EC 2.7 |
| 492 | 2 | 5.9 | 28 | 2 | D38578 | protein kinase 4 (|
| 493 | 2 | 5.9 | 28 | 2 | B39116 | epidermal growth f |
| 494 | 2 | 5.9 | 28 | 2 | A31859 | deoxycytidine kina |
| 495 | 2 | 5.9 | 28 | 2 | B54257 | deoxynucleoside ki |
| 496 | 2 | 5.9 | 28 | 2 | I55596 | lysosomal acid lip |
| 497 | 2 | 5.9 | 28 | 2 | B35948 | phospholipase A2 (|
| 498 | 2 | 5.9 | 28 | 2 | A35115 | hypothetical prote |
| 499 | 2 | 5.9 | 28 | 2 | A61281 | lysozyme homolog A |
| 500 | 2 | 5.9 | 28 | 2 | A61529 | chymotrypsin (EC 3 |
| 501 | 2 | 5.9 | 28 | 2 | A60291 | 24K proteinase (EC |
| 502 | 2 | 5.9 | 28 | 2 | S08186 | proteasome beta ch |
| 503 | 2 | 5.9 | 28 | 2 | S55729 | orotidine-5'-monop |
| 504 | 2 | 5.9 | 28 | 2 | I40034 | trpE protein - Bac |
| 505 | 2 | 5.9 | 28 | 2 | A32643 | deoxyribodipyrimid |
| 506 | 2 | 5.9 | 28 | 2 | S77854 | glutamate-tRNA lig |
| 507 | 2 | 5.9 | 28 | 2 | JX0059 | serine proteinase |
| 508 | 2 | 5.9 | 28 | 2 | S07156 | trypsin inhibitor |
| 509 | 2 | 5.9 | 28 | 2 | JX0058 | trypsin inhibitor |
| 510 | 2 | 5.9 | 28 | 2 | B45041 | trypsin inhibitor |
| 511 | 2 | 5.9 | 28 | 2 | S20393 | trypsin inhibitor |
| 512 | 2 | 5.9 | 28 | 2 | A25802 | 2S seed storage pr |
| 513 | 2 | 5.9 | 28 | 2 | T47196 | RAS protein [impor |
| 514 | 2 | 5.9 | 28 | 2 | A61322 | somatostatin-28 - |
| 515 | 2 | 5.9 | 28 | 2 | B60583 | glycoprotein hormo |
| 516 | 2 | 5.9 | 28 | 2 | A38232 | vasoactive intesti |
| 517 | 2 | 5.9 | 28 | 2 | A60303 | vasoactive intesti |
| 518 | 2 | 5.9 | 28 | 2 | JT0412 | bombyxin-IV chain |
| 519 | 2 | 5.9 | 28 | 2 | A56366 | intestinal trefoil |
| 520 | 2 | 5.9 | 28 | 2 | C44180 | alpha-neurotoxin-1 |
| 521 | 2 | 5.9 | 28 | 2 | C39327 | long neurotoxin - |
| 522 | 2 | 5.9 | 28 | 2 | I32529 | Ig lambda chain V |
| 523 | 2 | 5.9 | 28 | 2 | PC1001 | Ig light chain V r |
| 524 | 2 | 5.9 | 28 | 2 | B47719 | T-cell receptor al |
| 525 | 2 | 5.9 | 28 | 2 | D47719 | T-cell receptor al |
| 526 | 2 | 5.9 | 28 | 2 | S58389 | T-cell receptor be |

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|-----|---|-----|----|---|--------|--------------------|
| 527 | 2 | 5.9 | 28 | 2 | PH0250 | T-cell receptor Vb |
| 528 | 2 | 5.9 | 28 | 2 | PH0247 | T-cell receptor Vb |
| 529 | 2 | 5.9 | 28 | 2 | A49829 | T-cell receptor va |
| 530 | 2 | 5.9 | 28 | 2 | D49829 | T-cell receptor va |
| 531 | 2 | 5.9 | 28 | 2 | PH1908 | T-cell receptor al |
| 532 | 2 | 5.9 | 28 | 2 | D41912 | T-cell receptor be |
| 533 | 2 | 5.9 | 28 | 2 | G47719 | house-dust-mite-re |
| 534 | 2 | 5.9 | 28 | 2 | E49533 | T-cell receptor be |
| 535 | 2 | 5.9 | 28 | 2 | I46921 | gene Bota protein |
| 536 | 2 | 5.9 | 28 | 2 | S11618 | ribosomal protein |
| 537 | 2 | 5.9 | 28 | 2 | S51060 | ribosomal protein |
| 538 | 2 | 5.9 | 28 | 2 | S51067 | ribosomal protein |
| 539 | 2 | 5.9 | 28 | 2 | S72460 | ribosomal protein |
| 540 | 2 | 5.9 | 28 | 2 | S08569 | ribosomal protein |
| 541 | 2 | 5.9 | 28 | 2 | S55442 | beta A2 crystallin |
| 542 | 2 | 5.9 | 28 | 2 | A45626 | beta 2-tubulin - n |
| 543 | 2 | 5.9 | 28 | 2 | S21231 | calcium-binding pr |
| 544 | 2 | 5.9 | 28 | 2 | A23691 | apolipoprotein C-I |
| 545 | 2 | 5.9 | 28 | 2 | A05296 | fibrinogen alpha c |
| 546 | 2 | 5.9 | 28 | 2 | A61113 | cellular retinol-b |
| 547 | 2 | 5.9 | 28 | 2 | B35577 | cell adhesion rece |
| 548 | 2 | 5.9 | 28 | 2 | I48349 | fibronectin - mous |
| 549 | 2 | 5.9 | 28 | 2 | A61233 | retinol-binding pr |
| 550 | 2 | 5.9 | 28 | 2 | I45911 | dnaK-type molecula |
| 551 | 2 | 5.9 | 28 | 2 | PQ0263 | dnaK-type molecula |
| 552 | 2 | 5.9 | 28 | 2 | A03356 | omega-gliadin - ei |
| 553 | 2 | 5.9 | 28 | 2 | A60359 | pollen allergen DG |
| 554 | 2 | 5.9 | 28 | 2 | PQ0691 | photosystem I 5.6K |
| 555 | 2 | 5.9 | 28 | 2 | G32351 | 34K class B flagel |
| 556 | 2 | 5.9 | 28 | 2 | S47614 | zinc finger protei |
| 557 | 2 | 5.9 | 28 | 2 | S49924 | stp protein (Baker |
| 558 | 2 | 5.9 | 28 | 2 | PN0047 | signal transductio |
| 559 | 2 | 5.9 | 28 | 2 | B39227 | calcium channel pr |
| 560 | 2 | 5.9 | 28 | 2 | A36153 | major allergen Ole |
| 561 | 2 | 5.9 | 28 | 2 | B54127 | dolichyl-diphospho |
| 562 | 2 | 5.9 | 28 | 2 | S56746 | alpha-synuclein, N |
| 563 | 2 | 5.9 | 28 | 2 | I48178 | orphan receptor - |
| 564 | 2 | 5.9 | 28 | 2 | S29135 | aminopyrine N-deme |
| 565 | 2 | 5.9 | 28 | 2 | S29136 | aminopyrine N-deme |
| 566 | 2 | 5.9 | 28 | 2 | PN0625 | homeobox JRX prote |
| 567 | 2 | 5.9 | 28 | 2 | B56779 | tetM 5'-region lea |
| 568 | 2 | 5.9 | 28 | 2 | JU0297 | fruR-shl operon le |
| 569 | 2 | 5.9 | 28 | 2 | G90638 | leu operon leader |
| 570 | 2 | 5.9 | 28 | 2 | C90639 | fruR leader peptid |
| 571 | 2 | 5.9 | 28 | 2 | B47310 | MHVS28AA - murine |
| 572 | 2 | 5.9 | 28 | 2 | E64656 | hypothetical prote |
| 573 | 2 | 5.9 | 28 | 2 | B64669 | hypothetical prote |
| 574 | 2 | 5.9 | 28 | 2 | S15235 | hypothetical prote |
| 575 | 2 | 5.9 | 28 | 2 | C56262 | uvrB 3'-region hyp |
| 576 | 2 | 5.9 | 28 | 2 | E81239 | hypothetical prote |
| 577 | 2 | 5.9 | 28 | 2 | I60364 | phosphorybosylpyro |
| 578 | 2 | 5.9 | 28 | 2 | B39191 | hypothetical prote |
| 579 | 2 | 5.9 | 28 | 2 | T17391 | hypothetical prote |
| 580 | 2 | 5.9 | 28 | 2 | A56499 | brevicin-27 - Lact |
| 581 | 2 | 5.9 | 28 | 2 | A41476 | probable antigen 1 |
| 582 | 2 | 5.9 | 28 | 2 | S16228 | aryl acylamidase - |
| 583 | 2 | 5.9 | 28 | 2 | T37143 | hypothetical prote |

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|-----|---|-----|----|---|--------|--------------------|
| 584 | 2 | 5.9 | 28 | 2 | PS0106 | 2-phosphinomethylm |
| 585 | 2 | 5.9 | 28 | 2 | G69384 | conserved hypothet |
| 586 | 2 | 5.9 | 28 | 2 | A69259 | hypothetical prote |
| 587 | 2 | 5.9 | 28 | 2 | T06925 | hypothetical prote |
| 588 | 2 | 5.9 | 28 | 2 | S38524 | rRNA N-glycosidase |
| 589 | 2 | 5.9 | 28 | 2 | S21742 | 3-oxoacyl-[acyl-ca |
| 590 | 2 | 5.9 | 28 | 2 | PQ0800 | calmodulin antagon |
| 591 | 2 | 5.9 | 28 | 2 | T06340 | ribosomal protein |
| 592 | 2 | 5.9 | 28 | 2 | T07599 | hypothetical prote |
| 593 | 2 | 5.9 | 28 | 2 | PH0220 | peroxidase (EC 1.1 |
| 594 | 2 | 5.9 | 28 | 2 | JQ0272 | hypothetical 3K pr |
| 595 | 2 | 5.9 | 28 | 2 | S46250 | fatty-acid-binding |
| 596 | 2 | 5.9 | 28 | 2 | A44923 | carboxypeptidase 3 |
| 597 | 2 | 5.9 | 28 | 2 | S64701 | hypothetical prote |
| 598 | 2 | 5.9 | 28 | 2 | T38041 | similarity to yeas |
| 599 | 2 | 5.9 | 28 | 2 | A60698 | trichocyst protein |
| 600 | 2 | 5.9 | 28 | 2 | A27261 | proteinase inhibit |
| 601 | 2 | 5.9 | 28 | 2 | A61417 | bdellin B-3 - medi |
| 602 | 2 | 5.9 | 28 | 2 | S07826 | venom protein - Am |
| 603 | 2 | 5.9 | 28 | 2 | C34923 | omega-agatoxin IIA |
| 604 | 2 | 5.9 | 28 | 2 | A44877 | cell surface prote |
| 605 | 2 | 5.9 | 28 | 2 | JW0019 | mast cell degranul |
| 606 | 2 | 5.9 | 28 | 2 | A61273 | interleukin-1 - st |
| 607 | 2 | 5.9 | 28 | 2 | S68643 | nicotinic acetylch |
| 608 | 2 | 5.9 | 28 | 2 | PC2162 | angiotensin II rec |
| 609 | 2 | 5.9 | 28 | 2 | I54183 | cell adhesion regu |
| 610 | 2 | 5.9 | 28 | 2 | S54338 | cytochrome P450 CY |
| 611 | 2 | 5.9 | 28 | 2 | I52627 | erythrocyte chemok |
| 612 | 2 | 5.9 | 28 | 2 | JQ1035 | hypothetical 3.2K |
| 613 | 2 | 5.9 | 28 | 2 | PH1335 | Ig heavy chain DJ |
| 614 | 2 | 5.9 | 28 | 2 | PH1363 | Ig heavy chain DJ |
| 615 | 2 | 5.9 | 28 | 2 | S37683 | protein IEF SSP 91 |
| 616 | 2 | 5.9 | 28 | 2 | S37686 | protein IEF SSP 92 |
| 617 | 2 | 5.9 | 28 | 2 | PH1911 | T-cell receptor al |
| 618 | 2 | 5.9 | 28 | 2 | I39288 | ZF3 domain - human |
| 619 | 2 | 5.9 | 28 | 2 | PL0005 | pepsin A (EC 3.4.2 |
| 620 | 2 | 5.9 | 28 | 2 | A60692 | proline-rich prote |
| 621 | 2 | 5.9 | 28 | 2 | PC2239 | heat shock protein |
| 622 | 2 | 5.9 | 28 | 2 | PT0366 | T-cell receptor be |
| 623 | 2 | 5.9 | 28 | 2 | I58115 | cystic fibrosis tr |
| 624 | 2 | 5.9 | 28 | 2 | A46690 | sialic acid-specif |
| 625 | 2 | 5.9 | 28 | 2 | C83797 | hypothetical prote |
| 626 | 2 | 5.9 | 28 | 2 | C83969 | hypothetical prote |
| 627 | 2 | 5.9 | 28 | 2 | S51593 | myrB protein - Mic |
| 628 | 2 | 5.9 | 28 | 2 | C85490 | fruR leader peptid |
| 629 | 2 | 5.9 | 28 | 2 | C97078 | hypothetical prote |
| 630 | 2 | 5.9 | 28 | 2 | F97000 | hypothetical prote |
| 631 | 2 | 5.9 | 28 | 2 | G85489 | leu operon leader |
| 632 | 2 | 5.9 | 28 | 2 | AB1093 | hypothetical prote |
| 633 | 2 | 5.9 | 28 | 2 | T06490 | probable ribulose- |
| 634 | 2 | 5.9 | 28 | 2 | AG0516 | leu operon leader |
| 635 | 2 | 5.9 | 28 | 4 | I68614 | frame shifted FMR1 |
| 636 | 2 | 5.9 | 28 | 4 | JN0014 | GABA(A) receptor a |
| 637 | 2 | 5.9 | 29 | 1 | TIPU | trypsin inhibitor |
| 638 | 2 | 5.9 | 29 | 1 | TIPU3 | trypsin inhibitor |
| 639 | 2 | 5.9 | 29 | 1 | TIPU2B | trypsin inhibitor |
| 640 | 2 | 5.9 | 29 | 1 | GCOPV | glucagon - North A |

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|-----|---|-----|----|---|--------|--------------------|
| 641 | 2 | 5.9 | 29 | 1 | GC DK | glucagon - duck |
| 642 | 2 | 5.9 | 29 | 1 | A61583 | glucagon - ostrich |
| 643 | 2 | 5.9 | 29 | 1 | GCFLE | glucagon - Europea |
| 644 | 2 | 5.9 | 29 | 1 | GCDF | glucagon - smaller |
| 645 | 2 | 5.9 | 29 | 1 | GCEN | glucagon - elephan |
| 646 | 2 | 5.9 | 29 | 1 | GCTTS | glucagon - slider |
| 647 | 2 | 5.9 | 29 | 1 | TNLJBR | trans-activating t |
| 648 | 2 | 5.9 | 29 | 1 | Q1BP57 | gene 1.5 protein - |
| 649 | 2 | 5.9 | 29 | 2 | A60558 | cytochrome P450 HL |
| 650 | 2 | 5.9 | 29 | 2 | T17079 | NADH2 dehydrogenas |
| 651 | 2 | 5.9 | 29 | 2 | A48427 | flavohemoglobin hm |
| 652 | 2 | 5.9 | 29 | 2 | A54234 | cytochrome-c oxida |
| 653 | 2 | 5.9 | 29 | 2 | S08201 | peroxidase (EC 1.1 |
| 654 | 2 | 5.9 | 29 | 2 | A26208 | acetyl-CoA C-acety |
| 655 | 2 | 5.9 | 29 | 2 | A22018 | phosphotransferase |
| 656 | 2 | 5.9 | 29 | 2 | S46211 | kallikrein rK8 (pK |
| 657 | 2 | 5.9 | 29 | 2 | S28174 | heat-shock protein |
| 658 | 2 | 5.9 | 29 | 2 | A32414 | bothrolysin (EC 3. |
| 659 | 2 | 5.9 | 29 | 2 | S17432 | H+-transporting tw |
| 660 | 2 | 5.9 | 29 | 2 | S02578 | H+-transporting tw |
| 661 | 2 | 5.9 | 29 | 2 | S23122 | peptidylprolyl iso |
| 662 | 2 | 5.9 | 29 | 2 | JU0211 | squash-type trypsi |
| 663 | 2 | 5.9 | 29 | 2 | T03653 | phospholipid trans |
| 664 | 2 | 5.9 | 29 | 2 | C24536 | alpha-amylase/tryp |
| 665 | 2 | 5.9 | 29 | 2 | C25310 | alpha-amylase/tryp |
| 666 | 2 | 5.9 | 29 | 2 | D55998 | brevinin-2Ed - edi |
| 667 | 2 | 5.9 | 29 | 2 | D53578 | brevinin-2Ee - edi |
| 668 | 2 | 5.9 | 29 | 2 | A61509 | islet amyloid poly |
| 669 | 2 | 5.9 | 29 | 2 | A91740 | glucagon - turkey |
| 670 | 2 | 5.9 | 29 | 2 | A91741 | glucagon - rabbit |
| 671 | 2 | 5.9 | 29 | 2 | A91742 | glucagon - Arabian |
| 672 | 2 | 5.9 | 29 | 2 | S07211 | glucagon - marbled |
| 673 | 2 | 5.9 | 29 | 2 | A61135 | glucagon - bigeye |
| 674 | 2 | 5.9 | 29 | 2 | C39258 | glucagon - common |
| 675 | 2 | 5.9 | 29 | 2 | C60840 | glucagon I - Europ |
| 676 | 2 | 5.9 | 29 | 2 | S39018 | glucagon - bowfin |
| 677 | 2 | 5.9 | 29 | 2 | A39462 | cholestokinin - do |
| 678 | 2 | 5.9 | 29 | 2 | A60791 | toxin II.9 - scorp |
| 679 | 2 | 5.9 | 29 | 2 | A43620 | omega-conotoxin GV |
| 680 | 2 | 5.9 | 29 | 2 | B43620 | omega-conotoxin GV |
| 681 | 2 | 5.9 | 29 | 2 | A58537 | omega-conotoxin MV |
| 682 | 2 | 5.9 | 29 | 2 | I52628 | low affinity nerve |
| 683 | 2 | 5.9 | 29 | 2 | C61233 | conceptus protein |
| 684 | 2 | 5.9 | 29 | 2 | S10061 | Ig heavy chain (cl |
| 685 | 2 | 5.9 | 29 | 2 | PH1328 | Ig heavy chain DJ |
| 686 | 2 | 5.9 | 29 | 2 | PH0239 | T-cell receptor Vb |
| 687 | 2 | 5.9 | 29 | 2 | PH0251 | T-cell receptor Vb |
| 688 | 2 | 5.9 | 29 | 2 | PH0254 | T-cell receptor Vb |
| 689 | 2 | 5.9 | 29 | 2 | PH0233 | T-cell receptor Vb |
| 690 | 2 | 5.9 | 29 | 2 | E31485 | Ig heavy chain V r |
| 691 | 2 | 5.9 | 29 | 2 | H31485 | Ig kappa chain V r |
| 692 | 2 | 5.9 | 29 | 2 | G31461 | T-cell receptor de |
| 693 | 2 | 5.9 | 29 | 2 | C47719 | T-cell receptor al |
| 694 | 2 | 5.9 | 29 | 2 | E47719 | house-dust-mite-re |
| 695 | 2 | 5.9 | 29 | 2 | PS0134 | H-2 class I histoc |
| 696 | 2 | 5.9 | 29 | 2 | PS0132 | H-2 class I histoc |
| 697 | 2 | 5.9 | 29 | 2 | D32533 | class II histocomp |

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|-----|---|-----|----|---|--------|--------------------|
| 698 | 2 | 5.9 | 29 | 2 | I37534 | gene HLA-DRB prote |
| 699 | 2 | 5.9 | 29 | 2 | I37535 | gene HLA-DRB prote |
| 700 | 2 | 5.9 | 29 | 2 | I37536 | MHC class II histo |
| 701 | 2 | 5.9 | 29 | 2 | I37301 | MHC class II histo |
| 702 | 2 | 5.9 | 29 | 2 | I37303 | HLA-DR beta - huma |
| 703 | 2 | 5.9 | 29 | 2 | I37306 | HLA-DR beta - huma |
| 704 | 2 | 5.9 | 29 | 2 | I50214 | protein-tyrosine-p |
| 705 | 2 | 5.9 | 29 | 2 | S07771 | histone H2B.2, spe |
| 706 | 2 | 5.9 | 29 | 2 | T04412 | histone H3 - barle |
| 707 | 2 | 5.9 | 29 | 2 | S51070 | ribosomal protein |
| 708 | 2 | 5.9 | 29 | 2 | S08555 | ribosomal protein |
| 709 | 2 | 5.9 | 29 | 2 | PC4231 | ribosomal protein |
| 710 | 2 | 5.9 | 29 | 2 | S10050 | ribosomal protein |
| 711 | 2 | 5.9 | 29 | 2 | S10049 | ribosomal protein |
| 712 | 2 | 5.9 | 29 | 2 | S26229 | ribosomal protein |
| 713 | 2 | 5.9 | 29 | 2 | A27561 | ribosomal protein |
| 714 | 2 | 5.9 | 29 | 2 | S10725 | Meth A tumor-speci |
| 715 | 2 | 5.9 | 29 | 2 | E33208 | calmodulin-binding |
| 716 | 2 | 5.9 | 29 | 2 | C33208 | calreticulin, uter |
| 717 | 2 | 5.9 | 29 | 2 | D33208 | calreticulin, slow |
| 718 | 2 | 5.9 | 29 | 2 | A45474 | calreticulin, brai |
| 719 | 2 | 5.9 | 29 | 2 | G39690 | thrombospondin 2 - |
| 720 | 2 | 5.9 | 29 | 2 | A61166 | neural cell adhesi |
| 721 | 2 | 5.9 | 29 | 2 | I52402 | endometrial proges |
| 722 | 2 | 5.9 | 29 | 2 | S00564 | alpha-fetoprotein |
| 723 | 2 | 5.9 | 29 | 2 | S57232 | enamel protein - r |
| 724 | 2 | 5.9 | 29 | 2 | A43038 | homeotic protein s |
| 725 | 2 | 5.9 | 29 | 2 | T12082 | auxin-binding prot |
| 726 | 2 | 5.9 | 29 | 2 | S70328 | proline-rich prote |
| 727 | 2 | 5.9 | 29 | 2 | S29208 | gamma35 secalin - |
| 728 | 2 | 5.9 | 29 | 2 | S07055 | avenin gamma-3 - o |
| 729 | 2 | 5.9 | 29 | 2 | S05032 | photosystem I prot |
| 730 | 2 | 5.9 | 29 | 2 | S08088 | photosystem II pro |
| 731 | 2 | 5.9 | 29 | 2 | F42075 | gene VII protein - |
| 732 | 2 | 5.9 | 29 | 2 | T51116 | finger protein (cl |
| 733 | 2 | 5.9 | 29 | 2 | A53145 | probable precorrin |
| 734 | 2 | 5.9 | 29 | 2 | A35121 | high conductance c |
| 735 | 2 | 5.9 | 29 | 2 | S03277 | hypothetical prote |
| 736 | 2 | 5.9 | 29 | 2 | S63509 | photosystem II 5K |
| 737 | 2 | 5.9 | 29 | 2 | A55891 | glycine reductase |
| 738 | 2 | 5.9 | 29 | 2 | S32730 | delta-conotoxin Gm |
| 739 | 2 | 5.9 | 29 | 2 | S57225 | homeotic protein - |
| 740 | 2 | 5.9 | 29 | 2 | S32732 | labial protein (cl |
| 741 | 2 | 5.9 | 29 | 2 | S32734 | homeotic protein - |
| 742 | 2 | 5.9 | 29 | 2 | S32733 | homeotic protein - |
| 743 | 2 | 5.9 | 29 | 2 | S07513 | homeotic protein - |
| 744 | 2 | 5.9 | 29 | 2 | S14040 | gene 5.1 protein - |
| 745 | 2 | 5.9 | 29 | 2 | E64586 | hypothetical prote |
| 746 | 2 | 5.9 | 29 | 2 | B64607 | hypothetical prote |
| 747 | 2 | 5.9 | 29 | 2 | G83440 | hypothetical prote |
| 748 | 2 | 5.9 | 29 | 2 | A49288 | KdpF protein PA163 |
| 749 | 2 | 5.9 | 29 | 2 | B81136 | alcohol dehydrogen |
| 750 | 2 | 5.9 | 29 | 2 | A81078 | hypothetical prote |
| 751 | 2 | 5.9 | 29 | 2 | B81006 | hypothetical prote |
| 752 | 2 | 5.9 | 29 | 2 | A35445 | hypothetical prote |
| 753 | 2 | 5.9 | 29 | 2 | S19943 | repY protein - Esc |
| 754 | 2 | 5.9 | 29 | 2 | A49914 | aadB protein - Kle |
| | | | | | | S-layer protein va |

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|-----|---|-----|----|---|--------|--------------------|
| 755 | 2 | 5.9 | 29 | 2 | E64036 | hypothetical prote |
| 756 | 2 | 5.9 | 29 | 2 | B48363 | 2-hydroxyglutaryl- |
| 757 | 2 | 5.9 | 29 | 2 | C40638 | orf 3' of cycI - R |
| 758 | 2 | 5.9 | 29 | 2 | S05224 | photosystem I 4.8K |
| 759 | 2 | 5.9 | 29 | 2 | B56817 | photosystem I chai |
| 760 | 2 | 5.9 | 29 | 2 | S74572 | hypothetical prote |
| 761 | 2 | 5.9 | 29 | 2 | C60743 | putrescine carbamo |
| 762 | 2 | 5.9 | 29 | 2 | S67989 | HA-19/HA-52 protei |
| 763 | 2 | 5.9 | 29 | 2 | S14099 | 12-alpha-hydroxyst |
| 764 | 2 | 5.9 | 29 | 2 | S77569 | plantaricin SA6 - |
| 765 | 2 | 5.9 | 29 | 2 | S21222 | 48K protein - Euba |
| 766 | 2 | 5.9 | 29 | 2 | S03947 | hydrogen dehydroge |
| 767 | 2 | 5.9 | 29 | 2 | T34643 | hypothetical prote |
| 768 | 2 | 5.9 | 29 | 2 | T37120 | hypothetical prote |
| 769 | 2 | 5.9 | 29 | 2 | T36654 | probable small mem |
| 770 | 2 | 5.9 | 29 | 2 | B43937 | endo-1,4-beta-xyla |
| 771 | 2 | 5.9 | 29 | 2 | S09556 | hypothetical prote |
| 772 | 2 | 5.9 | 29 | 2 | T06904 | hypothetical prote |
| 773 | 2 | 5.9 | 29 | 2 | S73197 | hypothetical prote |
| 774 | 2 | 5.9 | 29 | 2 | S78326 | conserved hypothet |
| 775 | 2 | 5.9 | 29 | 2 | S78310 | hypothetical prote |
| 776 | 2 | 5.9 | 29 | 2 | S78360 | hypothetical prote |
| 777 | 2 | 5.9 | 29 | 2 | S01572 | hypothetical prote |
| 778 | 2 | 5.9 | 29 | 2 | T07450 | hypothetical prote |
| 779 | 2 | 5.9 | 29 | 2 | S01448 | hypothetical prote |
| 780 | 2 | 5.9 | 29 | 2 | S38525 | rRNA N-glycosidase |
| 781 | 2 | 5.9 | 29 | 2 | T52557 | translation elonga |
| 782 | 2 | 5.9 | 29 | 2 | PQ0862 | allantoinase (EC 3 |
| 783 | 2 | 5.9 | 29 | 2 | PQ0486 | globulin 2a - taro |
| 784 | 2 | 5.9 | 29 | 2 | S02200 | prolamin alpha-1 - |
| 785 | 2 | 5.9 | 29 | 2 | A60683 | malate dehydrogena |
| 786 | 2 | 5.9 | 29 | 2 | JQ0212 | hypothetical 3K pr |
| 787 | 2 | 5.9 | 29 | 2 | S58541 | hypothetical prote |
| 788 | 2 | 5.9 | 29 | 2 | PC2035 | alanine transamina |
| 789 | 2 | 5.9 | 29 | 2 | S78714 | protein YDR524w-a |
| 790 | 2 | 5.9 | 29 | 2 | S68094 | 2,3-dihydroxybenzo |
| 791 | 2 | 5.9 | 29 | 2 | B21112 | variant surface gl |
| 792 | 2 | 5.9 | 29 | 2 | C60110 | repetitive protein |
| 793 | 2 | 5.9 | 29 | 2 | D24802 | cuticle protein 36 |
| 794 | 2 | 5.9 | 29 | 2 | A56591 | E75 steroid recept |
| 795 | 2 | 5.9 | 29 | 2 | A61613 | ceratotoxin A - Me |
| 796 | 2 | 5.9 | 29 | 2 | B61613 | ceratotoxin B - Me |
| 797 | 2 | 5.9 | 29 | 2 | PH1230 | lectin - namazu (f |
| 798 | 2 | 5.9 | 29 | 2 | A32860 | biotin-binding pro |
| 799 | 2 | 5.9 | 29 | 2 | I50382 | c-mil protein - ch |
| 800 | 2 | 5.9 | 29 | 2 | I50695 | non-collagenous al |
| 801 | 2 | 5.9 | 29 | 2 | B54197 | 70k thyroid autoan |
| 802 | 2 | 5.9 | 29 | 2 | A35891 | carcinoembryonic a |
| 803 | 2 | 5.9 | 29 | 2 | I77372 | CD44SP - human |
| 804 | 2 | 5.9 | 29 | 2 | S54340 | diazepam binding i |
| 805 | 2 | 5.9 | 29 | 2 | A41683 | hyaluronate recept |
| 806 | 2 | 5.9 | 29 | 2 | C54037 | splicing regulator |
| 807 | 2 | 5.9 | 29 | 2 | S35924 | T-cell receptor ga |
| 808 | 2 | 5.9 | 29 | 2 | A60604 | glutathione peroxi |
| 809 | 2 | 5.9 | 29 | 2 | A27688 | mammary-derived gr |
| 810 | 2 | 5.9 | 29 | 2 | S57204 | oviduct-specific s |
| 811 | 2 | 5.9 | 29 | 2 | I47025 | antigen WC1 [impor |

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|-----|---|-----|----|---|--------|--------------------|
| 812 | 2 | 5.9 | 29 | 2 | A49410 | t-complex polypept |
| 813 | 2 | 5.9 | 29 | 2 | PS0125 | H-2 class I histoc |
| 814 | 2 | 5.9 | 29 | 2 | S46929 | teg169 protein - m |
| 815 | 2 | 5.9 | 29 | 2 | S38749 | vimentin homolog - |
| 816 | 2 | 5.9 | 29 | 2 | S42764 | Ca2+/calmodulin-de |
| 817 | 2 | 5.9 | 29 | 2 | A49708 | synaptosomal-assoc |
| 818 | 2 | 5.9 | 29 | 2 | H83777 | hypothetical prote |
| 819 | 2 | 5.9 | 29 | 2 | C83833 | hypothetical prote |
| 820 | 2 | 5.9 | 29 | 2 | F83870 | hypothetical prote |
| 821 | 2 | 5.9 | 29 | 2 | B84144 | hypothetical prote |
| 822 | 2 | 5.9 | 29 | 2 | PC4421 | multactivase (EC 3 |
| 823 | 2 | 5.9 | 29 | 2 | B85840 | hypothetical prote |
| 824 | 2 | 5.9 | 29 | 2 | C85840 | hypothetical prote |
| 825 | 2 | 5.9 | 29 | 2 | G86058 | hypothetical prote |
| 826 | 2 | 5.9 | 29 | 2 | E89904 | hypothetical prote |
| 827 | 2 | 5.9 | 29 | 2 | H89949 | hypothetical prote |
| 828 | 2 | 5.9 | 29 | 2 | S17496 | inorganic diphosph |
| 829 | 2 | 5.9 | 29 | 2 | PQ0782 | NADH2 dehydrogenas |
| 830 | 2 | 5.9 | 29 | 2 | S34762 | L-serine ammonia-l |
| 831 | 2 | 5.9 | 29 | 2 | AB0717 | hypothetical prote |
| 832 | 2 | 5.9 | 29 | 2 | AC0717 | hypothetical prote |
| 833 | 2 | 5.9 | 29 | 2 | AH2338 | PetN protein [impo |
| 834 | 2 | 5.9 | 29 | 4 | I58970 | hypothetical prote |
| 835 | 2 | 5.9 | 30 | 1 | AIBSAF | thermophilic amino |
| 836 | 2 | 5.9 | 30 | 1 | TIPU1W | trypsin inhibitor |
| 837 | 2 | 5.9 | 30 | 1 | OEON2K | beta-endorphin II |
| 838 | 2 | 5.9 | 30 | 1 | IRTRC3 | protamine CIII, ma |
| 839 | 2 | 5.9 | 30 | 1 | IRTRC2 | protamine Ia - rai |
| 840 | 2 | 5.9 | 30 | 1 | IRTR78 | protamine CIII, mi |
| 841 | 2 | 5.9 | 30 | 1 | IRTR4 | protamine PTP4 - r |
| 842 | 2 | 5.9 | 30 | 1 | CLHRY2 | protamine YII - Pa |
| 843 | 2 | 5.9 | 30 | 1 | CLHR2A | protamine YII - At |
| 844 | 2 | 5.9 | 30 | 1 | SNUMP | sillucin - Rhizomu |
| 845 | 2 | 5.9 | 30 | 2 | I57689 | ubiquinol-cytochro |
| 846 | 2 | 5.9 | 30 | 2 | I52254 | gene CYP11B2 prote |
| 847 | 2 | 5.9 | 30 | 2 | B56859 | fatty acid omega-h |
| 848 | 2 | 5.9 | 30 | 2 | A27375 | photosystem I iron |
| 849 | 2 | 5.9 | 30 | 2 | S11131 | NADH2 dehydrogenas |
| 850 | 2 | 5.9 | 30 | 2 | S14214 | NADH2 dehydrogenas |
| 851 | 2 | 5.9 | 30 | 2 | PQ0723 | parvalbumin [impor |
| 852 | 2 | 5.9 | 30 | 2 | S08202 | peroxidase (EC 1.1 |
| 853 | 2 | 5.9 | 30 | 2 | S08204 | peroxidase (EC 1.1 |
| 854 | 2 | 5.9 | 30 | 2 | S08203 | peroxidase (EC 1.1 |
| 855 | 2 | 5.9 | 30 | 2 | A39089 | hydrogenase (EC 1. |
| 856 | 2 | 5.9 | 30 | 2 | I38066 | nitric-oxide synth |
| 857 | 2 | 5.9 | 30 | 2 | I39799 | CAT-66 - Bacillus |
| 858 | 2 | 5.9 | 30 | 2 | A18780 | dimethylallyltrans |
| 859 | 2 | 5.9 | 30 | 2 | S03283 | methionine adenosy |
| 860 | 2 | 5.9 | 30 | 2 | A28562 | glutathione transf |
| 861 | 2 | 5.9 | 30 | 2 | B27103 | aspartate transami |
| 862 | 2 | 5.9 | 30 | 2 | A27103 | aspartate transami |
| 863 | 2 | 5.9 | 30 | 2 | I55427 | aspartate transami |
| 864 | 2 | 5.9 | 30 | 2 | A49955 | protein-tyrosine k |
| 865 | 2 | 5.9 | 30 | 2 | S68639 | nigroxin A - black |
| 866 | 2 | 5.9 | 30 | 2 | S68640 | nigroxin B - black |
| 867 | 2 | 5.9 | 30 | 2 | S15678 | acetylcholinestera |
| 868 | 2 | 5.9 | 30 | 2 | A05004 | pancreatic ribonuc |

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|-----|---|-----|----|---|--------|--------------------|
| 869 | 2 | 5.9 | 30 | 2 | A44598 | endo-1,4-beta-xyla |
| 870 | 2 | 5.9 | 30 | 2 | PC2361 | alpha-glucosidase |
| 871 | 2 | 5.9 | 30 | 2 | PX0073 | epoxide hydrolase |
| 872 | 2 | 5.9 | 30 | 2 | B60291 | 30K serine protein |
| 873 | 2 | 5.9 | 30 | 2 | A27634 | major fecal allerg |
| 874 | 2 | 5.9 | 30 | 2 | B27634 | major fecal allerg |
| 875 | 2 | 5.9 | 30 | 2 | I77411 | renin-2 - mouse (f |
| 876 | 2 | 5.9 | 30 | 2 | PC2328 | proteasome endopep |
| 877 | 2 | 5.9 | 30 | 2 | A34486 | inorganic diphosph |
| 878 | 2 | 5.9 | 30 | 2 | S21816 | H+-exporting ATPas |
| 879 | 2 | 5.9 | 30 | 2 | S21814 | H+-exporting ATPas |
| 880 | 2 | 5.9 | 30 | 2 | S74121 | fructose-bisphosph |
| 881 | 2 | 5.9 | 30 | 2 | S25666 | phosphopyruvate hy |
| 882 | 2 | 5.9 | 30 | 2 | S69600 | peptidylprolyl iso |
| 883 | 2 | 5.9 | 30 | 2 | A60517 | alpha-1-antitrypsi |
| 884 | 2 | 5.9 | 30 | 2 | S24979 | proteinase inhibit |
| 885 | 2 | 5.9 | 30 | 2 | JX0057 | trypsin inhibitor |
| 886 | 2 | 5.9 | 30 | 2 | JS0579 | squash-type trypsi |
| 887 | 2 | 5.9 | 30 | 2 | JQ1958 | trypsin inhibitor |
| 888 | 2 | 5.9 | 30 | 2 | PC1113 | proteinase inhibit |
| 889 | 2 | 5.9 | 30 | 2 | C42842 | antifungal 2S stor |
| 890 | 2 | 5.9 | 30 | 2 | S70341 | napin large chain |
| 891 | 2 | 5.9 | 30 | 2 | S70343 | napin large chain |
| 892 | 2 | 5.9 | 30 | 2 | A33308 | thrombomodulin - r |
| 893 | 2 | 5.9 | 30 | 2 | S01657 | atrial natriuretic |
| 894 | 2 | 5.9 | 30 | 2 | A61130 | somatotropin - Ame |
| 895 | 2 | 5.9 | 30 | 2 | S44473 | glucagon-like pept |
| 896 | 2 | 5.9 | 30 | 2 | A59076 | defensin alpha-1 - |
| 897 | 2 | 5.9 | 30 | 2 | B59076 | defensin alpha-2 - |
| 898 | 2 | 5.9 | 30 | 2 | C59076 | defensin alpha-3 - |
| 899 | 2 | 5.9 | 30 | 2 | B60791 | toxin II.6 - scorp |
| 900 | 2 | 5.9 | 30 | 2 | A31187 | neurotoxin II.22.5 |
| 901 | 2 | 5.9 | 30 | 2 | I68109 | interferon alpha-W |
| 902 | 2 | 5.9 | 30 | 2 | C49533 | T-cell receptor al |
| 903 | 2 | 5.9 | 30 | 2 | S20778 | Ig heavy chain V r |
| 904 | 2 | 5.9 | 30 | 2 | PL0092 | Ig heavy chain V r |
| 905 | 2 | 5.9 | 30 | 2 | PH0245 | T-cell receptor Vb |
| 906 | 2 | 5.9 | 30 | 2 | PH0228 | T-cell receptor Vb |
| 907 | 2 | 5.9 | 30 | 2 | PH0252 | T-cell receptor Vb |
| 908 | 2 | 5.9 | 30 | 2 | PH0882 | Ig kappa chain V r |
| 909 | 2 | 5.9 | 30 | 2 | E31461 | T-cell receptor de |
| 910 | 2 | 5.9 | 30 | 2 | PH0235 | T-cell receptor Vb |
| 911 | 2 | 5.9 | 30 | 2 | A49533 | T-cell receptor al |
| 912 | 2 | 5.9 | 30 | 2 | C27579 | T-cell receptor be |
| 913 | 2 | 5.9 | 30 | 2 | I37626 | Fc gamma (IgG) rec |
| 914 | 2 | 5.9 | 30 | 2 | PS0121 | H-2 class I histoc |
| 915 | 2 | 5.9 | 30 | 2 | S74192 | crotoxin inhibitor |
| 916 | 2 | 5.9 | 30 | 2 | A05253 | hemoglobin epsilon |
| 917 | 2 | 5.9 | 30 | 2 | A21680 | hemoglobin epsilon |
| 918 | 2 | 5.9 | 30 | 2 | A05254 | hemoglobin epsilon |
| 919 | 2 | 5.9 | 30 | 2 | S68618 | histone H2B - sea |
| 920 | 2 | 5.9 | 30 | 2 | PD0014 | cAMP response elem |
| 921 | 2 | 5.9 | 30 | 2 | PN0651 | restriction endonu |
| 922 | 2 | 5.9 | 30 | 2 | S11613 | ribosomal protein |
| 923 | 2 | 5.9 | 30 | 2 | B29164 | cartilage proteogl |
| 924 | 2 | 5.9 | 30 | 2 | A60511 | gamma-crystallin - |
| 925 | 2 | 5.9 | 30 | 2 | I49412 | gamma-crystallin-3 |

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| 926 | 2 | 5.9 | 30 | 2 | S12965 | gamma-crystallin - |
| 927 | 2 | 5.9 | 30 | 2 | S69269 | ezrin homolog - bo |
| 928 | 2 | 5.9 | 30 | 2 | A61189 | tubulin beta chain |
| 929 | 2 | 5.9 | 30 | 2 | I52806 | Duchenne muscular |
| 930 | 2 | 5.9 | 30 | 2 | S21153 | calcium-binding pr |
| 931 | 2 | 5.9 | 30 | 2 | A26188 | lipocortin I - pig |
| 932 | 2 | 5.9 | 30 | 2 | A56790 | annexin, isoform P |
| 933 | 2 | 5.9 | 30 | 2 | A34622 | fibrinogen beta ch |
| 934 | 2 | 5.9 | 30 | 2 | A03148 | retinol-binding pr |
| 935 | 2 | 5.9 | 30 | 2 | A48299 | taurine transporte |
| 936 | 2 | 5.9 | 30 | 2 | B61511 | serum albumin, mil |
| 937 | 2 | 5.9 | 30 | 2 | B39819 | neutrophil chemota |
| 938 | 2 | 5.9 | 30 | 2 | A38933 | vitronectin - bovi |
| 939 | 2 | 5.9 | 30 | 2 | S57234 | fushi tarazu segme |
| 940 | 2 | 5.9 | 30 | 2 | S69124 | rRNA N-glycosidase |
| 941 | 2 | 5.9 | 30 | 2 | S69125 | rRNA N-glycosidase |
| 942 | 2 | 5.9 | 30 | 2 | S07065 | rRNA N-glycosidase |
| 943 | 2 | 5.9 | 30 | 2 | A31836 | 17K antigen - Rick |
| 944 | 2 | 5.9 | 30 | 2 | PQ0669 | photosystem I 17.5 |
| 945 | 2 | 5.9 | 30 | 2 | E45095 | photosystem I ligh |
| 946 | 2 | 5.9 | 30 | 2 | B45095 | photosystem I ligh |
| 947 | 2 | 5.9 | 30 | 2 | A44913 | 34K core flagella |
| 948 | 2 | 5.9 | 30 | 2 | B24987 | regulatory protein |
| 949 | 2 | 5.9 | 30 | 2 | S30757 | genome polyprotein |
| 950 | 2 | 5.9 | 30 | 2 | S30760 | genome polyprotein |
| 951 | 2 | 5.9 | 30 | 2 | S30759 | genome polyprotein |
| 952 | 2 | 5.9 | 30 | 2 | B44314 | intracisternal A p |
| 953 | 2 | 5.9 | 30 | 2 | S13753 | replication initia |
| 954 | 2 | 5.9 | 30 | 2 | S26175 | tail tubular prote |
| 955 | 2 | 5.9 | 30 | 2 | S69352 | N-methylhydantoin |
| 956 | 2 | 5.9 | 30 | 2 | S68312 | glucuronosyltransf |
| 957 | 2 | 5.9 | 30 | 2 | PH1228 | D-aminoacylase (EC |
| 958 | 2 | 5.9 | 30 | 2 | S42364 | aromatic-amino-aci |
| 959 | 2 | 5.9 | 30 | 2 | S05223 | photosystem I 6.5K |
| 960 | 2 | 5.9 | 30 | 2 | S28991 | antifungal protein |
| 961 | 2 | 5.9 | 30 | 2 | PC2307 | X-Pro aminopeptida |
| 962 | 2 | 5.9 | 30 | 2 | PQ0484 | globulin lb - taro |
| 963 | 2 | 5.9 | 30 | 2 | C43591 | 51K outer membrane |
| 964 | 2 | 5.9 | 30 | 2 | B43591 | 45K outer membrane |
| 965 | 2 | 5.9 | 30 | 2 | S06411 | killer plasmid 28K |
| 966 | 2 | 5.9 | 30 | 2 | B49292 | GDP dissociation i |
| 967 | 2 | 5.9 | 30 | 2 | A60914 | pheromone-binding |
| 968 | 2 | 5.9 | 30 | 2 | PS0437 | potassium channel |
| 969 | 2 | 5.9 | 30 | 2 | PS0438 | potassium channel |
| 970 | 2 | 5.9 | 30 | 2 | A47607 | immunogenic protei |
| 971 | 2 | 5.9 | 30 | 2 | S02088 | blood group Rh-rel |
| 972 | 2 | 5.9 | 30 | 2 | S29138 | aniline monooxygen |
| 973 | 2 | 5.9 | 30 | 2 | S57227 | proboscipedia prot |
| 974 | 2 | 5.9 | 30 | 2 | H95008 | hypothetical prote |
| 975 | 2 | 5.9 | 30 | 2 | C95030 | hypothetical prote |
| 976 | 2 | 5.9 | 30 | 2 | G95031 | hypothetical prote |
| 977 | 2 | 5.9 | 30 | 2 | E95079 | hypothetical prote |
| 978 | 2 | 5.9 | 30 | 2 | F95118 | hypothetical prote |
| 979 | 2 | 5.9 | 30 | 2 | E95145 | hypothetical prote |
| 980 | 2 | 5.9 | 30 | 2 | F89406 | protein R10E8.7 [i |
| 981 | 2 | 5.9 | 30 | 2 | F87254 | hypothetical prote |
| 982 | 2 | 5.9 | 30 | 2 | E84786 | hypothetical prote |

| | | | | | | |
|------|---|-----|----|---|--------|--------------------|
| 983 | 2 | 5.9 | 30 | 2 | C84481 | hypothetical prote |
| 984 | 2 | 5.9 | 30 | 2 | B47483 | cysteine-rich para |
| 985 | 2 | 5.9 | 30 | 2 | S15141 | hypothetical prote |
| 986 | 2 | 5.9 | 30 | 2 | S13985 | hypothetical prote |
| 987 | 2 | 5.9 | 30 | 2 | S14038 | hypothetical prote |
| 988 | 2 | 5.9 | 30 | 2 | S13994 | hypothetical prote |
| 989 | 2 | 5.9 | 30 | 2 | A72205 | hypothetical prote |
| 990 | 2 | 5.9 | 30 | 2 | E72356 | hypothetical prote |
| 991 | 2 | 5.9 | 30 | 2 | H72312 | hypothetical prote |
| 992 | 2 | 5.9 | 30 | 2 | S66448 | trimethylamine deh |
| 993 | 2 | 5.9 | 30 | 2 | A70105 | conserved hypothet |
| 994 | 2 | 5.9 | 30 | 2 | F70118 | hypothetical prote |
| 995 | 2 | 5.9 | 30 | 2 | D70144 | hypothetical prote |
| 996 | 2 | 5.9 | 30 | 2 | H70152 | hypothetical prote |
| 997 | 2 | 5.9 | 30 | 2 | A70209 | hypothetical prote |
| 998 | 2 | 5.9 | 30 | 2 | E70246 | hypothetical prote |
| 999 | 2 | 5.9 | 30 | 2 | F70253 | hypothetical prote |
| 1000 | 2 | 5.9 | 30 | 2 | F70254 | hypothetical prote |

ALIGNMENTS

RESULT 1

A84241

hypothetical protein Vng0840h [imported] - Halobacterium sp. NRC-1

C;Species: Halobacterium sp. NRC-1

C;Date: 02-Feb-2001 #sequence_revision 02-Feb-2001 #text_change 02-Feb-2001

C;Accession: A84241

R;Ng, W.V.; Kennedy, S.P.; Mahairas, G.G.; Berquist, B.; Pan, M.; Shukla, H.D.; Lasky, S.R.; Baliga, N.; Thorsson, V.; Sbrogna, J.; Swartzell, S.; Weir, D.; Hall, J.; Dahl, T.A.; Welte, R.; Goo, Y.A.; Leithauser, B.; Keller, K.; Cruz, R.; Danson, M.J.; Hough, D.W.; Maddocks, D.G.; Jablonski, P.E.; Krebs, M.P.; Angevine, C.M.; Dale, H.; Isenbarger, T.A.; Peck, R.F.; Pohlschrod, M.; Spudich, J.L.; Jung, K.H.; Alam, M.; Freitas, T.

Proc. Natl. Acad. Sci. U.S.A. 97, 12176-12181, 2000

A;Authors: Hou, S.; Daniels, C.J.; Dennis, P.P.; Omer, A.D.; Ebhardt, H.; Lowe, T.M.; Liang, P.; Riley, M.; Hood, L.; DasSarma, S.

A;Title: Genome sequence of Halobacterium species NRC-1.

A;Reference number: A84160; MUID:20504483; PMID:11016950

A;Accession: A84241

A;Status: preliminary

A;Molecule type: DNA

A;Residues: 1-34 <STO>

A;Cross-references: GB:AE004437; NID:g10580410; PIDN:AAG19293.1; GSPDB:GN00138

C;Genetics:

A;Gene: VNG0840H

Query Match 14.7%; Score 5; DB 2; Length 34;
 Best Local Similarity 100.0%; Pred. No. 97;
 Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 24 LRKKL 28
 |||||
 Db 26 LRKKL 30

RESULT 2

B97032

transcription regulator, AcrR family [imported] - *Clostridium acetobutylicum*

C;Species: *Clostridium acetobutylicum*

C;Date: 14-Sep-2001 #sequence_revision 14-Sep-2001 #text_change 14-Sep-2001

C;Accession: B97032

R;Nolling, J.; Breton, G.; Omelchenko, M.V.; Markarova, K.S.; Zeng, Q.; Gibson, R.; Lee, H.M.; Dubois, J.; Qiu, D.; Hitti, J.; Wolf, Y.I.; Tatusov, R.L.; Sabathe, F.; Doucette-Stamm, L.; Soucaille, P.; Daly, M.J.; Bennett, G.N.; Koonin, E.V.; Smith, D.R.

J. Bacteriol. 183, 4823-4838, 2001

A;Title: Genome Sequence and Comparative Analysis of the Solvent-Producing Bacterium *Clostridium acetobutylicum*.

A;Reference number: A96900; MUID:21359325; PMID:21359325

A;Accession: B97032

A;Status: preliminary

A;Molecule type: DNA

A;Residues: 1-34 <KUR>

A;Cross-references: GB:AE001437; PIDN:AAK79045.1; PID:g15023984; GSPDB:GN00168

A;Experimental source: *Clostridium acetobutylicum* ATCC824

C;Genetics:

A;Gene: CAC1071

Query Match 14.7%; Score 5; DB 2; Length 34;

Best Local Similarity 100.0%; Pred. No. 97;

Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 SVSEI 5

|||||

Db 30 SVSEI 34

RESULT 3

E95098

hypothetical protein SP0853 [imported] - *Streptococcus pneumoniae* (strain TIGR4)

C;Species: *Streptococcus pneumoniae*

C;Date: 03-Aug-2001 #sequence_revision 03-Aug-2001 #text_change 03-Aug-2001

C;Accession: E95098

R;Tettelin, H.; Nelson, K.E.; Paulsen, I.T.; Eisen, J.A.; Read, T.D.; Peterson, S.; Heidelberg, J.; DeBoy, R.T.; Haft, D.H.; Dodson, R.J.; Durkin, A.S.; Gwinn, M.; Kolonay, J.F.; Nelson, W.C.; Peterson, J.D.; Umayam, L.A.; White, O.; Salzberg, S.L.; Lewis, M.R.; Radune, D.; Holtzapple, E.; Khouri, H.; Wolf, A.M.; Utterback, T.R.; Hansen, C.L.; McDonald, L.A.; Feldblyum, T.V.; Angiuoli, S.; Dickinson, T.; Hickey, E.K.; Holt, I.E.

Science 293, 498-506, 2001

A;Authors: Loftus, B.J.; Yang, F.; Smith, H.O.; Venter, J.C.; Dougherty, B.A.; Morrison, D.A.; Hollingshead, S.K.; Fraser, C.M.

A;Title: Complete Genome Sequence of a virulent isolate of *Streptococcus pneumoniae*.

A;Reference number: A95000; MUID:21357209; PMID:11463916

A;Accession: E95098

A;Status: preliminary

A;Molecule type: DNA

A;Residues: 1-35 <KUR>

A;Cross-references: GB:AE005672; PIDN:AAK74982.1; PID:g14972326; GSPDB:GN00164; TIGR:SP4SP0853

A;Experimental source: strain TIGR4

C;Genetics:
A;Gene: SP0853

Query Match 14.7%; Score 5; DB 2; Length 35;
Best Local Similarity 100.0%; Pred. No. 1e+02;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 26 KKLQD 30
|||||
Db 30 KKLQD 34

RESULT 4

T09594

gene LFY protein - Monterey pine (fragment)

C;Species: Pinus radiata (Monterey pine)

C;Date: 16-Jul-1999 #sequence_revision 16-Jul-1999 #text_change 16-Jul-1999

C;Accession: T09594

R;Izquierdo, L.Y.; Vergara, R.F.; Alvarez-Buylla, E.R.

submitted to the EMBL Data Library, August 1996

A;Description: Partial characterization of Pinus radiata meristem identity homolog gene (LFY).

A;Reference number: Z16756

A;Accession: T09594

A;Status: preliminary; translated from GB/EMBL/DDBJ

A;Molecule type: DNA

A;Residues: 1-28 <IZQ>

A;Cross-references: EMBL:U66725; NID:g1513305; PID:g1513306

C;Genetics:

A;Gene: LFY

C;Function:

A;Description: controls meristem identity

Query Match 11.8%; Score 4; DB 2; Length 28;
Best Local Similarity 100.0%; Pred. No. 9.7e+02;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 24 LRKK 27
|||||
Db 15 LRKK 18

RESULT 5

A55527

pyrroloquinoline quinone precursor pqqD - Methylobacterium extorquens

C;Species: Methylobacterium extorquens

C;Date: 18-Feb-2000 #sequence_revision 18-Feb-2000 #text_change 18-Feb-2000

C;Accession: A55527

R;Morris, C.J.; Biville, F.; Turlin, E.; Lee, E.; Ellermann, K.; Fan, W.H.; Ramamoorthi, R.; Springer, A.L.; Lidstrom, M.E.

J. Bacteriol. 176, 1746-1755, 1994

A;Title: Isolation, phenotypic characterization, and complementation analysis of mutants of Methylobacterium extorquens AM1 unable to synthesize pyrroloquinoline quinone and sequences of pqqD, pqqG, and pqqC.

A;Reference number: A55527; MUID:94179111; PMID:8132470

A;Accession: A55527

A;Status: preliminary

A;Molecule type: DNA
A;Residues: 1-29 <MOR>
A;Cross-references: GB:L25889; NID:g414589; PIDN:AAA17878.1; PID:g414590
C;Genetics:
A;Gene: pqqD
C;Superfamily: pyrroloquinoline quinone precursor pqqA
C;Keywords: quinoprotein
F;16,20/Product: pyrroloquinoline quinone #status predicted <MAT>
F;16-20/Cross-link: pyrroloquinoline quinone (Glu, Tyr) #status predicted

Query Match 11.8%; Score 4; DB 1; Length 29;
Best Local Similarity 100.0%; Pred. No. 1e+03;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 VSEI 5
|||
Db 8 VSEI 11

RESULT 6

S01614

dystrophin - rat (fragment)

C;Species: Rattus norvegicus (Norway rat)

C;Date: 07-Sep-1990 #sequence_revision 07-Sep-1990 #text_change 20-Jun-2000

C;Accession: S01614

R;Nudel, U.; Robzyk, K.; Yaffe, D.

Nature 331, 635-638, 1988

A;Title: Expression of the putative Duchenne muscular dystrophy gene in differentiated myogenic cell cultures and in the brain.

A;Reference number: S01614; MUID:88122671; PMID:3340214

A;Accession: S01614

A;Status: translation not shown

A;Molecule type: DNA

A;Residues: 1-29 <NUD>

A;Cross-references: EMBL:X07000; NID:g56137; PIDN:CAA30057.1; PID:g1334214

C;Genetics:

A;Map position: X

C;Superfamily: dystrophin; alpha-actinin actin-binding domain homology; spectrin/dystrophin repeat homology; WW repeat homology

C;Keywords: actin binding; cytoskeleton

Query Match 11.8%; Score 4; DB 2; Length 29;
Best Local Similarity 100.0%; Pred. No. 1e+03;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 27 KLQD 30
|||
Db 12 KLQD 15

RESULT 7

I78537

copper transporting P-type ATPase - human (fragment)

C;Species: Homo sapiens (man)

C;Date: 29-May-1998 #sequence_revision 29-May-1998 #text_change 21-Jul-2000

C;Accession: I78537

R;Thomas, G.R.; Forbes, J.R.; Roberts, E.A.; Walshe, J.M.; Cox, D.W.

Nature Genet. 9, 210-217, 1995

A;Title: The Wilson disease gene: spectrum of mutations and their consequences.

A;Reference number: I58128; MUID:95235569; PMID:7626145

A;Accession: I78537

A;Status: preliminary; translated from GB/EMBL/DDBJ

A;Molecule type: DNA

A;Residues: 1-29 <RES>

A;Cross-references: GB:S77450; NID:g957354; PIDN:AAB34087.1; PID:g957355

C;Genetics:

A;Gene: GDB:ATP7B

A;Cross-references: GDB:120494; OMIM:277900

A;Map position: 13q14.3-13q21.1

Query Match 11.8%; Score 4; DB 2; Length 29;
Best Local Similarity 100.0%; Pred. No. 1e+03;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 3 SEIQ 6
|||
Db 14 SEIQ 17

RESULT 8

S78412

ribosomal protein RL22/RL24, mitochondrial [validated] - rat (tentative sequence) (fragment)

C;Species: Rattus norvegicus (Norway rat)

C;Date: 25-Feb-1998 #sequence_revision 13-Mar-1998 #text_change 21-Jul-2000

C;Accession: S78412; S78413

R;Goldschmidt-Reisin, S.; Graack, H.R.

submitted to the Protein Sequence Database, February 1998

A;Reference number: S78411

A;Accession: S78412

A;Molecule type: protein

A;Residues: 1-29 <GOL>

A;Note: the protein is designated as mitochondrial ribosomal protein L22

A;Accession: S78413

A;Molecule type: protein

A;Residues: 1-10, 'XXP', 14-15, 'X', 17-24 <GO2>

A;Note: the protein is designated as mitochondrial ribosomal protein L24

C;Keywords: mitochondrion; protein biosynthesis; ribosome

Query Match 11.8%; Score 4; DB 2; Length 29;
Best Local Similarity 100.0%; Pred. No. 1e+03;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 24 LRKK 27
|||
Db 4 LRKK 7

RESULT 9

S63531

hypothetical protein 1 - Sulfolobus solfataricus (fragment)

C;Species: Sulfolobus solfataricus

C;Date: 28-Oct-1996 #sequence_revision 13-Mar-1997 #text_change 17-Mar-1999

C;Accession: S63531

R;Jones, C.E.; Fleming, T.M.; Cowan, D.A.; Littlechild, J.A.; Piper, P.W.
Eur. J. Biochem. 233, 800-808, 1995

A;Title: The phosphoglycerate kinase and glyceraldehyde-3-phosphate
dehydrogenase genes from the thermophilic archaeon *Sulfolobus solfataricus*
overlap by 8-bp: isolation, sequencing of the genes and expression in
Escherichia coli.

A;Reference number: S63528; MUID:96085144; PMID:8521845

A;Accession: S63531

A;Status: preliminary

A;Molecule type: DNA

A;Residues: 1-30 <JON>

A;Cross-references: EMBL:X80178

Query Match 11.8%; Score 4; DB 2; Length 30;
Best Local Similarity 100.0%; Pred. No. 1e+03;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 23 WLRK 26

||||

Db 11 WLRK 14

RESULT 10

S44471

glucagon G1 - North American paddlefish (*Polyodon spathula*)

C;Species: *Polyodon spathula*

C;Date: 18-Sep-1997 #sequence_revision 18-Sep-1997 #text_change 07-May-1999

C;Accession: S44471

R;Nguyen, T.M.; Mommsen, T.P.; Mims, S.M.; Conlon, J.M.

Biochem. J. 300, 339-345, 1994

A;Title: Characterization of insulins and proglucagon-derived peptides from a
phylogenetically ancient fish, the paddlefish (*Polyodon spathula*).

A;Reference number: S44467; MUID:94271144; PMID:8002937

A;Accession: S44471

A;Molecule type: protein

A;Residues: 1-31 <NGU>

A;Experimental source: pancreas

C;Superfamily: glucagon

C;Keywords: carbohydrate metabolism; duplication; hormone; pancreas

F;1-31/Product: glucagon G1 #status predicted <MAT>

Query Match 11.8%; Score 4; DB 2; Length 31;
Best Local Similarity 100.0%; Pred. No. 1.1e+03;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 21 VEWL 24

||||

Db 23 VEWL 26

RESULT 11

S44472

glucagon G2 - North American paddlefish (*Polyodon spathula*)

C;Species: *Polyodon spathula*

C;Date: 19-Mar-1997 #sequence_revision 12-Dec-1997 #text_change 07-May-1999

C;Accession: S44472

R;Nguyen, T.M.; Mommsen, T.P.; Mims, S.M.; Conlon, J.M.

Biochem. J. 300, 339-345, 1994

A;Title: Characterization of insulins and proglucagon-derived peptides from a phylogenetically ancient fish, the paddlefish (*Polyodon spathula*).

A;Reference number: S44467; MUID:94271144; PMID:8002937

A;Accession: S44472

A;Molecule type: protein

A;Residues: 1-31 <NGU>

A;Note: the sequence from Fig. 3 is inconsistent with that from Fig. 5 in having 29-Glu

C;Superfamily: glucagon

C;Keywords: carbohydrate metabolism; duplication; hormone; pancreas

F;1-31/Product: glucagon G2 #status predicted <GCN>

Query Match 11.8%; Score 4; DB 2; Length 31;
Best Local Similarity 100.0%; Pred. No. 1.1e+03;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 21 VEWL 24
|||
Db 23 VEWL 26

RESULT 12

D70236

hypothetical protein BBH11 - Lyme disease spirochete plasmid H/lp28-3

C;Species: *Borrelia burgdorferi* (Lyme disease spirochete)

C;Date: 13-Feb-1998 #sequence_revision 13-Feb-1998 #text_change 08-Oct-1999

C;Accession: D70236

R;Fraser, C.M.; Casjens, S.; Huang, W.M.; Sutton, G.G.; Clayton, R.; Lathigra, R.; White, O.; Ketchum, K.A.; Dodson, R.; Hickey, E.K.; Gwinn, M.; Dougherty, B.; Tomb, J.F.; Fleischmann, R.D.; Richardson, D.; Peterson, J.; Kerlavage, A.R.; Quackenbush, J.; Salzberg, S.; Hanson, M.; Vugt, R.V.; Palmer, N.; Adams, M.D.; Gocayne, J.; Weidman, J.; Utterback, T.; Watthey, L.; McDonald, L.; Artiach, P.; Bowman, C.; Garland, S.; Fujii, C.; Cotton, M.D.; Horst, K.; Roberts, K.; Hatch, B.

Nature 390, 580-586, 1997

A;Authors: Smith, H.O.; Venter, J.C.

A;Title: Genomic sequence of a Lyme disease spirochaete, *Borrelia burgdorferi*.

A;Reference number: A70100; MUID:98065943; PMID:9403685

A;Accession: D70236

A;Status: preliminary; nucleic acid sequence not shown; translation not shown

A;Molecule type: DNA

A;Residues: 1-31 <KLE>

A;Cross-references: GB:AE000784; NID:g2690041; PIDN:AAC66002.1; PID:g2690058; TIGR:BBH11

A;Experimental source: strain B31

C;Genetics:

A;Genome: plasmid

Query Match 11.8%; Score 4; DB 2; Length 31;
Best Local Similarity 100.0%; Pred. No. 1.1e+03;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 26 KKLQ 29
|||
Db 26 KKLQ 29

RESULT 13

F23454

ovalbumin phosphoserine peptide - fulvous whistling-duck (fragments)

C;Species: Dendrocygna bicolor (fulvous whistling-duck)

C;Date: 05-Jun-1987 #sequence_revision 05-Jun-1987 #text_change 13-Mar-1998

C;Accession: F23454

R;Henderson, J.Y.; Moir, A.J.G.; Fothergill, L.A.; Fothergill, J.E.

Eur. J. Biochem. 114, 439-450, 1981

A;Title: Sequences of sixteen phosphoserine peptides from ovalbumins of eight species.

A;Reference number: A91106; MUID:81164535; PMID:6783411

A;Accession: F23454

A;Molecule type: protein

A;Residues: 1-32 <HEN>

C;Superfamily: antithrombin III

Query Match 11.8%; Score 4; DB 2; Length 32;
Best Local Similarity 100.0%; Pred. No. 1.1e+03;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 SVSE 4
|||
Db 26 SVSE 29

RESULT 14

D31461

T-cell receptor delta chain BDN7, thymus - mouse (fragment)

C;Species: Mus musculus (house mouse)

C;Date: 05-Oct-1989 #sequence_revision 05-Oct-1989 #text_change 30-May-1997

C;Accession: D31461

R;Lacy, M.J.; McNeil, L.K.; Roth, M.E.; Kranz, D.M.

Proc. Natl. Acad. Sci. U.S.A. 86, 1023-1026, 1989

A;Title: T-cell receptor delta-chain diversity in peripheral lymphocytes.

A;Reference number: A31461; MUID:89128840; PMID:2783779

A;Accession: D31461

A;Status: preliminary; not compared with conceptual translation

A;Molecule type: mRNA

A;Residues: 1-32 <LAC>

C;Superfamily: immunoglobulin V region; immunoglobulin homology

C;Keywords: T-cell receptor

Query Match 11.8%; Score 4; DB 2; Length 32;
Best Local Similarity 100.0%; Pred. No. 1.1e+03;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 18 MERV 21
|||
Db 8 MERV 11

RESULT 15

G84161

hypothetical protein Vng0019h [imported] - Halobacterium sp. NRC-1

C;Species: Halobacterium sp. NRC-1

C;Date: 02-Feb-2001 #sequence_revision 02-Feb-2001 #text_change 02-Feb-2001

C;Accession: G84161
 R;Ng, W.V.; Kennedy, S.P.; Mahairas, G.G.; Berquist, B.; Pan, M.; Shukla, H.D.;
 Lasky, S.R.; Baliga, N.; Thorsson, V.; Sbrogna, J.; Swartzell, S.; Weir, D.;
 Hall, J.; Dahl, T.A.; Welte, R.; Goo, Y.A.; Leithauser, B.; Keller, K.; Cruz,
 R.; Danson, M.J.; Hough, D.W.; Maddocks, D.G.; Jablonski, P.E.; Krebs, M.P.;
 Angevine, C.M.; Dale, H.; Isenbarger, T.A.; Peck, R.F.; Pohlschrod, M.; Spudich,
 J.L.; Jung, K.H.; Alam, M.; Freitas, T.
 Proc. Natl. Acad. Sci. U.S.A. 97, 12176-12181, 2000
 A;Authors: Hou, S.; Daniels, C.J.; Dennis, P.P.; Omer, A.D.; Ebhardt, H.; Lowe,
 T.M.; Liang, P.; Riley, M.; Hood, L.; DasSarma, S.
 A;Title: Genome sequence of Halobacterium species NRC-1.
 A;Reference number: A84160; MUID:20504483; PMID:11016950
 A;Accession: G84161
 A;Status: preliminary
 A;Molecule type: DNA
 A;Residues: 1-32 <STO>
 A;Cross-references: GB:AE004437; NID:g10579667; PIDN:AAG18659.1; GSPDB:GN00138
 C;Genetics:
 A;Gene: VNG0019H

Query Match 11.8%; Score 4; DB 2; Length 32;
 Best Local Similarity 100.0%; Pred. No. 1.1e+03;
 Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 27 KLQD 30
 ||||
 Db 13 KLQD 16

RESULT 16

E81714
 hypothetical protein TC0337 [imported] - Chlamydia muridarum (strain Nigg)
 C;Species: Chlamydia muridarum, Chlamydia trachomatis MoPn
 C;Date: 31-Mar-2000 #sequence_revision 31-Mar-2000 #text_change 11-May-2000
 C;Accession: E81714
 R;Read, T.D.; Brunham, R.C.; Shen, C.; Gill, S.R.; Heidelberg, J.F.; White, O.;
 Hickey, E.K.; Peterson, J.; Utterback, T.; Berry, K.; Bass, S.; Linher, K.;
 Weidman, J.; Khouri, H.; Craven, B.; Bowman, C.; Dodson, R.; Gwinn, M.; Nelson,
 W.; DeBoy, R.; Kolonay, J.; McClarty, G.; Salzberg, S.L.; Eisen, J.; Fraser,
 C.M.
 Nucleic Acids Res. 28, 1397-1406, 2000
 A;Title: Genome sequences of Chlamydia trachomatis MoPn and Chlamydia pneumoniae
 AR39.
 A;Reference number: A81500; MUID:20150255; PMID:10684935
 A;Accession: E81714
 A;Status: preliminary
 A;Molecule type: DNA
 A;Residues: 1-33 <TET>
 A;Cross-references: GB:AE002301; GB:AE002160; NID:g7190372; PIDN:AAF39200.1;
 PID:g7190379; GSPDB:GN00121; TIGR:TC0337
 A;Experimental source: strain Nigg (MoPn)
 C;Genetics:
 A;Gene: TC0337

Query Match 11.8%; Score 4; DB 2; Length 33;
 Best Local Similarity 100.0%; Pred. No. 1.1e+03;
 Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 24 LRKK 27
|||
Db 26 LRKK 29

RESULT 17

D23454

ovalbumin phosphoserine peptide - golden pheasant (fragments)

C;Species: Chrysolophus pictus (golden pheasant)

C;Date: 05-Jun-1987 #sequence_revision 05-Jun-1987 #text_change 13-Mar-1998

C;Accession: D23454

R;Henderson, J.Y.; Moir, A.J.G.; Fothergill, L.A.; Fothergill, J.E.

Eur. J. Biochem. 114, 439-450, 1981

A;Title: Sequences of sixteen phosphoserine peptides from ovalbumins of eight species.

A;Reference number: A91106; MUID:81164535; PMID:6783411

A;Accession: D23454

A;Molecule type: protein

A;Residues: 1-35 <HEN>

C;Superfamily: antithrombin III

Query Match 11.8%; Score 4; DB 2; Length 35;
Best Local Similarity 100.0%; Pred. No. 1.2e+03;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 SVSE 4
|||
Db 29 SVSE 32

RESULT 18

G23454

ovalbumin phosphoserine peptide - magpie goose (fragments)

C;Species: Anseranas semipalmata (magpie goose)

C;Date: 05-Jun-1987 #sequence_revision 05-Jun-1987 #text_change 13-Mar-1998

C;Accession: G23454

R;Henderson, J.Y.; Moir, A.J.G.; Fothergill, L.A.; Fothergill, J.E.

Eur. J. Biochem. 114, 439-450, 1981

A;Title: Sequences of sixteen phosphoserine peptides from ovalbumins of eight species.

A;Reference number: A91106; MUID:81164535; PMID:6783411

A;Accession: G23454

A;Molecule type: protein

A;Residues: 1-35 <HEN>

C;Superfamily: antithrombin III

Query Match 11.8%; Score 4; DB 2; Length 35;
Best Local Similarity 100.0%; Pred. No. 1.2e+03;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 SVSE 4
|||
Db 29 SVSE 32

RESULT 19

D82125

hypothetical protein VC2034 [imported] - *Vibrio cholerae* (strain N16961 serogroup O1)

C;Species: *Vibrio cholerae*

C;Date: 18-Aug-2000 #sequence_revision 20-Aug-2000 #text_change 02-Feb-2001

C;Accession: D82125

R;Heidelberg, J.F.; Eisen, J.A.; Nelson, W.C.; Clayton, R.A.; Gwinn, M.L.; Dodson, R.J.; Haft, D.H.; Hickey, E.K.; Peterson, J.D.; Umayam, L.A.; Gill, S.R.; Nelson, K.E.; Read, T.D.; Tettelin, H.; Richardson, D.; Ermolaeva, M.D.; Vamathevan, J.; Bass, S.; Qin, H.; Dragoi, I.; Sellers, P.; McDonald, L.; Utterback, T.; Fleishmann, R.D.; Nierman, W.C.; White, O.; Salzberg, S.L.; Smith, H.O.; Colwell, R.R.; Mekalanos, J.J.; Venter, J.C.; Fraser, C.M.
Nature 406, 477-483, 2000

A;Title: DNA Sequence of both chromosomes of the cholera pathogen *Vibrio cholerae*.

A;Reference number: A82035; MUID:20406833; PMID:10952301

A;Accession: D82125

A;Status: preliminary

A;Molecule type: DNA

A;Residues: 1-35 <HEI>

A;Cross-references: GB:AE004278; GB:AE003852; NID:g9656579; PIDN:AAF95182.1;

GSPDB:GN00126; TIGR:VC2034

A;Experimental source: serogroup O1; strain N16961; biotype El Tor

C;Genetics:

A;Gene: VC2034

A;Map position: 1

Query Match 11.8%; Score 4; DB 2; Length 35;
Best Local Similarity 100.0%; Pred. No. 1.2e+03;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 26 KKLQ 29

||||

Db 24 KKLQ 27

RESULT 20

S70806

hypothetical protein 5 - *Vibrio cholerae* (fragment)

N;Alternate names: flagellar protein flaA homolog

C;Species: *Vibrio cholerae*

C;Date: 12-Feb-1998 #sequence_revision 20-Feb-1998 #text_change 26-Aug-1999

C;Accession: S70806

R;Camilli, A.; Mekalanos, J.J.

Mol. Microbiol. 18, 671-683, 1995

A;Title: Use of recombinase gene fusions to identify *Vibrio cholerae* genes induced during infection.

A;Reference number: S70798; MUID:96414469; PMID:8817490

A;Accession: S70806

A;Status: preliminary; nucleic acid sequence not shown

A;Molecule type: DNA

A;Residues: 1-36 <CAM>

A;Cross-references: EMBL:U25820; NID:g1165195; PIDN:AAC43560.1; PID:g1165196

C;Superfamily: flagellin

Query Match 11.8%; Score 4; DB 2; Length 36;
Best Local Similarity 100.0%; Pred. No. 1.2e+03;

Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 17 SMER 20
 ||||
Db 14 SMER 17

RESULT 21

F95057

hypothetical protein SP0497 [imported] - Streptococcus pneumoniae (strain TIGR4)

C;Species: Streptococcus pneumoniae

C;Date: 03-Aug-2001 #sequence_revision 03-Aug-2001 #text_change 03-Aug-2001

C;Accession: F95057

R;Tettelin, H.; Nelson, K.E.; Paulsen, I.T.; Eisen, J.A.; Read, T.D.; Peterson, S.; Heidelberg, J.; DeBoy, R.T.; Haft, D.H.; Dodson, R.J.; Durkin, A.S.; Gwinn, M.; Kolonay, J.F.; Nelson, W.C.; Peterson, J.D.; Umayam, L.A.; White, O.; Salzberg, S.L.; Lewis, M.R.; Radune, D.; Holtzapple, E.; Khouri, H.; Wolf, A.M.; Utterback, T.R.; Hansen, C.L.; McDonald, L.A.; Feldblyum, T.V.; Angiuoli, S.; Dickinson, T.; Hickey, E.K.; Holt, I.E.

Science 293, 498-506, 2001

A;Authors: Loftus, B.J.; Yang, F.; Smith, H.O.; Venter, J.C.; Dougherty, B.A.;

Morrison, D.A.; Hollingshead, S.K.; Fraser, C.M.

A;Title: Complete Genome Sequence of a virulent isolate of Streptococcus pneumoniae.

A;Reference number: A95000; MUID:21357209; PMID:11463916

A;Accession: F95057

A;Status: preliminary

A;Molecule type: DNA

A;Residues: 1-36 <KUR>

A;Cross-references: GB:AE005672; PIDN:AAK74655.1; PID:g14971969; GSPDB:GN00164; TIGR:SP4SP0497

A;Experimental source: strain TIGR4

C;Genetics:

A;Gene: SP0497

Query Match 11.8%; Score 4; DB 2; Length 36;
Best Local Similarity 100.0%; Pred. No. 1.2e+03;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 26 KKLQ 29
 ||||
Db 10 KKLQ 13

RESULT 22

A84774

hypothetical protein At2g35870 [imported] - Arabidopsis thaliana

C;Species: Arabidopsis thaliana (mouse-ear cress)

C;Date: 02-Feb-2001 #sequence_revision 02-Feb-2001 #text_change 02-Feb-2001

C;Accession: A84774

R;Lin, X.; Kaul, S.; Rounsley, S.D.; Shea, T.P.; Benito, M.I.; Town, C.D.; Fujii, C.Y.; Mason, T.M.; Bowman, C.L.; Barnstead, M.E.; Feldblyum, T.V.; Buell, C.R.; Ketchum, K.A.; Lee, J.J.; Ronning, C.M.; Koo, H.; Moffat, K.S.; Cronin, L.A.; Shen, M.; VanAken, S.E.; Umayam, L.; Tallon, L.J.; Gill, J.E.; Adams, M.D.; Carrera, A.J.; Creasy, T.H.; Goodman, H.M.; Somerville, C.R.; Copenhaver, G.P.; Preuss, D.; Nierman, W.C.; White, O.; Eisen, J.A.; Salzberg, S.L.; Fraser, C.M.; Venter, J.C.

Nature 402, 761-768, 1999

A;Title: Sequence and analysis of chromosome 2 of the plant *Arabidopsis thaliana*.

A;Reference number: A84420; MUID:20083487; PMID:10617197

A;Accession: A84774

A;Status: preliminary

A;Molecule type: DNA

A;Residues: 1-36 <STO>

A;Cross-references: GB:AE002093; NID:g4510382; PIDN:AAD21470.1; GSPDB:GN00139

C;Genetics:

A;Gene: At2g35870

A;Map position: 2

Query Match 11.8%; Score 4; DB 2; Length 36;
Best Local Similarity 100.0%; Pred. No. 1.2e+03;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 26 KKLQ 29
 ||||
Db 4 KKLQ 7

RESULT 23

S46227

hypothetical protein - *Streptomyces chrysomallus* (fragment)

C;Species: *Streptomyces chrysomallus*

C;Date: 19-Mar-1997 #sequence_revision 29-Aug-1997 #text_change 28-May-1999

C;Accession: S46227

R;Pahl, A.; Keller, U.

EMBO J. 13, 3472-3480, 1994

A;Title: *Streptomyces chrysomallus* FKBP-33 is a novel immunophilin consisting of two FK506 binding domains; its gene is transcriptionally coupled to the FKBP-12 gene.

A;Reference number: S46227; MUID:94341259; PMID:8062824

A;Accession: S46227

A;Molecule type: DNA

A;Residues: 1-36 <PAH>

A;Cross-references: GB:Z34523; NID:g535270; PIDN:CAA84281.1; PID:g633645

A;Experimental source: strain ATCC 11523

Query Match 11.8%; Score 4; DB 2; Length 36;
Best Local Similarity 100.0%; Pred. No. 1.2e+03;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 19 ERVE 22
 ||||
Db 27 ERVE 30

RESULT 24

S71912

hemoglobin, extracellular, chain A1 - polychaete (*Perinereis aibuhitensis*) (fragment)

C;Species: *Perinereis aibuhitensis*

C;Date: 14-Apr-1998 #sequence_revision 08-May-1998 #text_change 02-Jul-1998

C;Accession: S71912

R;Matsubara, K.; Yamaki, M.; Nagayama, K.; Imai, K.; Ishii, H.; Gotoh, T.; Ebina, S.

Biochim. Biophys. Acta 1290, 215-223, 1996

A;Title: Wheat germ agglutinin-reactive chains of giant hemoglobin from the polychaete *Perinereis aibuhitensis*.

A;Reference number: S71912; MUID:96350431; PMID:8765123

A;Accession: S71912

A;Molecule type: protein

A;Residues: 1-37 <MAT>

C;Superfamily: globin; globin homology

C;Keywords: chromoprotein; heme; iron; oxygen carrier

Query Match 11.8%; Score 4; DB 2; Length 37;
Best Local Similarity 100.0%; Pred. No. 1.2e+03;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 19 ERVE 22
 ||||
Db 25 ERVE 28

RESULT 25

T12635

homeotic protein HAHB-2 - common sunflower (fragment)

C;Species: *Helianthus annuus* (common sunflower)

C;Date: 13-Aug-1999 #sequence_revision 13-Aug-1999 #text_change 21-Jul-2000

C;Accession: T12635

R;Chan, R.L.; Gonzalez, D.H.

Plant Physiol. 106, 1687-1688, 1994

A;Title: A cDNA encoding an HD-zip protein from sunflower.

A;Reference number: Z17563; MUID:95148747; PMID:7846169

A;Accession: T12635

A;Status: preliminary; translated from GB/EMBL/DDBJ

A;Molecule type: mRNA

A;Residues: 1-37 <CHA>

A;Cross-references: EMBL:L22849; NID:g349258; PIDN:AAA63766.1; PID:g349259

C;Keywords: DNA binding; homeobox; transcription regulation

Query Match 11.8%; Score 4; DB 2; Length 37;
Best Local Similarity 100.0%; Pred. No. 1.2e+03;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 25 RKKL 28
 ||||
Db 6 RKKL 9

RESULT 26

A43933

antigen 5 epitope - tapeworm (*Echinococcus granulosus*) (fragment)

C;Species: *Echinococcus granulosus*

C;Date: 10-Mar-1993 #sequence_revision 18-Nov-1994 #text_change 18-Nov-1994

C;Accession: A43933

R;Chamekh, M.; Gras-Masse, H.; Bossus, M.; Facon, B.; Dissous, C.; Tartar, A.; Capron, A.

J. Clin. Invest. 89, 458-464, 1992

A;Title: Diagnostic value of a synthetic peptide derived from Echinococcus granulosus recombinant protein.

A;Reference number: A43933; MUID:92147859; PMID:1737836

A;Accession: A43933

A;Status: preliminary; not compared with conceptual translation

A;Molecule type: mRNA

A;Residues: 1-37 <CHA>

A;Cross-references: GB:M74034

A;Note: sequence extracted from NCBI backbone (NCBIP:81239)

Query Match 11.8%; Score 4; DB 2; Length 37;
Best Local Similarity 100.0%; Pred. No. 1.2e+03;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 10 NKGK 13
 ||||
Db 10 NKGK 13

RESULT 27

CKFHCS

sarcotoxin IC - flesh fly (Sarcophaga peregrina)

C;Species: Sarcophaga peregrina

C;Date: 31-Mar-1988 #sequence_revision 31-Mar-1988 #text_change 08-Dec-1995

C;Accession: C22625

R;Okada, M.; Natori, S.

J. Biol. Chem. 260, 7174-7177, 1985

A;Title: Primary structure of sarcotoxin I, an antibacterial protein induced in the hemolymph of Sarcophaga peregrina (flesh fly) larvae.

A;Reference number: A92536; MUID:85207747; PMID:3888997

A;Accession: C22625

A;Molecule type: protein

A;Residues: 1-39 <OKA>

C;Comment: Sarcotoxins, which are potent bactericidal proteins, are produced in response to injury. They are cytotoxic to both Gram positive and Gram negative bacteria.

C;Superfamily: cecropin

C;Keywords: amidated carboxyl end; antibacterial; hemolymph

F;39/Modified site: amidated carboxyl end (Arg) #status predicted

Query Match 11.8%; Score 4; DB 1; Length 39;
Best Local Similarity 100.0%; Pred. No. 1.3e+03;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 23 WLRK 26
 ||||
Db 2 WLRK 5

RESULT 28

S71913

hemoglobin, extracellular, chain A2 - polychaete (Perinereis aibuhitensis) (fragment)

C;Species: Perinereis aibuhitensis

C;Date: 14-Apr-1998 #sequence_revision 08-May-1998 #text_change 02-Jul-1998

C;Accession: S71913

R;Matsubara, K.; Yamaki, M.; Nagayama, K.; Imai, K.; Ishii, H.; Gotoh, T.; Ebina, S.
Biochim. Biophys. Acta 1290, 215-223, 1996
A;Title: Wheat germ agglutinin-reactive chains of giant hemoglobin from the polychaete *Perinereis aibuhitensis*.
A;Reference number: S71912; MUID:96350431; PMID:8765123
A;Accession: S71913
A;Molecule type: protein
A;Residues: 1-39 <MAT>
C;Superfamily: globin; globin homology
C;Keywords: chromoprotein; heme; iron; oxygen carrier

Query Match 11.8%; Score 4; DB 2; Length 39;
Best Local Similarity 100.0%; Pred. No. 1.3e+03;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 19 ERVE 22
|||
Db 27 ERVE 30

RESULT 29

S77164

ycf32 protein - *Synechocystis* sp. (strain PCC 6803)

N;Alternate names: protein sml0007

C;Species: *Synechocystis* sp.

A;Variety: PCC 6803

C;Date: 25-Apr-1997 #sequence_revision 25-Apr-1997 #text_change 20-Jun-2000

C;Accession: S77164

R;Kaneko, T.; Sato, S.; Kotani, H.; Tanaka, A.; Asamizu, E.; Nakamura, Y.; Miyajima, N.; Hirosawa, M.; Sugiura, M.; Sasamoto, S.; Kimura, T.; Hosouchi, T.; Matsuno, A.; Muraki, A.; Nakazaki, N.; Naruo, K.; Okumura, S.; Shimpō, S.; Takeuchi, C.; Wada, T.; Watanabe, A.; Yamada, M.; Yasuda, M.; Tabata, S.

DNA Res. 3, 109-136, 1996

A;Title: Sequence analysis of the genome of the unicellular cyanobacterium *Synechocystis* sp. PCC6803. II. Sequence determination of the entire genome and assignment of potential protein-coding regions.

A;Reference number: S74322; MUID:97061201; PMID:8905231

A;Accession: S77164

A;Status: nucleic acid sequence not shown; translation not shown

A;Molecule type: DNA

A;Residues: 1-39 <KAN>

A;Cross-references: EMBL:D90908; GB:AB001339; NID:g1652725; PIDN:BAA17722.1; PID:g1652803

A;Note: the nucleotide sequence was submitted to the EMBL Data Library, June 1996

C;Genetics:

A;Gene: ycf32

C;Superfamily: hypothetical protein ycf32

Query Match 11.8%; Score 4; DB 2; Length 39;
Best Local Similarity 100.0%; Pred. No. 1.3e+03;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 28 LQDV 31
|||
Db 31 LQDV 34

RESULT 30

A42272

brain-type creatine kinase, peptide, B - spiny dogfish (fragment)

C;Species: Squalus acanthias (spiny dogfish)

C;Date: 04-Mar-1993 #sequence_revision 18-Nov-1994 #text_change 11-Apr-1997

C;Accession: A42272

R;Friedman, D.L.; Roberts, R.

J. Biol. Chem. 267, 4270-4276, 1992

A;Title: Purification and localization of brain-type creatine kinase in sodium chloride transporting epithelia of the spiny dogfish, Squalus acanthias.

A;Reference number: A42272; MUID:92156175; PMID:1310991

A;Accession: A42272

A;Status: preliminary

A;Molecule type: protein

A;Residues: 1-28 <FRI>

A;Note: sequence extracted from NCBI backbone (NCBIP:82919)

C;Superfamily: creatine kinase; creatine kinase repeat homology

Query Match 8.8%; Score 3; DB 2; Length 28;
Best Local Similarity 100.0%; Pred. No. 1.1e+04;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 26 KKL 28

|||

Db 10 KKL 12

RESULT 31

C32416

phospholipase A2 (EC 3.1.1.4) pseudexin chain C - red-bellied black snake (fragment)

C;Species: Pseudechis porphyriacus (red-bellied black snake)

C;Date: 05-Oct-1989 #sequence_revision 05-Oct-1989 #text_change 23-Jun-1993

C;Accession: C32416

R;Schmidt, J.J.; Middlebrook, J.L.

Toxicon 27, 805-818, 1989

A;Title: Purification, sequencing and characterization of pseudexin phospholipases A-2 from Pseudechis porphyriacus (Australian red-bellied black snake).

A;Reference number: A32416; MUID:89388835; PMID:2675391

A;Accession: C32416

A;Status: preliminary

A;Molecule type: protein

A;Residues: 1-28 <SCH>

C;Superfamily: phospholipase A2

C;Keywords: carboxylic ester hydrolase

Query Match 8.8%; Score 3; DB 2; Length 28;
Best Local Similarity 100.0%; Pred. No. 1.1e+04;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 5 IQL 7

|||

Db 3 IQL 5

RESULT 32

B60071

vasoactive intestinal peptide - rhesus macaque

C;Species: Macaca mulatta (rhesus macaque)

C;Date: 28-Apr-1993 #sequence_revision 28-Apr-1993 #text_change 20-Mar-1998

C;Accession: B60071

R;Yu, J.; Xin, Y.; Eng, J.; Yalow, R.S.

Regul. Pept. 32, 39-45, 1991

A;Title: Rhesus monkey gastroenteropancreatic hormones: relationship to human sequences.

A;Reference number: A60071; MUID:91164506; PMID:2003150

A;Accession: B60071

A;Status: protein sequence not shown

A;Molecule type: protein

A;Residues: 1-28 <YUA>

A;Note: the sequence is identical with the human sequence

C;Superfamily: glucagon

C;Keywords: duplication; hormone; intestine; neuropeptide; vasodilator

Query Match 8.8%; Score 3; DB 2; Length 28;
Best Local Similarity 100.0%; Pred. No. 1.1e+04;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 15 LNS 17
|||
Db 23 LNS 25

RESULT 33

A60304

vasoactive intestinal peptide - dog

N;Alternate names: VIP

C;Species: Canis lupus familiaris (dog)

C;Date: 15-Jan-1993 #sequence_revision 15-Jan-1993 #text_change 20-Mar-1998

C;Accession: A60304

R;Eng, J.; Pan, Y.C.E.; Raufman, J.P.; Yalow, R.S.

Regul. Pept. Suppl. 3, S14, 1985

A;Title: Purification and sequencing of dog and guinea pig VIP's.

A;Reference number: A60304

A;Accession: A60304

A;Molecule type: protein

A;Residues: 1-28 <ENG>

C;Superfamily: glucagon

C;Keywords: duplication; hormone; intestine; neuropeptide; vasodilator

Query Match 8.8%; Score 3; DB 2; Length 28;
Best Local Similarity 100.0%; Pred. No. 1.1e+04;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 15 LNS 17
|||
Db 23 LNS 25

RESULT 34

S58386

T-cell receptor beta-chain Vb11-Jb2.4 - mouse (fragment)
 C;Species: Mus musculus (house mouse)
 C;Date: 29-Nov-1995 #sequence_revision 01-Mar-1996 #text_change 23-Jul-1999
 C;Accession: S58386
 R;Johnston, S.L.; Strausbauch, M.; Sarkar, G.; Wettstein, P.J.
 Nucleic Acids Res. 23, 3074-3075, 1995
 A;Title: A novel method for sequencing members of multi-gene families.
 A;Reference number: S58384; MUID:95388532; PMID:7659534
 A;Accession: S58386
 A;Status: preliminary; nucleic acid sequence not shown
 A;Molecule type: mRNA
 A;Residues: 1-28 <JOH>
 A;Cross-references: EMBL:U20300; NID:g663123; PIDN:AAA62247.1; PID:g663124
 A;Note: the nucleotide sequence was submitted to the EMBL Data Library, January 1995
 A;Note: only a part of the coding sequence is given
 C;Superfamily: immunoglobulin V region; immunoglobulin homology
 C;Keywords: T-cell receptor

Query Match 8.8%; Score 3; DB 2; Length 28;
 Best Local Similarity 100.0%; Pred. No. 1.1e+04;
 Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 19 ERV 21
 |||
 Db 12 ERV 14

RESULT 35

S10052
 ribosomal protein L37.e - fission yeast (Schizosaccharomyces pombe) (fragment)
 N;Alternate names: ribosomal protein SP-L27
 C;Species: Schizosaccharomyces pombe
 C;Date: 31-Dec-1990 #sequence_revision 31-Dec-1990 #text_change 30-Sep-1993
 C;Accession: S10052
 R;Otaka, E.; Higo, K.I.; Itoh, T.
 Mol. Gen. Genet. 191, 519-524, 1983
 A;Title: Yeast ribosomal proteins: VII. Cytoplasmic ribosomal proteins from Schizosaccharomyces pombe.
 A;Reference number: S07293; MUID:84038947; PMID:6355773
 A;Accession: S10052
 A;Molecule type: protein
 A;Residues: 1-28 <OTA>
 C;Superfamily: rat ribosomal protein L37
 C;Keywords: protein biosynthesis; ribosome

Query Match 8.8%; Score 3; DB 2; Length 28;
 Best Local Similarity 100.0%; Pred. No. 1.1e+04;
 Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 11 KGK 13
 |||
 Db 21 KGK 23

RESULT 36

A60752

outer membrane protein A - *Yersinia pseudotuberculosis* (fragment)
 N;Alternate names: heat-modifiable protein; outer membrane protein II
 C;Species: *Yersinia pseudotuberculosis*
 C;Date: 14-May-1993 #sequence_revision 14-May-1993 #text_change 17-Mar-1999
 C;Accession: A60752
 R;Zhang, J.J.; Hamachi, M.; Hamachi, T.; Zhao, Y.P.; Yu, D.T.Y.
 J. Immunol. 143, 2955-2960, 1989
 A;Title: The bacterial outer membrane protein that reacts with anti-HLA-B27
 antibodies is the OmpA protein.
 A;Reference number: A60752; MUID:90038529; PMID:2478630
 A;Accession: A60752
 A;Molecule type: protein
 A;Residues: 1-28 <ZHA>
 C;Genetics:
 A;Gene: ompA
 C;Superfamily: outer membrane protein A
 C;Keywords: membrane protein

Query Match 8.8%; Score 3; DB 2; Length 28;
 Best Local Similarity 100.0%; Pred. No. 1.1e+04;
 Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 10 NKG 12
 |||
 Db 26 NKG 28

RESULT 37

S56121

type I DNA methyltransferase M.EcoR124I chain HsdS - *Escherichia coli*
 (fragments)

C;Species: *Escherichia coli*
 C;Date: 27-Oct-1995 #sequence_revision 03-Nov-1995 #text_change 03-Nov-1995
 C;Accession: S56121
 R;Webb, M.; Taylor, I.A.; Firman, K.; Kneale, G.G.
 J. Mol. Biol. 250, 181-190, 1995
 A;Title: Probing the domain structure of the type IC DNA methyltransferase
 M.EcoR124I by limited proteolysis.
 A;Reference number: S56121; MUID:95333175; PMID:7608969
 A;Accession: S56121
 A;Status: preliminary
 A;Molecule type: protein
 A;Residues: 1-28 <WEB>

Query Match 8.8%; Score 3; DB 2; Length 28;
 Best Local Similarity 100.0%; Pred. No. 1.1e+04;
 Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 30 DVH 32
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 Db 8 DVH 10

RESULT 38

S70894

hypothetical protein 1 - *Vibrio anguillarum* (fragment)
 C;Species: *Vibrio anguillarum*

C;Date: 19-Mar-1997 #sequence_revision 25-Apr-1997 #text_change 08-Oct-1999
 C;Accession: S70894
 R;O'Toole, R.; Milton, D.L.; Wolf-Watz, H.
 Mol. Microbiol. 19, 625-637, 1996
 A;Title: Chemotactic motility is required for invasion of the host by the fish
 pathogen *Vibrio anguillarum*.
 A;Reference number: S70894; MUID:96228710; PMID:8830252
 A;Accession: S70894
 A;Status: preliminary
 A;Molecule type: DNA
 A;Residues: 1-28 <OTO>
 A;Cross-references: GB:U36378; EMBL:L47344; NID:g1020321; PIDN:AAB38488.1;
 PID:g1723992

Query Match 8.8%; Score 3; DB 2; Length 28;
 Best Local Similarity 100.0%; Pred. No. 1.1e+04;
 Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 15 LNS 17
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 Db 18 LNS 20

RESULT 39

S22469

hypothetical protein 1 - *Prochlorothrix hollandica*

C;Species: *Prochlorothrix hollandica*

C;Date: 13-Jan-1995 #sequence_revision 13-Jan-1995 #text_change 15-Oct-1999

C;Accession: S22469; S16850

R;Greer, K.L.; Golden, S.S.

Plant Mol. Biol. 19, 355-365, 1992

A;Title: Conserved relationship between psbH and petBD genes: presence of a
 shared upstream element in *Prochlorothrix hollandica*.

A;Reference number: S22469; MUID:92322967; PMID:1623188

A;Accession: S22469

A;Status: preliminary

A;Molecule type: DNA

A;Residues: 1-28 <GRE>

A;Cross-references: EMBL:X60313; NID:g45528; PIDN:CAA42858.1; PID:g45529

Query Match 8.8%; Score 3; DB 2; Length 28;
 Best Local Similarity 100.0%; Pred. No. 1.1e+04;
 Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 SVS 3
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 Db 4 SVS 6

RESULT 40

C60683

malate dehydrogenase (decarboxylating) (EC 1.1.1.39) - *tampala* (fragment)

N;Alternate names: NAD-malic enzyme

C;Species: *Amaranthus tricolor* (*tampala*)

C;Date: 30-Sep-1993 #sequence_revision 30-Sep-1993 #text_change 07-Feb-1997

C;Accession: C60683

R;Murata, T.; Ikeda, J.; Takano, M.; Ohsugi, R.

Plant Cell Physiol. 30, 429-437, 1989

A;Title: Comparative studies of NAD-malic enzyme from leaves of various C-4 plants.

A;Reference number: A60683

A;Accession: C60683

A;Molecule type: protein

A;Residues: 1-28 <MUR>

C;Keywords: NAD; oxidoreductase; photosynthesis

Query Match 8.8%; Score 3; DB 2; Length 28;

Best Local Similarity 100.0%; Pred. No. 1.1e+04;

Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 10 NKG 12

|||

Db 25 NKG 27

Search completed: January 14, 2004, 10:37:23

Job time : 11.0623 secs

GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: January 14, 2004, 10:37:44 ; Search time 22.8785 Seconds
(without alignments)
303.882 Million cell updates/sec

Title: US-09-843-221A-163
Perfect score: 34
Sequence: 1 SVSEIQLMHNKGKHLNSMERVEWLRKKLQDVHNF 34

Scoring table: OLIGO
Gapop 60.0 , Gapext 60.0

Searched: 762491 seqs, 204481190 residues

Word size : 0

Total number of hits satisfying chosen parameters: 28045

Minimum DB seq length: 28
Maximum DB seq length: 40

Post-processing: Listing first 1000 summaries

Database : Published_Applications_AA:*
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18: /cgn2_6/ptodata/1/pubpaa/US60_PUBCOMB.pep:*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

| Result | % | Query | | | | |
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| 2 | 34 | 100.0 | 34 | 11 | US-09-843-221A-163 | Sequence 163, App |
| 3 | 30 | 88.2 | 30 | 11 | US-09-843-221A-41 | Sequence 41, Appl |
| 4 | 23 | 67.6 | 28 | 11 | US-09-843-221A-32 | Sequence 32, Appl |
| 5 | 23 | 67.6 | 34 | 9 | US-09-169-786-3 | Sequence 3, Appli |
| 6 | 23 | 67.6 | 34 | 10 | US-09-928-047B-6 | Sequence 6, Appli |
| 7 | 23 | 67.6 | 34 | 11 | US-09-843-221A-16 | Sequence 16, Appl |
| 8 | 23 | 67.6 | 34 | 11 | US-09-843-221A-17 | Sequence 17, Appl |
| 9 | 23 | 67.6 | 34 | 11 | US-09-843-221A-20 | Sequence 20, Appl |
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| 45 | 18 | 52.9 | 40 | 15 | US-10-014-162-111 | Sequence 111, App |
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| 168 | 6 | 17.6 | 31 | 14 | US-10-097-079-82 | Sequence 82, Appl |
| 169 | 6 | 17.6 | 31 | 14 | US-10-097-079-83 | Sequence 83, Appl |
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| 182 | 5 | 14.7 | 34 | 11 | US-09-843-221A-123 | Sequence 123, App |
| 183 | 5 | 14.7 | 34 | 12 | US-10-317-832-178 | Sequence 178, App |
| 184 | 5 | 14.7 | 38 | 9 | US-09-864-761-49110 | Sequence 49110, A |
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| 187 | 4 | 11.8 | 28 | 9 | US-09-929-818-122 | Sequence 122, App |
| 188 | 4 | 11.8 | 28 | 9 | US-09-929-818-200 | Sequence 200, App |
| 189 | 4 | 11.8 | 28 | 10 | US-09-003-869-153 | Sequence 153, App |
| 190 | 4 | 11.8 | 28 | 10 | US-09-999-745-38 | Sequence 38, Appl |
| 191 | 4 | 11.8 | 28 | 10 | US-09-554-000-22 | Sequence 22, Appl |
| 192 | 4 | 11.8 | 28 | 11 | US-09-756-690A-153 | Sequence 153, App |
| 193 | 4 | 11.8 | 28 | 11 | US-09-899-495-104 | Sequence 104, App |
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| 195 | 4 | 11.8 | 28 | 15 | US-10-157-224A-153 | Sequence 153, App |
| 196 | 4 | 11.8 | 28 | 15 | US-10-187-051-153 | Sequence 153, App |
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| 198 | 4 | 11.8 | 29 | 9 | US-09-815-248-18 | Sequence 18, Appl |
| 199 | 4 | 11.8 | 29 | 11 | US-09-983-802-386 | Sequence 386, App |
| 200 | 4 | 11.8 | 29 | 11 | US-09-983-802-480 | Sequence 480, App |
| 201 | 4 | 11.8 | 29 | 11 | US-09-969-730-133 | Sequence 133, App |
| 202 | 4 | 11.8 | 29 | 11 | US-09-095-478-24 | Sequence 24, Appl |
| 203 | 4 | 11.8 | 29 | 12 | US-10-131-909A-4 | Sequence 4, Appli |
| 204 | 4 | 11.8 | 29 | 12 | US-09-933-767-1006 | Sequence 1006, Ap |
| 205 | 4 | 11.8 | 29 | 15 | US-10-018-103A-4 | Sequence 4, Appli |
| 206 | 4 | 11.8 | 29 | 15 | US-10-023-282-1006 | Sequence 1006, Ap |
| 207 | 4 | 11.8 | 29 | 15 | US-10-106-698-5404 | Sequence 5404, Ap |
| 208 | 4 | 11.8 | 29 | 15 | US-10-197-954-111 | Sequence 111, App |
| 209 | 4 | 11.8 | 30 | 9 | US-09-864-761-41441 | Sequence 41441, A |
| 210 | 4 | 11.8 | 30 | 9 | US-09-864-761-46868 | Sequence 46868, A |
| 211 | 4 | 11.8 | 30 | 10 | US-09-756-983-20 | Sequence 20, Appl |
| 212 | 4 | 11.8 | 30 | 11 | US-09-774-639-191 | Sequence 191, App |
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| 214 | 4 | 11.8 | 30 | 12 | US-10-310-113-19 | Sequence 19, Appl |
| 215 | 4 | 11.8 | 30 | 12 | US-09-933-767-821 | Sequence 821, App |
| 216 | 4 | 11.8 | 30 | 12 | US-10-173-551-40 | Sequence 40, Appl |
| 217 | 4 | 11.8 | 30 | 15 | US-10-188-947-11 | Sequence 11, Appl |
| 218 | 4 | 11.8 | 30 | 15 | US-10-057-408-20 | Sequence 20, Appl |
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| 223 | 4 | 11.8 | 31 | 9 | US-09-864-761-44182 | Sequence 44182, A |
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| 226 | 4 | 11.8 | 31 | 12 | US-09-933-767-1001 | Sequence 1001, Ap |
| 227 | 4 | 11.8 | 31 | 12 | US-10-029-386-32285 | Sequence 32285, A |

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| 229 | 4 | 11.8 | 31 | 15 | US-10-023-282-1001 | Sequence 1001, Ap |
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| 240 | 4 | 11.8 | 32 | 12 | US-10-164-279-43 | Sequence 43, Appl |
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| 250 | 4 | 11.8 | 33 | 11 | US-09-809-391-660 | Sequence 660, App |
| 251 | 4 | 11.8 | 33 | 12 | US-09-882-171-660 | Sequence 660, App |
| 252 | 4 | 11.8 | 33 | 12 | US-09-933-767-368 | Sequence 368, App |
| 253 | 4 | 11.8 | 33 | 12 | US-10-164-279-63 | Sequence 63, Appl |
| 254 | 4 | 11.8 | 33 | 14 | US-10-215-297-4 | Sequence 4, Appli |
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| 259 | 4 | 11.8 | 34 | 9 | US-09-864-761-45430 | Sequence 45430, A |
| 260 | 4 | 11.8 | 34 | 9 | US-09-864-761-48511 | Sequence 48511, A |
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| 263 | 4 | 11.8 | 34 | 15 | US-10-106-698-8037 | Sequence 8037, Ap |
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| 267 | 4 | 11.8 | 35 | 11 | US-09-820-843A-106 | Sequence 106, App |
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| 272 | 4 | 11.8 | 35 | 15 | US-10-133-128-75 | Sequence 75, Appl |
| 273 | 4 | 11.8 | 35 | 15 | US-10-062-831-138 | Sequence 138, App |
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| 283 | 4 | 11.8 | 36 | 15 | US-10-050-704-192 | Sequence 192, App |
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| 304 | 4 | 11.8 | 39 | 9 | US-09-864-761-41410 | Sequence 41410, A |
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| 309 | 4 | 11.8 | 39 | 15 | US-10-187-051-25 | Sequence 25, Appl |
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| 312 | 4 | 11.8 | 40 | 12 | US-10-058-053A-81 | Sequence 81, Appl |
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| 315 | 4 | 11.8 | 40 | 15 | US-10-091-572-223 | Sequence 223, App |
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| 322 | 3 | 8.8 | 28 | 9 | US-09-765-527-140 | Sequence 140, App |
| 323 | 3 | 8.8 | 28 | 9 | US-09-765-527-142 | Sequence 142, App |
| 324 | 3 | 8.8 | 28 | 9 | US-09-765-527-143 | Sequence 143, App |
| 325 | 3 | 8.8 | 28 | 9 | US-09-895-072-27 | Sequence 27, Appl |
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| 359 | 3 | 8.8 | 28 | 9 | US-09-864-761-48316 | Sequence 48316, A |
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| 370 | 3 | 8.8 | 28 | 9 | US-09-881-490-114 | Sequence 114, App |
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| 455 | 3 | 8.8 | 28 | 9 | US-09-929-818-117 | Sequence 117, App |

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| 457 | 3 | 8.8 | 28 | 9 | US-09-929-818-119 | Sequence 119, App |
| 458 | 3 | 8.8 | 28 | 9 | US-09-929-818-120 | Sequence 120, App |
| 459 | 3 | 8.8 | 28 | 9 | US-09-929-818-121 | Sequence 121, App |
| 460 | 3 | 8.8 | 28 | 9 | US-09-929-818-123 | Sequence 123, App |
| 461 | 3 | 8.8 | 28 | 9 | US-09-929-818-124 | Sequence 124, App |
| 462 | 3 | 8.8 | 28 | 9 | US-09-929-818-125 | Sequence 125, App |
| 463 | 3 | 8.8 | 28 | 9 | US-09-929-818-126 | Sequence 126, App |
| 464 | 3 | 8.8 | 28 | 9 | US-09-929-818-127 | Sequence 127, App |
| 465 | 3 | 8.8 | 28 | 9 | US-09-929-818-128 | Sequence 128, App |
| 466 | 3 | 8.8 | 28 | 9 | US-09-929-818-129 | Sequence 129, App |
| 467 | 3 | 8.8 | 28 | 9 | US-09-929-818-130 | Sequence 130, App |
| 468 | 3 | 8.8 | 28 | 9 | US-09-929-818-131 | Sequence 131, App |
| 469 | 3 | 8.8 | 28 | 9 | US-09-929-818-132 | Sequence 132, App |
| 470 | 3 | 8.8 | 28 | 9 | US-09-929-818-133 | Sequence 133, App |
| 471 | 3 | 8.8 | 28 | 9 | US-09-929-818-134 | Sequence 134, App |
| 472 | 3 | 8.8 | 28 | 9 | US-09-929-818-135 | Sequence 135, App |
| 473 | 3 | 8.8 | 28 | 9 | US-09-929-818-136 | Sequence 136, App |
| 474 | 3 | 8.8 | 28 | 9 | US-09-929-818-137 | Sequence 137, App |
| 475 | 3 | 8.8 | 28 | 9 | US-09-929-818-138 | Sequence 138, App |
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| 477 | 3 | 8.8 | 28 | 9 | US-09-929-818-140 | Sequence 140, App |
| 478 | 3 | 8.8 | 28 | 9 | US-09-929-818-141 | Sequence 141, App |
| 479 | 3 | 8.8 | 28 | 9 | US-09-929-818-142 | Sequence 142, App |
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| 481 | 3 | 8.8 | 28 | 9 | US-09-929-818-144 | Sequence 144, App |
| 482 | 3 | 8.8 | 28 | 9 | US-09-929-818-145 | Sequence 145, App |
| 483 | 3 | 8.8 | 28 | 9 | US-09-929-818-146 | Sequence 146, App |
| 484 | 3 | 8.8 | 28 | 9 | US-09-929-818-147 | Sequence 147, App |
| 485 | 3 | 8.8 | 28 | 9 | US-09-929-818-148 | Sequence 148, App |
| 486 | 3 | 8.8 | 28 | 9 | US-09-929-818-149 | Sequence 149, App |
| 487 | 3 | 8.8 | 28 | 9 | US-09-929-818-150 | Sequence 150, App |
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| 494 | 3 | 8.8 | 28 | 9 | US-09-929-818-157 | Sequence 157, App |
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| 499 | 3 | 8.8 | 28 | 9 | US-09-929-818-162 | Sequence 162, App |
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| 503 | 3 | 8.8 | 28 | 9 | US-09-929-818-166 | Sequence 166, App |
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| 509 | 3 | 8.8 | 28 | 9 | US-09-929-818-172 | Sequence 172, App |
| 510 | 3 | 8.8 | 28 | 9 | US-09-929-818-173 | Sequence 173, App |
| 511 | 3 | 8.8 | 28 | 9 | US-09-929-818-174 | Sequence 174, App |
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| 517 | 3 | 8.8 | 28 | 9 | US-09-929-818-180 | Sequence 180, App |
| 518 | 3 | 8.8 | 28 | 9 | US-09-929-818-181 | Sequence 181, App |
| 519 | 3 | 8.8 | 28 | 9 | US-09-929-818-182 | Sequence 182, App |
| 520 | 3 | 8.8 | 28 | 9 | US-09-929-818-183 | Sequence 183, App |
| 521 | 3 | 8.8 | 28 | 9 | US-09-929-818-184 | Sequence 184, App |
| 522 | 3 | 8.8 | 28 | 9 | US-09-929-818-185 | Sequence 185, App |
| 523 | 3 | 8.8 | 28 | 9 | US-09-929-818-186 | Sequence 186, App |
| 524 | 3 | 8.8 | 28 | 9 | US-09-929-818-187 | Sequence 187, App |
| 525 | 3 | 8.8 | 28 | 9 | US-09-929-818-188 | Sequence 188, App |
| 526 | 3 | 8.8 | 28 | 9 | US-09-929-818-189 | Sequence 189, App |
| 527 | 3 | 8.8 | 28 | 9 | US-09-929-818-190 | Sequence 190, App |
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| 529 | 3 | 8.8 | 28 | 9 | US-09-929-818-192 | Sequence 192, App |
| 530 | 3 | 8.8 | 28 | 9 | US-09-929-818-193 | Sequence 193, App |
| 531 | 3 | 8.8 | 28 | 9 | US-09-929-818-194 | Sequence 194, App |
| 532 | 3 | 8.8 | 28 | 9 | US-09-929-818-195 | Sequence 195, App |
| 533 | 3 | 8.8 | 28 | 9 | US-09-929-818-196 | Sequence 196, App |
| 534 | 3 | 8.8 | 28 | 9 | US-09-929-818-197 | Sequence 197, App |
| 535 | 3 | 8.8 | 28 | 9 | US-09-929-818-198 | Sequence 198, App |
| 536 | 3 | 8.8 | 28 | 9 | US-09-929-818-199 | Sequence 199, App |
| 537 | 3 | 8.8 | 28 | 9 | US-09-929-818-201 | Sequence 201, App |
| 538 | 3 | 8.8 | 28 | 9 | US-09-929-818-202 | Sequence 202, App |
| 539 | 3 | 8.8 | 28 | 9 | US-09-929-818-207 | Sequence 207, App |
| 540 | 3 | 8.8 | 28 | 10 | US-09-117-380B-4 | Sequence 4, Appli |
| 541 | 3 | 8.8 | 28 | 10 | US-09-003-869-40 | Sequence 40, Appl |
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| 543 | 3 | 8.8 | 28 | 10 | US-09-003-869-91 | Sequence 91, Appl |
| 544 | 3 | 8.8 | 28 | 10 | US-09-003-869-92 | Sequence 92, Appl |
| 545 | 3 | 8.8 | 28 | 10 | US-09-003-869-95 | Sequence 95, Appl |
| 546 | 3 | 8.8 | 28 | 10 | US-09-003-869-104 | Sequence 104, App |
| 547 | 3 | 8.8 | 28 | 10 | US-09-003-869-105 | Sequence 105, App |
| 548 | 3 | 8.8 | 28 | 10 | US-09-003-869-106 | Sequence 106, App |
| 549 | 3 | 8.8 | 28 | 10 | US-09-003-869-107 | Sequence 107, App |
| 550 | 3 | 8.8 | 28 | 10 | US-09-003-869-108 | Sequence 108, App |
| 551 | 3 | 8.8 | 28 | 10 | US-09-003-869-109 | Sequence 109, App |
| 552 | 3 | 8.8 | 28 | 10 | US-09-003-869-111 | Sequence 111, App |
| 553 | 3 | 8.8 | 28 | 10 | US-09-003-869-113 | Sequence 113, App |
| 554 | 3 | 8.8 | 28 | 10 | US-09-003-869-115 | Sequence 115, App |
| 555 | 3 | 8.8 | 28 | 10 | US-09-003-869-117 | Sequence 117, App |
| 556 | 3 | 8.8 | 28 | 10 | US-09-003-869-119 | Sequence 119, App |
| 557 | 3 | 8.8 | 28 | 10 | US-09-003-869-121 | Sequence 121, App |
| 558 | 3 | 8.8 | 28 | 10 | US-09-003-869-123 | Sequence 123, App |
| 559 | 3 | 8.8 | 28 | 10 | US-09-003-869-125 | Sequence 125, App |
| 560 | 3 | 8.8 | 28 | 10 | US-09-003-869-127 | Sequence 127, App |
| 561 | 3 | 8.8 | 28 | 10 | US-09-003-869-129 | Sequence 129, App |
| 562 | 3 | 8.8 | 28 | 10 | US-09-003-869-131 | Sequence 131, App |
| 563 | 3 | 8.8 | 28 | 10 | US-09-003-869-133 | Sequence 133, App |
| 564 | 3 | 8.8 | 28 | 10 | US-09-003-869-135 | Sequence 135, App |
| 565 | 3 | 8.8 | 28 | 10 | US-09-003-869-137 | Sequence 137, App |
| 566 | 3 | 8.8 | 28 | 10 | US-09-003-869-139 | Sequence 139, App |
| 567 | 3 | 8.8 | 28 | 10 | US-09-003-869-141 | Sequence 141, App |
| 568 | 3 | 8.8 | 28 | 10 | US-09-003-869-143 | Sequence 143, App |
| 569 | 3 | 8.8 | 28 | 10 | US-09-003-869-145 | Sequence 145, App |

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| 570 | 3 | 8.8 | 28 | 10 | US-09-003-869-147 | Sequence 147, App |
| 571 | 3 | 8.8 | 28 | 10 | US-09-003-869-149 | Sequence 149, App |
| 572 | 3 | 8.8 | 28 | 10 | US-09-003-869-151 | Sequence 151, App |
| 573 | 3 | 8.8 | 28 | 10 | US-09-003-869-155 | Sequence 155, App |
| 574 | 3 | 8.8 | 28 | 10 | US-09-003-869-163 | Sequence 163, App |
| 575 | 3 | 8.8 | 28 | 10 | US-09-003-869-165 | Sequence 165, App |
| 576 | 3 | 8.8 | 28 | 10 | US-09-903-456-116 | Sequence 116, App |
| 577 | 3 | 8.8 | 28 | 10 | US-09-989-903-23 | Sequence 23, Appl |
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| 579 | 3 | 8.8 | 28 | 10 | US-09-880-149-11 | Sequence 11, Appl |
| 580 | 3 | 8.8 | 28 | 10 | US-09-986-552-27 | Sequence 27, Appl |
| 581 | 3 | 8.8 | 28 | 10 | US-09-999-745-53 | Sequence 53, Appl |
| 582 | 3 | 8.8 | 28 | 10 | US-09-981-876-241 | Sequence 241, App |
| 583 | 3 | 8.8 | 28 | 10 | US-09-880-498-1 | Sequence 1, Appli |
| 584 | 3 | 8.8 | 28 | 10 | US-09-554-000-37 | Sequence 37, Appl |
| 585 | 3 | 8.8 | 28 | 10 | US-09-880-132-10 | Sequence 10, Appl |
| 586 | 3 | 8.8 | 28 | 10 | US-09-880-132-11 | Sequence 11, Appl |
| 587 | 3 | 8.8 | 28 | 10 | US-09-848-967-3 | Sequence 3, Appli |
| 588 | 3 | 8.8 | 28 | 10 | US-09-848-967-4 | Sequence 4, Appli |
| 589 | 3 | 8.8 | 28 | 10 | US-09-976-740-26 | Sequence 26, Appl |
| 590 | 3 | 8.8 | 28 | 11 | US-09-983-802-481 | Sequence 481, App |
| 591 | 3 | 8.8 | 28 | 11 | US-09-983-802-531 | Sequence 531, App |
| 592 | 3 | 8.8 | 28 | 11 | US-09-999-724-28 | Sequence 28, Appl |
| 593 | 3 | 8.8 | 28 | 11 | US-09-148-545-241 | Sequence 241, App |
| 594 | 3 | 8.8 | 28 | 11 | US-09-974-879-269 | Sequence 269, App |
| 595 | 3 | 8.8 | 28 | 11 | US-09-974-879-520 | Sequence 520, App |
| 596 | 3 | 8.8 | 28 | 11 | US-09-974-879-546 | Sequence 546, App |
| 597 | 3 | 8.8 | 28 | 11 | US-09-756-690A-40 | Sequence 40, Appl |
| 598 | 3 | 8.8 | 28 | 11 | US-09-756-690A-90 | Sequence 90, Appl |
| 599 | 3 | 8.8 | 28 | 11 | US-09-756-690A-91 | Sequence 91, Appl |
| 600 | 3 | 8.8 | 28 | 11 | US-09-756-690A-92 | Sequence 92, Appl |
| 601 | 3 | 8.8 | 28 | 11 | US-09-756-690A-95 | Sequence 95, Appl |
| 602 | 3 | 8.8 | 28 | 11 | US-09-756-690A-104 | Sequence 104, App |
| 603 | 3 | 8.8 | 28 | 11 | US-09-756-690A-105 | Sequence 105, App |
| 604 | 3 | 8.8 | 28 | 11 | US-09-756-690A-106 | Sequence 106, App |
| 605 | 3 | 8.8 | 28 | 11 | US-09-756-690A-107 | Sequence 107, App |
| 606 | 3 | 8.8 | 28 | 11 | US-09-756-690A-108 | Sequence 108, App |
| 607 | 3 | 8.8 | 28 | 11 | US-09-756-690A-109 | Sequence 109, App |
| 608 | 3 | 8.8 | 28 | 11 | US-09-756-690A-111 | Sequence 111, App |
| 609 | 3 | 8.8 | 28 | 11 | US-09-756-690A-113 | Sequence 113, App |
| 610 | 3 | 8.8 | 28 | 11 | US-09-756-690A-115 | Sequence 115, App |
| 611 | 3 | 8.8 | 28 | 11 | US-09-756-690A-117 | Sequence 117, App |
| 612 | 3 | 8.8 | 28 | 11 | US-09-756-690A-119 | Sequence 119, App |
| 613 | 3 | 8.8 | 28 | 11 | US-09-756-690A-121 | Sequence 121, App |
| 614 | 3 | 8.8 | 28 | 11 | US-09-756-690A-123 | Sequence 123, App |
| 615 | 3 | 8.8 | 28 | 11 | US-09-756-690A-125 | Sequence 125, App |
| 616 | 3 | 8.8 | 28 | 11 | US-09-756-690A-127 | Sequence 127, App |
| 617 | 3 | 8.8 | 28 | 11 | US-09-756-690A-129 | Sequence 129, App |
| 618 | 3 | 8.8 | 28 | 11 | US-09-756-690A-131 | Sequence 131, App |
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| 620 | 3 | 8.8 | 28 | 11 | US-09-756-690A-135 | Sequence 135, App |
| 621 | 3 | 8.8 | 28 | 11 | US-09-756-690A-137 | Sequence 137, App |
| 622 | 3 | 8.8 | 28 | 11 | US-09-756-690A-139 | Sequence 139, App |
| 623 | 3 | 8.8 | 28 | 11 | US-09-756-690A-141 | Sequence 141, App |
| 624 | 3 | 8.8 | 28 | 11 | US-09-756-690A-143 | Sequence 143, App |
| 625 | 3 | 8.8 | 28 | 11 | US-09-756-690A-145 | Sequence 145, App |
| 626 | 3 | 8.8 | 28 | 11 | US-09-756-690A-147 | Sequence 147, App |

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| 627 | 3 | 8.8 | 28 | 11 | US-09-756-690A-149 | Sequence 149, App |
| 628 | 3 | 8.8 | 28 | 11 | US-09-756-690A-151 | Sequence 151, App |
| 629 | 3 | 8.8 | 28 | 11 | US-09-756-690A-155 | Sequence 155, App |
| 630 | 3 | 8.8 | 28 | 11 | US-09-756-690A-163 | Sequence 163, App |
| 631 | 3 | 8.8 | 28 | 11 | US-09-756-690A-165 | Sequence 165, App |
| 632 | 3 | 8.8 | 28 | 11 | US-09-843-221A-68 | Sequence 68, Appl |
| 633 | 3 | 8.8 | 28 | 11 | US-09-843-221A-70 | Sequence 70, Appl |
| 634 | 3 | 8.8 | 28 | 11 | US-09-843-221A-103 | Sequence 103, App |
| 635 | 3 | 8.8 | 28 | 11 | US-09-843-221A-104 | Sequence 104, App |
| 636 | 3 | 8.8 | 28 | 11 | US-09-843-221A-105 | Sequence 105, App |
| 637 | 3 | 8.8 | 28 | 11 | US-09-843-221A-106 | Sequence 106, App |
| 638 | 3 | 8.8 | 28 | 11 | US-09-843-221A-107 | Sequence 107, App |
| 639 | 3 | 8.8 | 28 | 11 | US-09-925-299-1173 | Sequence 1173, Ap |
| 640 | 3 | 8.8 | 28 | 11 | US-09-945-917-23 | Sequence 23, Appl |
| 641 | 3 | 8.8 | 28 | 11 | US-09-813-153-220 | Sequence 220, App |
| 642 | 3 | 8.8 | 28 | 11 | US-09-776-724A-198 | Sequence 198, App |
| 643 | 3 | 8.8 | 28 | 11 | US-09-876-904A-230 | Sequence 230, App |
| 644 | 3 | 8.8 | 28 | 11 | US-09-892-877-335 | Sequence 335, App |
| 645 | 3 | 8.8 | 28 | 11 | US-09-910-180-19 | Sequence 19, Appl |
| 646 | 3 | 8.8 | 28 | 11 | US-09-305-736-285 | Sequence 285, App |
| 647 | 3 | 8.8 | 28 | 11 | US-09-305-736-522 | Sequence 522, App |
| 648 | 3 | 8.8 | 28 | 11 | US-09-305-736-548 | Sequence 548, App |
| 649 | 3 | 8.8 | 28 | 11 | US-09-948-783-348 | Sequence 348, App |
| 650 | 3 | 8.8 | 28 | 11 | US-09-866-066-31 | Sequence 31, Appl |
| 651 | 3 | 8.8 | 28 | 12 | US-10-195-730-307 | Sequence 307, App |
| 652 | 3 | 8.8 | 28 | 12 | US-10-195-730-354 | Sequence 354, App |
| 653 | 3 | 8.8 | 28 | 12 | US-10-293-086-57 | Sequence 57, Appl |
| 654 | 3 | 8.8 | 28 | 12 | US-10-309-422-4 | Sequence 4, Appli |
| 655 | 3 | 8.8 | 28 | 12 | US-10-334-405-4 | Sequence 4, Appli |
| 656 | 3 | 8.8 | 28 | 12 | US-10-251-703-21 | Sequence 21, Appl |
| 657 | 3 | 8.8 | 28 | 12 | US-10-306-686-27 | Sequence 27, Appl |
| 658 | 3 | 8.8 | 28 | 12 | US-09-991-225-35 | Sequence 35, Appl |
| 659 | 3 | 8.8 | 28 | 12 | US-10-100-256B-1 | Sequence 1, Appli |
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| 661 | 3 | 8.8 | 28 | 12 | US-10-345-281-11 | Sequence 11, Appl |
| 662 | 3 | 8.8 | 28 | 12 | US-10-254-569A-1 | Sequence 1, Appli |
| 663 | 3 | 8.8 | 28 | 12 | US-10-254-569A-2 | Sequence 2, Appli |
| 664 | 3 | 8.8 | 28 | 12 | US-10-254-569A-3 | Sequence 3, Appli |
| 665 | 3 | 8.8 | 28 | 12 | US-10-254-569A-4 | Sequence 4, Appli |
| 666 | 3 | 8.8 | 28 | 12 | US-10-254-569A-5 | Sequence 5, Appli |
| 667 | 3 | 8.8 | 28 | 12 | US-10-254-569A-6 | Sequence 6, Appli |
| 668 | 3 | 8.8 | 28 | 12 | US-10-254-569A-7 | Sequence 7, Appli |
| 669 | 3 | 8.8 | 28 | 12 | US-10-254-569A-8 | Sequence 8, Appli |
| 670 | 3 | 8.8 | 28 | 12 | US-10-254-569A-9 | Sequence 9, Appli |
| 671 | 3 | 8.8 | 28 | 12 | US-10-254-569A-10 | Sequence 10, Appl |
| 672 | 3 | 8.8 | 28 | 12 | US-10-254-569A-11 | Sequence 11, Appl |
| 673 | 3 | 8.8 | 28 | 12 | US-10-254-569A-12 | Sequence 12, Appl |
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| 675 | 3 | 8.8 | 28 | 12 | US-09-845-917A-23 | Sequence 23, Appl |
| 676 | 3 | 8.8 | 28 | 12 | US-10-322-746-7 | Sequence 7, Appli |
| 677 | 3 | 8.8 | 28 | 12 | US-10-411-224-108 | Sequence 108, App |
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| 679 | 3 | 8.8 | 28 | 12 | US-10-231-417-591 | Sequence 591, App |
| 680 | 3 | 8.8 | 28 | 12 | US-10-312-691-2 | Sequence 2, Appli |
| 681 | 3 | 8.8 | 28 | 12 | US-10-314-506-16 | Sequence 16, Appl |
| 682 | 3 | 8.8 | 28 | 12 | US-10-314-506-17 | Sequence 17, Appl |
| 683 | 3 | 8.8 | 28 | 12 | US-10-408-736-81 | Sequence 81, Appl |

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| 684 | 3 | 8.8 | 28 | 12 | US-09-933-767-626 | Sequence 626, App |
| 685 | 3 | 8.8 | 28 | 12 | US-09-933-767-638 | Sequence 638, App |
| 686 | 3 | 8.8 | 28 | 12 | US-09-933-767-1089 | Sequence 1089, Ap |
| 687 | 3 | 8.8 | 28 | 12 | US-10-105-232-329 | Sequence 329, App |
| 688 | 3 | 8.8 | 28 | 12 | US-10-131-686A-19 | Sequence 19, Appl |
| 689 | 3 | 8.8 | 28 | 12 | US-10-289-135A-36 | Sequence 36, Appl |
| 690 | 3 | 8.8 | 28 | 12 | US-10-082-014-39 | Sequence 39, Appl |
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| 692 | 3 | 8.8 | 28 | 12 | US-10-276-392-7 | Sequence 7, Appli |
| 693 | 3 | 8.8 | 28 | 12 | US-10-276-392-8 | Sequence 8, Appli |
| 694 | 3 | 8.8 | 28 | 12 | US-10-276-392-9 | Sequence 9, Appli |
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| 696 | 3 | 8.8 | 28 | 12 | US-10-276-392-11 | Sequence 11, Appl |
| 697 | 3 | 8.8 | 28 | 12 | US-10-276-392-12 | Sequence 12, Appl |
| 698 | 3 | 8.8 | 28 | 12 | US-10-276-392-13 | Sequence 13, Appl |
| 699 | 3 | 8.8 | 28 | 12 | US-10-276-392-14 | Sequence 14, Appl |
| 700 | 3 | 8.8 | 28 | 12 | US-10-276-392-15 | Sequence 15, Appl |
| 701 | 3 | 8.8 | 28 | 12 | US-10-276-392-16 | Sequence 16, Appl |
| 702 | 3 | 8.8 | 28 | 12 | US-10-276-392-17 | Sequence 17, Appl |
| 703 | 3 | 8.8 | 28 | 12 | US-10-276-392-18 | Sequence 18, Appl |
| 704 | 3 | 8.8 | 28 | 12 | US-10-276-392-19 | Sequence 19, Appl |
| 705 | 3 | 8.8 | 28 | 12 | US-10-276-392-20 | Sequence 20, Appl |
| 706 | 3 | 8.8 | 28 | 12 | US-10-276-392-21 | Sequence 21, Appl |
| 707 | 3 | 8.8 | 28 | 12 | US-10-330-872-9 | Sequence 9, Appli |
| 708 | 3 | 8.8 | 28 | 12 | US-10-351-641-54 | Sequence 54, Appl |
| 709 | 3 | 8.8 | 28 | 12 | US-10-351-641-62 | Sequence 62, Appl |
| 710 | 3 | 8.8 | 28 | 12 | US-10-351-641-982 | Sequence 982, App |
| 711 | 3 | 8.8 | 28 | 12 | US-10-351-641-1279 | Sequence 1279, Ap |
| 712 | 3 | 8.8 | 28 | 12 | US-10-351-641-1280 | Sequence 1280, Ap |
| 713 | 3 | 8.8 | 28 | 12 | US-10-351-641-1314 | Sequence 1314, Ap |
| 714 | 3 | 8.8 | 28 | 12 | US-10-351-641-1315 | Sequence 1315, Ap |
| 715 | 3 | 8.8 | 28 | 12 | US-10-351-641-1689 | Sequence 1689, Ap |
| 716 | 3 | 8.8 | 28 | 12 | US-10-029-386-27629 | Sequence 27629, A |
| 717 | 3 | 8.8 | 28 | 12 | US-10-029-386-27986 | Sequence 27986, A |
| 718 | 3 | 8.8 | 28 | 12 | US-10-029-386-28154 | Sequence 28154, A |
| 719 | 3 | 8.8 | 28 | 12 | US-10-029-386-28548 | Sequence 28548, A |
| 720 | 3 | 8.8 | 28 | 12 | US-10-029-386-31090 | Sequence 31090, A |
| 721 | 3 | 8.8 | 28 | 12 | US-10-029-386-31267 | Sequence 31267, A |
| 722 | 3 | 8.8 | 28 | 12 | US-10-029-386-31429 | Sequence 31429, A |
| 723 | 3 | 8.8 | 28 | 12 | US-10-029-386-33289 | Sequence 33289, A |
| 724 | 3 | 8.8 | 28 | 12 | US-10-029-386-33582 | Sequence 33582, A |
| 725 | 3 | 8.8 | 28 | 12 | US-10-189-437-316 | Sequence 316, App |
| 726 | 3 | 8.8 | 28 | 12 | US-10-189-437-669 | Sequence 669, App |
| 727 | 3 | 8.8 | 28 | 12 | US-10-080-254-100 | Sequence 100, App |
| 728 | 3 | 8.8 | 28 | 12 | US-10-080-608A-1 | Sequence 1, Appli |
| 729 | 3 | 8.8 | 28 | 12 | US-10-372-076-40 | Sequence 40, Appl |
| 730 | 3 | 8.8 | 28 | 12 | US-09-818-683-285 | Sequence 285, App |
| 731 | 3 | 8.8 | 28 | 12 | US-09-818-683-522 | Sequence 522, App |
| 732 | 3 | 8.8 | 28 | 12 | US-09-818-683-548 | Sequence 548, App |
| 733 | 3 | 8.8 | 28 | 12 | US-10-370-685-90 | Sequence 90, Appl |
| 734 | 3 | 8.8 | 28 | 12 | US-09-873-155-43 | Sequence 43, Appl |
| 735 | 3 | 8.8 | 28 | 12 | US-10-366-493-24 | Sequence 24, Appl |
| 736 | 3 | 8.8 | 28 | 12 | US-10-391-399-86 | Sequence 86, Appl |
| 737 | 3 | 8.8 | 28 | 12 | US-10-211-689-8 | Sequence 8, Appli |
| 738 | 3 | 8.8 | 28 | 12 | US-10-324-143-148 | Sequence 148, App |
| 739 | 3 | 8.8 | 28 | 12 | US-10-397-160-30 | Sequence 30, Appl |
| 740 | 3 | 8.8 | 28 | 12 | US-10-242-355-646 | Sequence 646, App |

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| 741 | 3 | 8.8 | 28 | 12 | US-10-245-871-32 | Sequence 32, Appl |
| 742 | 3 | 8.8 | 28 | 12 | US-10-264-049-2573 | Sequence 2573, Ap |
| 743 | 3 | 8.8 | 28 | 14 | US-10-014-269-16 | Sequence 16, Appl |
| 744 | 3 | 8.8 | 28 | 14 | US-10-014-269-17 | Sequence 17, Appl |
| 745 | 3 | 8.8 | 28 | 14 | US-10-023-529-26 | Sequence 26, Appl |
| 746 | 3 | 8.8 | 28 | 14 | US-10-097-079-77 | Sequence 77, Appl |
| 747 | 3 | 8.8 | 28 | 14 | US-10-105-931-23 | Sequence 23, Appl |
| 748 | 3 | 8.8 | 28 | 14 | US-10-090-109A-1 | Sequence 1, Appli |
| 749 | 3 | 8.8 | 28 | 14 | US-10-023-523-26 | Sequence 26, Appl |
| 750 | 3 | 8.8 | 28 | 14 | US-10-044-359-23 | Sequence 23, Appl |
| 751 | 3 | 8.8 | 28 | 14 | US-10-044-722-8 | Sequence 8, Appli |
| 752 | 3 | 8.8 | 28 | 14 | US-10-002-974-16 | Sequence 16, Appl |
| 753 | 3 | 8.8 | 28 | 14 | US-10-002-974-17 | Sequence 17, Appl |
| 754 | 3 | 8.8 | 28 | 14 | US-10-118-984-23 | Sequence 23, Appl |
| 755 | 3 | 8.8 | 28 | 15 | US-10-014-162-48 | Sequence 48, Appl |
| 756 | 3 | 8.8 | 28 | 15 | US-10-000-256A-219 | Sequence 219, App |
| 757 | 3 | 8.8 | 28 | 15 | US-10-068-564-23 | Sequence 23, Appl |
| 758 | 3 | 8.8 | 28 | 15 | US-10-078-090-126 | Sequence 126, App |
| 759 | 3 | 8.8 | 28 | 15 | US-10-004-530A-17 | Sequence 17, Appl |
| 760 | 3 | 8.8 | 28 | 15 | US-10-131-433-6 | Sequence 6, Appli |
| 761 | 3 | 8.8 | 28 | 15 | US-10-097-065-486 | Sequence 486, App |
| 762 | 3 | 8.8 | 28 | 15 | US-10-097-065-598 | Sequence 598, App |
| 763 | 3 | 8.8 | 28 | 15 | US-10-059-261-324 | Sequence 324, App |
| 764 | 3 | 8.8 | 28 | 15 | US-10-150-111-131 | Sequence 131, App |
| 765 | 3 | 8.8 | 28 | 15 | US-10-211-994-1 | Sequence 1, Appli |
| 766 | 3 | 8.8 | 28 | 15 | US-10-157-224A-40 | Sequence 40, Appl |
| 767 | 3 | 8.8 | 28 | 15 | US-10-157-224A-90 | Sequence 90, Appl |
| 768 | 3 | 8.8 | 28 | 15 | US-10-157-224A-91 | Sequence 91, Appl |
| 769 | 3 | 8.8 | 28 | 15 | US-10-157-224A-92 | Sequence 92, Appl |
| 770 | 3 | 8.8 | 28 | 15 | US-10-157-224A-95 | Sequence 95, Appl |
| 771 | 3 | 8.8 | 28 | 15 | US-10-157-224A-104 | Sequence 104, App |
| 772 | 3 | 8.8 | 28 | 15 | US-10-157-224A-105 | Sequence 105, App |
| 773 | 3 | 8.8 | 28 | 15 | US-10-157-224A-106 | Sequence 106, App |
| 774 | 3 | 8.8 | 28 | 15 | US-10-157-224A-107 | Sequence 107, App |
| 775 | 3 | 8.8 | 28 | 15 | US-10-157-224A-108 | Sequence 108, App |
| 776 | 3 | 8.8 | 28 | 15 | US-10-157-224A-109 | Sequence 109, App |
| 777 | 3 | 8.8 | 28 | 15 | US-10-157-224A-111 | Sequence 111, App |
| 778 | 3 | 8.8 | 28 | 15 | US-10-157-224A-113 | Sequence 113, App |
| 779 | 3 | 8.8 | 28 | 15 | US-10-157-224A-115 | Sequence 115, App |
| 780 | 3 | 8.8 | 28 | 15 | US-10-157-224A-117 | Sequence 117, App |
| 781 | 3 | 8.8 | 28 | 15 | US-10-157-224A-119 | Sequence 119, App |
| 782 | 3 | 8.8 | 28 | 15 | US-10-157-224A-121 | Sequence 121, App |
| 783 | 3 | 8.8 | 28 | 15 | US-10-157-224A-123 | Sequence 123, App |
| 784 | 3 | 8.8 | 28 | 15 | US-10-157-224A-125 | Sequence 125, App |
| 785 | 3 | 8.8 | 28 | 15 | US-10-157-224A-127 | Sequence 127, App |
| 786 | 3 | 8.8 | 28 | 15 | US-10-157-224A-129 | Sequence 129, App |
| 787 | 3 | 8.8 | 28 | 15 | US-10-157-224A-131 | Sequence 131, App |
| 788 | 3 | 8.8 | 28 | 15 | US-10-157-224A-133 | Sequence 133, App |
| 789 | 3 | 8.8 | 28 | 15 | US-10-157-224A-135 | Sequence 135, App |
| 790 | 3 | 8.8 | 28 | 15 | US-10-157-224A-137 | Sequence 137, App |
| 791 | 3 | 8.8 | 28 | 15 | US-10-157-224A-139 | Sequence 139, App |
| 792 | 3 | 8.8 | 28 | 15 | US-10-157-224A-141 | Sequence 141, App |
| 793 | 3 | 8.8 | 28 | 15 | US-10-157-224A-143 | Sequence 143, App |
| 794 | 3 | 8.8 | 28 | 15 | US-10-157-224A-145 | Sequence 145, App |
| 795 | 3 | 8.8 | 28 | 15 | US-10-157-224A-147 | Sequence 147, App |
| 796 | 3 | 8.8 | 28 | 15 | US-10-157-224A-149 | Sequence 149, App |
| 797 | 3 | 8.8 | 28 | 15 | US-10-157-224A-151 | Sequence 151, App |

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| 798 | 3 | 8.8 | 28 | 15 | US-10-157-224A-155 | Sequence 155, App |
| 799 | 3 | 8.8 | 28 | 15 | US-10-157-224A-163 | Sequence 163, App |
| 800 | 3 | 8.8 | 28 | 15 | US-10-157-224A-165 | Sequence 165, App |
| 801 | 3 | 8.8 | 28 | 15 | US-10-187-051-40 | Sequence 40, Appl |
| 802 | 3 | 8.8 | 28 | 15 | US-10-187-051-90 | Sequence 90, Appl |
| 803 | 3 | 8.8 | 28 | 15 | US-10-187-051-91 | Sequence 91, Appl |
| 804 | 3 | 8.8 | 28 | 15 | US-10-187-051-92 | Sequence 92, Appl |
| 805 | 3 | 8.8 | 28 | 15 | US-10-187-051-95 | Sequence 95, Appl |
| 806 | 3 | 8.8 | 28 | 15 | US-10-187-051-104 | Sequence 104, App |
| 807 | 3 | 8.8 | 28 | 15 | US-10-187-051-105 | Sequence 105, App |
| 808 | 3 | 8.8 | 28 | 15 | US-10-187-051-106 | Sequence 106, App |
| 809 | 3 | 8.8 | 28 | 15 | US-10-187-051-107 | Sequence 107, App |
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| 811 | 3 | 8.8 | 28 | 15 | US-10-187-051-109 | Sequence 109, App |
| 812 | 3 | 8.8 | 28 | 15 | US-10-187-051-111 | Sequence 111, App |
| 813 | 3 | 8.8 | 28 | 15 | US-10-187-051-113 | Sequence 113, App |
| 814 | 3 | 8.8 | 28 | 15 | US-10-187-051-115 | Sequence 115, App |
| 815 | 3 | 8.8 | 28 | 15 | US-10-187-051-117 | Sequence 117, App |
| 816 | 3 | 8.8 | 28 | 15 | US-10-187-051-119 | Sequence 119, App |
| 817 | 3 | 8.8 | 28 | 15 | US-10-187-051-121 | Sequence 121, App |
| 818 | 3 | 8.8 | 28 | 15 | US-10-187-051-123 | Sequence 123, App |
| 819 | 3 | 8.8 | 28 | 15 | US-10-187-051-125 | Sequence 125, App |
| 820 | 3 | 8.8 | 28 | 15 | US-10-187-051-127 | Sequence 127, App |
| 821 | 3 | 8.8 | 28 | 15 | US-10-187-051-129 | Sequence 129, App |
| 822 | 3 | 8.8 | 28 | 15 | US-10-187-051-131 | Sequence 131, App |
| 823 | 3 | 8.8 | 28 | 15 | US-10-187-051-133 | Sequence 133, App |
| 824 | 3 | 8.8 | 28 | 15 | US-10-187-051-135 | Sequence 135, App |
| 825 | 3 | 8.8 | 28 | 15 | US-10-187-051-137 | Sequence 137, App |
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| 827 | 3 | 8.8 | 28 | 15 | US-10-187-051-141 | Sequence 141, App |
| 828 | 3 | 8.8 | 28 | 15 | US-10-187-051-143 | Sequence 143, App |
| 829 | 3 | 8.8 | 28 | 15 | US-10-187-051-145 | Sequence 145, App |
| 830 | 3 | 8.8 | 28 | 15 | US-10-187-051-147 | Sequence 147, App |
| 831 | 3 | 8.8 | 28 | 15 | US-10-187-051-149 | Sequence 149, App |
| 832 | 3 | 8.8 | 28 | 15 | US-10-187-051-151 | Sequence 151, App |
| 833 | 3 | 8.8 | 28 | 15 | US-10-187-051-155 | Sequence 155, App |
| 834 | 3 | 8.8 | 28 | 15 | US-10-187-051-163 | Sequence 163, App |
| 835 | 3 | 8.8 | 28 | 15 | US-10-187-051-165 | Sequence 165, App |
| 836 | 3 | 8.8 | 28 | 15 | US-10-023-282-626 | Sequence 626, App |
| 837 | 3 | 8.8 | 28 | 15 | US-10-023-282-638 | Sequence 638, App |
| 838 | 3 | 8.8 | 28 | 15 | US-10-023-282-1089 | Sequence 1089, Ap |
| 839 | 3 | 8.8 | 28 | 15 | US-10-255-532-6 | Sequence 6, Appli |
| 840 | 3 | 8.8 | 28 | 15 | US-10-075-869-24 | Sequence 24, Appl |
| 841 | 3 | 8.8 | 28 | 15 | US-10-202-724-3 | Sequence 3, Appli |
| 842 | 3 | 8.8 | 28 | 15 | US-10-262-017-3 | Sequence 3, Appli |
| 843 | 3 | 8.8 | 28 | 15 | US-10-106-698-5608 | Sequence 5608, Ap |
| 844 | 3 | 8.8 | 28 | 15 | US-10-106-698-6764 | Sequence 6764, Ap |
| 845 | 3 | 8.8 | 28 | 15 | US-10-106-698-7736 | Sequence 7736, Ap |
| 846 | 3 | 8.8 | 28 | 15 | US-10-106-698-7875 | Sequence 7875, Ap |
| 847 | 3 | 8.8 | 28 | 15 | US-10-106-698-8447 | Sequence 8447, Ap |
| 848 | 3 | 8.8 | 28 | 15 | US-10-295-809-20 | Sequence 20, Appl |
| 849 | 3 | 8.8 | 28 | 15 | US-10-322-579-2 | Sequence 2, Appli |
| 850 | 3 | 8.8 | 28 | 15 | US-10-192-283A-12 | Sequence 12, Appl |
| 851 | 3 | 8.8 | 28 | 15 | US-10-197-954-62 | Sequence 62, Appl |
| 852 | 3 | 8.8 | 28 | 15 | US-10-197-954-145 | Sequence 145, App |
| 853 | 3 | 8.8 | 28 | 15 | US-10-283-500-19 | Sequence 19, Appl |
| 854 | 3 | 8.8 | 28 | 15 | US-10-295-981-23 | Sequence 23, Appl |

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| 855 | 3 | 8.8 | 28 | 15 | US-10-160-290-22 | Sequence 22, Appl |
| 856 | 3 | 8.8 | 29 | 9 | US-09-730-379B-4 | Sequence 4, Appli |
| 857 | 3 | 8.8 | 29 | 9 | US-09-765-527-13 | Sequence 13, Appl |
| 858 | 3 | 8.8 | 29 | 9 | US-09-765-527-64 | Sequence 64, Appl |
| 859 | 3 | 8.8 | 29 | 9 | US-09-005-243-73 | Sequence 73, Appl |
| 860 | 3 | 8.8 | 29 | 9 | US-09-904-380-23 | Sequence 23, Appl |
| 861 | 3 | 8.8 | 29 | 9 | US-09-224-683-73 | Sequence 73, Appl |
| 862 | 3 | 8.8 | 29 | 9 | US-09-932-161-1 | Sequence 1, Appli |
| 863 | 3 | 8.8 | 29 | 9 | US-09-864-761-33834 | Sequence 33834, A |
| 864 | 3 | 8.8 | 29 | 9 | US-09-864-761-34011 | Sequence 34011, A |
| 865 | 3 | 8.8 | 29 | 9 | US-09-864-761-34337 | Sequence 34337, A |
| 866 | 3 | 8.8 | 29 | 9 | US-09-864-761-35314 | Sequence 35314, A |
| 867 | 3 | 8.8 | 29 | 9 | US-09-864-761-36235 | Sequence 36235, A |
| 868 | 3 | 8.8 | 29 | 9 | US-09-864-761-37068 | Sequence 37068, A |
| 869 | 3 | 8.8 | 29 | 9 | US-09-864-761-37579 | Sequence 37579, A |
| 870 | 3 | 8.8 | 29 | 9 | US-09-864-761-37814 | Sequence 37814, A |
| 871 | 3 | 8.8 | 29 | 9 | US-09-864-761-37955 | Sequence 37955, A |
| 872 | 3 | 8.8 | 29 | 9 | US-09-864-761-38222 | Sequence 38222, A |
| 873 | 3 | 8.8 | 29 | 9 | US-09-864-761-38638 | Sequence 38638, A |
| 874 | 3 | 8.8 | 29 | 9 | US-09-864-761-38968 | Sequence 38968, A |
| 875 | 3 | 8.8 | 29 | 9 | US-09-864-761-40067 | Sequence 40067, A |
| 876 | 3 | 8.8 | 29 | 9 | US-09-864-761-40393 | Sequence 40393, A |
| 877 | 3 | 8.8 | 29 | 9 | US-09-864-761-40727 | Sequence 40727, A |
| 878 | 3 | 8.8 | 29 | 9 | US-09-864-761-40944 | Sequence 40944, A |
| 879 | 3 | 8.8 | 29 | 9 | US-09-864-761-41199 | Sequence 41199, A |
| 880 | 3 | 8.8 | 29 | 9 | US-09-864-761-41596 | Sequence 41596, A |
| 881 | 3 | 8.8 | 29 | 9 | US-09-864-761-42035 | Sequence 42035, A |
| 882 | 3 | 8.8 | 29 | 9 | US-09-864-761-42321 | Sequence 42321, A |
| 883 | 3 | 8.8 | 29 | 9 | US-09-864-761-42342 | Sequence 42342, A |
| 884 | 3 | 8.8 | 29 | 9 | US-09-864-761-42467 | Sequence 42467, A |
| 885 | 3 | 8.8 | 29 | 9 | US-09-864-761-42832 | Sequence 42832, A |
| 886 | 3 | 8.8 | 29 | 9 | US-09-864-761-42924 | Sequence 42924, A |
| 887 | 3 | 8.8 | 29 | 9 | US-09-864-761-43064 | Sequence 43064, A |
| 888 | 3 | 8.8 | 29 | 9 | US-09-864-761-43487 | Sequence 43487, A |
| 889 | 3 | 8.8 | 29 | 9 | US-09-864-761-43635 | Sequence 43635, A |
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| 892 | 3 | 8.8 | 29 | 9 | US-09-864-761-45036 | Sequence 45036, A |
| 893 | 3 | 8.8 | 29 | 9 | US-09-864-761-45207 | Sequence 45207, A |
| 894 | 3 | 8.8 | 29 | 9 | US-09-864-761-45777 | Sequence 45777, A |
| 895 | 3 | 8.8 | 29 | 9 | US-09-864-761-45815 | Sequence 45815, A |
| 896 | 3 | 8.8 | 29 | 9 | US-09-864-761-46618 | Sequence 46618, A |
| 897 | 3 | 8.8 | 29 | 9 | US-09-864-761-47028 | Sequence 47028, A |
| 898 | 3 | 8.8 | 29 | 9 | US-09-864-761-47383 | Sequence 47383, A |
| 899 | 3 | 8.8 | 29 | 9 | US-09-864-761-47524 | Sequence 47524, A |
| 900 | 3 | 8.8 | 29 | 9 | US-09-864-761-48176 | Sequence 48176, A |
| 901 | 3 | 8.8 | 29 | 9 | US-09-864-761-48505 | Sequence 48505, A |
| 902 | 3 | 8.8 | 29 | 9 | US-09-864-761-48518 | Sequence 48518, A |
| 903 | 3 | 8.8 | 29 | 9 | US-09-864-761-48746 | Sequence 48746, A |
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| 906 | 3 | 8.8 | 29 | 9 | US-09-764-869-638 | Sequence 638, App |
| 907 | 3 | 8.8 | 29 | 9 | US-09-881-490-3 | Sequence 3, Appli |
| 908 | 3 | 8.8 | 29 | 9 | US-09-789-836-13 | Sequence 13, Appl |
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| 910 | 3 | 8.8 | 29 | 10 | US-09-927-112-6 | Sequence 6, Appli |
| 911 | 3 | 8.8 | 29 | 10 | US-09-872-864-17 | Sequence 17, Appl |

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| 912 | 3 | 8.8 | 29 | 10 | US-09-872-864-18 | Sequence 18, Appl |
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| 914 | 3 | 8.8 | 29 | 10 | US-09-872-864-20 | Sequence 20, Appl |
| 915 | 3 | 8.8 | 29 | 10 | US-09-922-261-258 | Sequence 258, App |
| 916 | 3 | 8.8 | 29 | 10 | US-09-908-664-8 | Sequence 8, Appli |
| 917 | 3 | 8.8 | 29 | 10 | US-09-908-664-9 | Sequence 9, Appli |
| 918 | 3 | 8.8 | 29 | 10 | US-09-908-664-18 | Sequence 18, Appl |
| 919 | 3 | 8.8 | 29 | 10 | US-09-905-831-12 | Sequence 12, Appl |
| 920 | 3 | 8.8 | 29 | 10 | US-09-905-831-15 | Sequence 15, Appl |
| 921 | 3 | 8.8 | 29 | 10 | US-09-003-869-79 | Sequence 79, Appl |
| 922 | 3 | 8.8 | 29 | 10 | US-09-003-869-98 | Sequence 98, Appl |
| 923 | 3 | 8.8 | 29 | 10 | US-09-911-969-7 | Sequence 7, Appli |
| 924 | 3 | 8.8 | 29 | 10 | US-09-880-149-52 | Sequence 52, Appl |
| 925 | 3 | 8.8 | 29 | 10 | US-09-880-149-55 | Sequence 55, Appl |
| 926 | 3 | 8.8 | 29 | 10 | US-09-764-877-1395 | Sequence 1395, Ap |
| 927 | 3 | 8.8 | 29 | 10 | US-09-071-838-189 | Sequence 189, App |
| 928 | 3 | 8.8 | 29 | 10 | US-09-071-838-242 | Sequence 242, App |
| 929 | 3 | 8.8 | 29 | 10 | US-09-956-206A-1 | Sequence 1, Appli |
| 930 | 3 | 8.8 | 29 | 10 | US-09-984-245-227 | Sequence 227, App |
| 931 | 3 | 8.8 | 29 | 10 | US-09-880-132-52 | Sequence 52, Appl |
| 932 | 3 | 8.8 | 29 | 10 | US-09-880-132-55 | Sequence 55, Appl |
| 933 | 3 | 8.8 | 29 | 11 | US-09-983-802-620 | Sequence 620, App |
| 934 | 3 | 8.8 | 29 | 11 | US-09-956-940-38 | Sequence 38, Appl |
| 935 | 3 | 8.8 | 29 | 11 | US-09-974-879-406 | Sequence 406, App |
| 936 | 3 | 8.8 | 29 | 11 | US-09-974-879-511 | Sequence 511, App |
| 937 | 3 | 8.8 | 29 | 11 | US-09-974-879-527 | Sequence 527, App |
| 938 | 3 | 8.8 | 29 | 11 | US-09-259-658-15 | Sequence 15, Appl |
| 939 | 3 | 8.8 | 29 | 11 | US-09-756-690A-79 | Sequence 79, Appl |
| 940 | 3 | 8.8 | 29 | 11 | US-09-756-690A-98 | Sequence 98, Appl |
| 941 | 3 | 8.8 | 29 | 11 | US-09-843-221A-152 | Sequence 152, App |
| 942 | 3 | 8.8 | 29 | 11 | US-09-925-299-1270 | Sequence 1270, Ap |
| 943 | 3 | 8.8 | 29 | 11 | US-09-847-102A-80 | Sequence 80, Appl |
| 944 | 3 | 8.8 | 29 | 11 | US-09-813-153-218 | Sequence 218, App |
| 945 | 3 | 8.8 | 29 | 11 | US-09-966-262-227 | Sequence 227, App |
| 946 | 3 | 8.8 | 29 | 11 | US-09-969-730-196 | Sequence 196, App |
| 947 | 3 | 8.8 | 29 | 11 | US-09-281-495-51 | Sequence 51, Appl |
| 948 | 3 | 8.8 | 29 | 11 | US-09-983-966-227 | Sequence 227, App |
| 949 | 3 | 8.8 | 29 | 11 | US-09-876-904A-28 | Sequence 28, Appl |
| 950 | 3 | 8.8 | 29 | 11 | US-09-764-891-4191 | Sequence 4191, Ap |
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| 953 | 3 | 8.8 | 29 | 11 | US-09-847-208-125 | Sequence 125, App |
| 954 | 3 | 8.8 | 29 | 11 | US-09-305-736-406 | Sequence 406, App |
| 955 | 3 | 8.8 | 29 | 11 | US-09-305-736-512 | Sequence 512, App |
| 956 | 3 | 8.8 | 29 | 11 | US-09-305-736-529 | Sequence 529, App |
| 957 | 3 | 8.8 | 29 | 11 | US-09-095-478-25 | Sequence 25, Appl |
| 958 | 3 | 8.8 | 29 | 11 | US-09-908-139-19 | Sequence 19, Appl |
| 959 | 3 | 8.8 | 29 | 11 | US-09-908-139-21 | Sequence 21, Appl |
| 960 | 3 | 8.8 | 29 | 11 | US-09-491-614-14 | Sequence 14, Appl |
| 961 | 3 | 8.8 | 29 | 11 | US-09-491-614-15 | Sequence 15, Appl |
| 962 | 3 | 8.8 | 29 | 11 | US-09-948-783-438 | Sequence 438, App |
| 963 | 3 | 8.8 | 29 | 11 | US-09-910-082A-158 | Sequence 158, App |
| 964 | 3 | 8.8 | 29 | 11 | US-09-910-082A-368 | Sequence 368, App |
| 965 | 3 | 8.8 | 29 | 12 | US-10-153-604A-72 | Sequence 72, Appl |
| 966 | 3 | 8.8 | 29 | 12 | US-10-231-894-44 | Sequence 44, Appl |
| 967 | 3 | 8.8 | 29 | 12 | US-10-345-281-52 | Sequence 52, Appl |
| 968 | 3 | 8.8 | 29 | 12 | US-10-345-281-55 | Sequence 55, Appl |

| | | | | | | |
|------|---|-----|----|----|---------------------|-------------------|
| 969 | 3 | 8.8 | 29 | 12 | US-10-234-816-95 | Sequence 95, Appl |
| 970 | 3 | 8.8 | 29 | 12 | US-09-789-831-13 | Sequence 13, Appl |
| 971 | 3 | 8.8 | 29 | 12 | US-09-935-384-757 | Sequence 757, App |
| 972 | 3 | 8.8 | 29 | 12 | US-09-935-384-758 | Sequence 758, App |
| 973 | 3 | 8.8 | 29 | 12 | US-10-131-909A-7 | Sequence 7, Appli |
| 974 | 3 | 8.8 | 29 | 12 | US-10-160-162-232 | Sequence 232, App |
| 975 | 3 | 8.8 | 29 | 12 | US-10-096-777-1 | Sequence 1, Appli |
| 976 | 3 | 8.8 | 29 | 12 | US-10-008-524A-123 | Sequence 123, App |
| 977 | 3 | 8.8 | 29 | 12 | US-10-340-458-4 | Sequence 4, Appli |
| 978 | 3 | 8.8 | 29 | 12 | US-10-340-458-21 | Sequence 21, Appl |
| 979 | 3 | 8.8 | 29 | 12 | US-09-933-767-660 | Sequence 660, App |
| 980 | 3 | 8.8 | 29 | 12 | US-09-933-767-1182 | Sequence 1182, Ap |
| 981 | 3 | 8.8 | 29 | 12 | US-10-105-232-304 | Sequence 304, App |
| 982 | 3 | 8.8 | 29 | 12 | US-10-105-232-319 | Sequence 319, App |
| 983 | 3 | 8.8 | 29 | 12 | US-10-105-232-343 | Sequence 343, App |
| 984 | 3 | 8.8 | 29 | 12 | US-10-105-232-512 | Sequence 512, App |
| 985 | 3 | 8.8 | 29 | 12 | US-10-280-066-334 | Sequence 334, App |
| 986 | 3 | 8.8 | 29 | 12 | US-10-289-135A-25 | Sequence 25, Appl |
| 987 | 3 | 8.8 | 29 | 12 | US-10-029-386-27545 | Sequence 27545, A |
| 988 | 3 | 8.8 | 29 | 12 | US-10-029-386-27995 | Sequence 27995, A |
| 989 | 3 | 8.8 | 29 | 12 | US-10-029-386-29238 | Sequence 29238, A |
| 990 | 3 | 8.8 | 29 | 12 | US-10-029-386-30063 | Sequence 30063, A |
| 991 | 3 | 8.8 | 29 | 12 | US-10-029-386-31071 | Sequence 31071, A |
| 992 | 3 | 8.8 | 29 | 12 | US-10-029-386-31232 | Sequence 31232, A |
| 993 | 3 | 8.8 | 29 | 12 | US-10-029-386-31577 | Sequence 31577, A |
| 994 | 3 | 8.8 | 29 | 12 | US-10-029-386-32473 | Sequence 32473, A |
| 995 | 3 | 8.8 | 29 | 12 | US-10-029-386-32650 | Sequence 32650, A |
| 996 | 3 | 8.8 | 29 | 12 | US-10-029-386-33620 | Sequence 33620, A |
| 997 | 3 | 8.8 | 29 | 12 | US-10-189-437-291 | Sequence 291, App |
| 998 | 3 | 8.8 | 29 | 12 | US-10-189-437-306 | Sequence 306, App |
| 999 | 3 | 8.8 | 29 | 12 | US-10-189-437-330 | Sequence 330, App |
| 1000 | 3 | 8.8 | 29 | 12 | US-10-189-437-499 | Sequence 499, App |

ALIGNMENTS

RESULT 1

US-09-843-221A-18

; Sequence 18, Application US/09843221A

; Publication No. US20030039654A1

; GENERAL INFORMATION:

; APPLICANT: KOSTENUIK, PAUL

; APPLICANT: LIU, CHUAN-FA

; APPLICANT: LACEY, DAVID LEE

; TITLE OF INVENTION: MODULATORS OF RECEPTORS FOR PARATHYROID HORMONE AND
PARATHYROID HORMONE-

; TITLE OF INVENTION: RELATED PROTEIN

; FILE REFERENCE: A-665B

; CURRENT APPLICATION NUMBER: US/09/843,221A

; CURRENT FILING DATE: 2001-04-26

; PRIOR APPLICATION NUMBER: 60/266,673

; PRIOR FILING DATE: 2001-02-06

; PRIOR APPLICATION NUMBER: 60/214,860

; PRIOR FILING DATE: 2000-06-28

; PRIOR APPLICATION NUMBER: 60/200,053

; PRIOR FILING DATE: 2000-04-27

```

; NUMBER OF SEQ ID NOS: 170
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 18
;   LENGTH: 34
;   TYPE: PRT
;   ORGANISM: Artificial Sequence
;   FEATURE:
;   OTHER INFORMATION: modified human PTH
US-09-843-221A-18

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Query Match 100.0%; Score 34; DB 11; Length 34;
Best Local Similarity 100.0%; Pred. No. 6e-28;
Matches 34; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 SVSEIQLMHNKGKHLNSMERVEWLRKKLQDVHNF 34
 |||||
 Db 1 SVSEIOLMHNKGKHLNSMERVEWLRKKLODVHNF 34

RESULT 2

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US-09-843-221A-163
; Sequence 163, Application US/09843221A
; Publication No. US20030039654A1
; GENERAL INFORMATION:
; APPLICANT: KOSTENUK, PAUL
; APPLICANT: LIU, CHUAN-FA
; APPLICANT: LACEY, DAVID LEE
; TITLE OF INVENTION: MODULATORS OF RECEPTORS FOR PARATHYROID HORMONE AND
PARATHYROID HORMONE-
; TITLE OF INVENTION: RELATED PROTEIN
; FILE REFERENCE: A-665B
; CURRENT APPLICATION NUMBER: US/09/843,221A
; CURRENT FILING DATE: 2001-04-26
; PRIOR APPLICATION NUMBER: 60/266,673
; PRIOR FILING DATE: 2001-02-06
; PRIOR APPLICATION NUMBER: 60/214,860
; PRIOR FILING DATE: 2000-06-28
; PRIOR APPLICATION NUMBER: 60/200,053
; PRIOR FILING DATE: 2000-04-27
; NUMBER OF SEQ ID NOS: 170
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 163
; LENGTH: 34
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Preferred embodiments - PTH
; NAME/KEY: misc_feature
; LOCATION: (34)..(34)
; OTHER INFORMATION: Optional linker and Fc domain attached at the C-terminus
US-09-843-221A-163

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Query Match 100.0%; Score 34; DB 11; Length 34;
Best Local Similarity 100.0%; Pred. No. 6e-28;
Matches 34; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 SVSEIQLMHNKGKHLNSMERVEWLRKKLODVHNF 34

Db 1 SVSEIQLMHNKGKHLNSMERVEWLRKKLQDVHNF 34

RESULT 3

US-09-843-221A-41

; Sequence 41, Application US/09843221A
; Publication No. US20030039654A1
; GENERAL INFORMATION:
; APPLICANT: KOSTENUIK, PAUL
; APPLICANT: LIU, CHUAN-FA
; APPLICANT: LACEY, DAVID LEE
; TITLE OF INVENTION: MODULATORS OF RECEPTORS FOR PARATHYROID HORMONE AND
PARATHYROID HORMONE-
; TITLE OF INVENTION: RELATED PROTEIN
; FILE REFERENCE: A-665B
; CURRENT APPLICATION NUMBER: US/09/843,221A
; CURRENT FILING DATE: 2001-04-26
; PRIOR APPLICATION NUMBER: 60/266,673
; PRIOR FILING DATE: 2001-02-06
; PRIOR APPLICATION NUMBER: 60/214,860
; PRIOR FILING DATE: 2000-06-28
; PRIOR APPLICATION NUMBER: 60/200,053
; PRIOR FILING DATE: 2000-04-27
; NUMBER OF SEQ ID NOS: 170
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 41
; LENGTH: 30
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: modified human PTH
US-09-843-221A-41

Query Match 88.2%; Score 30; DB 11; Length 30;
Best Local Similarity 100.0%; Pred. No. 6.9e-24;
Matches 30; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 SVSEIQLMHNKGKHLNSMERVEWLRKKLQD 30
|||
Db 1 SVSEIQLMHNKGKHLNSMERVEWLRKKLQD 30

RESULT 4

US-09-843-221A-32

; Sequence 32, Application US/09843221A
; Publication No. US20030039654A1
; GENERAL INFORMATION:
; APPLICANT: KOSTENUIK, PAUL
; APPLICANT: LIU, CHUAN-FA
; APPLICANT: LACEY, DAVID LEE
; TITLE OF INVENTION: MODULATORS OF RECEPTORS FOR PARATHYROID HORMONE AND
PARATHYROID HORMONE-
; TITLE OF INVENTION: RELATED PROTEIN
; FILE REFERENCE: A-665B
; CURRENT APPLICATION NUMBER: US/09/843,221A
; CURRENT FILING DATE: 2001-04-26

; PRIOR APPLICATION NUMBER: 60/266,673
; PRIOR FILING DATE: 2001-02-06
; PRIOR APPLICATION NUMBER: 60/214,860
; PRIOR FILING DATE: 2000-06-28
; PRIOR APPLICATION NUMBER: 60/200,053
; PRIOR FILING DATE: 2000-04-27
; NUMBER OF SEQ ID NOS: 170
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 32
; LENGTH: 28
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-843-221A-32

Query Match 67.6%; Score 23; DB 11; Length 28;
Best Local Similarity 100.0%; Pred. No. 9.8e-17;
Matches 23; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 12 GKHLNSMERVEWLRKKLQDVHNF 34
|||
Db 6 GKHLNSMERVEWLRKKLQDVHNF 28

RESULT 5

US-09-169-786-3

; Sequence 3, Application US/09169786B
; Patent No. US20020025929A1
; GENERAL INFORMATION:
; APPLICANT: Sato, Masahiko
; TITLE OF INVENTION: METHOD OF BUILDING AND MAINTAINING BONE
; FILE REFERENCE: X-11480
; CURRENT APPLICATION NUMBER: US/09/169,786B
; CURRENT FILING DATE: 1998-10-09
; EARLIER APPLICATION NUMBER: US 60/061,800
; EARLIER FILING DATE: 1997-10-14
; NUMBER OF SEQ ID NOS: 12
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 3
; LENGTH: 34
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-169-786-3

Query Match 67.6%; Score 23; DB 9; Length 34;
Best Local Similarity 100.0%; Pred. No. 1.1e-16;
Matches 23; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 12 GKHLNSMERVEWLRKKLQDVHNF 34
|||
Db 12 GKHLNSMERVEWLRKKLQDVHNF 34

RESULT 6

US-09-928-047B-6

; Sequence 6, Application US/09928047B
; Patent No. US20020160945A1
; GENERAL INFORMATION:

; APPLICANT: Cantor, Thomas
; TITLE OF INVENTION: CYCLASE INHIBITING PARATHYROID HORMONE
; TITLE OF INVENTION: ANTAGONIST OR MODULATORS AND OSTEOPOROSIS
; FILE REFERENCE: 53221-20002.00
; CURRENT APPLICATION NUMBER: US/09/928,047B
; CURRENT FILING DATE: 2001-08-10
; PRIOR APPLICATION NUMBER: US 60/224,446
; PRIOR FILING DATE: 2000-08-10
; NUMBER OF SEQ ID NOS: 8
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 6
; LENGTH: 34
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-928-047B-6

Query Match 67.6%; Score 23; DB 10; Length 34;
Best Local Similarity 100.0%; Pred. No. 1.1e-16;
Matches 23; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 12 GKHLNSMERVEWLRKKLQDVHNF 34
| | | | | | | | | | | | | | | | | |
Db 12 GKHLNSMERVEWLRKKLQDVHNF 34

RESULT 7

US-09-843-221A-16
; Sequence 16, Application US/09843221A
; Publication No. US20030039654A1
; GENERAL INFORMATION:
; APPLICANT: KOSTENUIK, PAUL
; APPLICANT: LIU, CHUAN-FA
; APPLICANT: LACEY, DAVID LEE
; TITLE OF INVENTION: MODULATORS OF RECEPTORS FOR PARATHYROID HORMONE AND
PARATHYROID HORMONE-
; TITLE OF INVENTION: RELATED PROTEIN
; FILE REFERENCE: A-665B
; CURRENT APPLICATION NUMBER: US/09/843,221A
; CURRENT FILING DATE: 2001-04-26
; PRIOR APPLICATION NUMBER: 60/266,673
; PRIOR FILING DATE: 2001-02-06
; PRIOR APPLICATION NUMBER: 60/214,860
; PRIOR FILING DATE: 2000-06-28
; PRIOR APPLICATION NUMBER: 60/200,053
; PRIOR FILING DATE: 2000-04-27
; NUMBER OF SEQ ID NOS: 170
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 16
; LENGTH: 34
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-843-221A-16

Query Match 67.6%; Score 23; DB 11; Length 34;
Best Local Similarity 100.0%; Pred. No. 1.1e-16;
Matches 23; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 12 GKHLNSMERVEWLRKKLQDVHNF 34
|||||
Db 12 GKHLNSMERVEWLRKKLQDVHNF 34

RESULT 8

US-09-843-221A-17

; Sequence 17, Application US/09843221A
; Publication No. US20030039654A1
; GENERAL INFORMATION:
; APPLICANT: KOSTENUIK, PAUL
; APPLICANT: LIU, CHUAN-FA
; APPLICANT: LACEY, DAVID LEE
; TITLE OF INVENTION: MODULATORS OF RECEPTORS FOR PARATHYROID HORMONE AND
PARATHYROID HORMONE-
; TITLE OF INVENTION: RELATED PROTEIN
; FILE REFERENCE: A-665B
; CURRENT APPLICATION NUMBER: US/09/843,221A
; CURRENT FILING DATE: 2001-04-26
; PRIOR APPLICATION NUMBER: 60/266,673
; PRIOR FILING DATE: 2001-02-06
; PRIOR APPLICATION NUMBER: 60/214,860
; PRIOR FILING DATE: 2000-06-28
; PRIOR APPLICATION NUMBER: 60/200,053
; PRIOR FILING DATE: 2000-04-27
; NUMBER OF SEQ ID NOS: 170
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 17
; LENGTH: 34
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: modified human PTH
US-09-843-221A-17

Query Match 67.6%; Score 23; DB 11; Length 34;
Best Local Similarity 100.0%; Pred. No. 1.1e-16;
Matches 23; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 12 GKHLNSMERVEWLRKKLQDVHNF 34
|||||
Db 12 GKHLNSMERVEWLRKKLQDVHNF 34

RESULT 9

US-09-843-221A-20

; Sequence 20, Application US/09843221A
; Publication No. US20030039654A1
; GENERAL INFORMATION:
; APPLICANT: KOSTENUIK, PAUL
; APPLICANT: LIU, CHUAN-FA
; APPLICANT: LACEY, DAVID LEE
; TITLE OF INVENTION: MODULATORS OF RECEPTORS FOR PARATHYROID HORMONE AND
PARATHYROID HORMONE-
; TITLE OF INVENTION: RELATED PROTEIN
; FILE REFERENCE: A-665B
; CURRENT APPLICATION NUMBER: US/09/843,221A

; CURRENT FILING DATE: 2001-04-26
; PRIOR APPLICATION NUMBER: 60/266,673
; PRIOR FILING DATE: 2001-02-06
; PRIOR APPLICATION NUMBER: 60/214,860
; PRIOR FILING DATE: 2000-06-28
; PRIOR APPLICATION NUMBER: 60/200,053
; PRIOR FILING DATE: 2000-04-27
; NUMBER OF SEQ ID NOS: 170
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 20
; LENGTH: 34
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: modified human PTH
US-09-843-221A-20

Query Match 67.6%; Score 23; DB 11; Length 34;
Best Local Similarity 100.0%; Pred. No. 1.1e-16;
Matches 23; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 12 GKHLNSMERVEWLRKKLQDVHNF 34
|||
Db 12 GKHLNSMERVEWLRKKLQDVHNF 34

RESULT 10

US-09-843-221A-161

; Sequence 161, Application US/09843221A
; Publication No. US20030039654A1
; GENERAL INFORMATION:
; APPLICANT: KOSTENUIK, PAUL
; APPLICANT: LIU, CHUAN-FA
; APPLICANT: LACEY, DAVID LEE
; TITLE OF INVENTION: MODULATORS OF RECEPTORS FOR PARATHYROID HORMONE AND
PARATHYROID HORMONE-
; TITLE OF INVENTION: RELATED PROTEIN
; FILE REFERENCE: A-665B
; CURRENT APPLICATION NUMBER: US/09/843,221A
; CURRENT FILING DATE: 2001-04-26
; PRIOR APPLICATION NUMBER: 60/266,673
; PRIOR FILING DATE: 2001-02-06
; PRIOR APPLICATION NUMBER: 60/214,860
; PRIOR FILING DATE: 2000-06-28
; PRIOR APPLICATION NUMBER: 60/200,053
; PRIOR FILING DATE: 2000-04-27
; NUMBER OF SEQ ID NOS: 170
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 161
; LENGTH: 34
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Preferred embodiments - PTH
; NAME/KEY: misc_feature
; LOCATION: (34)..(34)
; OTHER INFORMATION: Optional linker and Fc domain attached at the C-terminus

US-09-843-221A-161

Query Match 67.6%; Score 23; DB 11; Length 34;
Best Local Similarity 100.0%; Pred. No. 1.1e-16;
Matches 23; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 12 GKHLNSMERVEWLRKKLQDVHNF 34
|||||
Db 12 GKHLNSMERVEWLRKKLQDVHNF 34

RESULT 11

US-09-843-221A-162

; Sequence 162, Application US/09843221A
; Publication No. US20030039654A1
; GENERAL INFORMATION:
; APPLICANT: KOSTENUIK, PAUL
; APPLICANT: LIU, CHUAN-FA
; APPLICANT: LACEY, DAVID LEE
; TITLE OF INVENTION: MODULATORS OF RECEPTORS FOR PARATHYROID HORMONE AND
PARATHYROID HORMONE-
; TITLE OF INVENTION: RELATED PROTEIN
; FILE REFERENCE: A-665B
; CURRENT APPLICATION NUMBER: US/09/843,221A
; CURRENT FILING DATE: 2001-04-26
; PRIOR APPLICATION NUMBER: 60/266,673
; PRIOR FILING DATE: 2001-02-06
; PRIOR APPLICATION NUMBER: 60/214,860
; PRIOR FILING DATE: 2000-06-28
; PRIOR APPLICATION NUMBER: 60/200,053
; PRIOR FILING DATE: 2000-04-27
; NUMBER OF SEQ ID NOS: 170
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 162
; LENGTH: 34
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Preferred embodiments - PTH
; NAME/KEY: misc_feature
; LOCATION: (34)..(34)
; OTHER INFORMATION: Optional linker and Fc domain attached at the C-terminus
US-09-843-221A-162

Query Match 67.6%; Score 23; DB 11; Length 34;
Best Local Similarity 100.0%; Pred. No. 1.1e-16;
Matches 23; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 12 GKHLNSMERVEWLRKKLQDVHNF 34
|||||
Db 12 GKHLNSMERVEWLRKKLQDVHNF 34

RESULT 12

US-09-928-048A-6

; Sequence 6, Application US/09928048A
; Publication No. US20030138858A1

```
; GENERAL INFORMATION:
; APPLICANT: Scantibodies Laboratory, Inc.
; APPLICANT: Cantor, Thomas L.
; TITLE OF INVENTION: METHODS AND DEVICES FOR DIRECT
; TITLE OF INVENTION: DETERMINATION OF CYCLASE INHIBITING PARATHYROID HORMONE
; FILE REFERENCE: 53221-20015.00
; CURRENT APPLICATION NUMBER: US/09/928,048A
; CURRENT FILING DATE: 2000-08-10
; NUMBER OF SEQ ID NOS: 8
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 6
; LENGTH: 34
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-928-048A-6
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Query Match          67.6%; Score 23; DB 12; Length 34;
Best Local Similarity 100.0%; Pred. No. 1.1e-16;
Matches 23; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
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Qy      12 GKHLNSMERVEWLRKKLQDVHNF 34
          ||||||||||||||||||||
Db      12 GKHLNSMERVEWLRKKLQDVHNF 34
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RESULT 13

US-10-361-928-1

```
; Sequence 1, Application US/10361928
; Publication No. US20030144209A1
; GENERAL INFORMATION:
; APPLICANT: BRINGHURST, F. RICHARD
; APPLICANT: TAKASU, HISASHI
; APPLICANT: GARDELLA, THOMAS J.
; TITLE OF INVENTION: AMINO-TERMINAL MODIFIED PARATHYROID HORMONE (PTH)
; TITLE OF INVENTION: ANALOGS
; FILE REFERENCE: 0609.4630002
; CURRENT APPLICATION NUMBER: US/10/361,928
; CURRENT FILING DATE: 2003-02-11
; PRIOR APPLICATION NUMBER: 09/447,800
; PRIOR FILING DATE: 1999-11-23
; PRIOR APPLICATION NUMBER: 60/110,152
; PRIOR FILING DATE: 1998-11-25
; NUMBER OF SEQ ID NOS: 10
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 1
; LENGTH: 34
; TYPE: PRT
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: UNSURE
; LOCATION: (1)
; OTHER INFORMATION: Can be desamino Ser, desamino Ala, or desamino Gly
US-10-361-928-1
```

```
Query Match          67.6%; Score 23; DB 12; Length 34;
Best Local Similarity 100.0%; Pred. No. 1.1e-16;
Matches 23; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
```

Qy 12 GKHLNSMERVEWLRKKLQDVHNF 34
| | | | | | | | | | | | | | | | | | | |
Db 12 GKHLNSMERVEWLRKKLQDVHNF 34

RESULT 14

US-10-361-928-2

; Sequence 2, Application US/10361928
; Publication No. US20030144209A1
; GENERAL INFORMATION:
; APPLICANT: BRINGHURST, F. RICHARD
; APPLICANT: TAKASU, HISASHI
; APPLICANT: GARDELLA, THOMAS J.
; TITLE OF INVENTION: AMINO-TERMINAL MODIFIED PARATHYROID HORMONE (PTH)
; TITLE OF INVENTION: ANALOGS
; FILE REFERENCE: 0609.4630002
; CURRENT APPLICATION NUMBER: US/10/361,928
; CURRENT FILING DATE: 2003-02-11
; PRIOR APPLICATION NUMBER: 09/447,800
; PRIOR FILING DATE: 1999-11-23
; PRIOR APPLICATION NUMBER: 60/110,152
; PRIOR FILING DATE: 1998-11-25
; NUMBER OF SEQ ID NOS: 10
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 2
; LENGTH: 34
; TYPE: PRT
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: MOD_RES
; LOCATION: (1)
; OTHER INFORMATION: Desamino Gly
US-10-361-928-2

Query Match 67.6%; Score 23; DB 12; Length 34;
Best Local Similarity 100.0%; Pred. No. 1.1e-16;
Matches 23; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 12 GKHLNSMERVEWLRKKLQDVHNF 34
| | | | | | | | | | | | | | | | | | | |
Db 12 GKHLNSMERVEWLRKKLQDVHNF 34

RESULT 15

US-10-361-928-5

; Sequence 5, Application US/10361928
; Publication No. US20030144209A1
; GENERAL INFORMATION:
; APPLICANT: BRINGHURST, F. RICHARD
; APPLICANT: TAKASU, HISASHI
; APPLICANT: GARDELLA, THOMAS J.
; TITLE OF INVENTION: AMINO-TERMINAL MODIFIED PARATHYROID HORMONE (PTH)
; TITLE OF INVENTION: ANALOGS
; FILE REFERENCE: 0609.4630002
; CURRENT APPLICATION NUMBER: US/10/361,928
; CURRENT FILING DATE: 2003-02-11

; PRIOR APPLICATION NUMBER: 09/447,800
; PRIOR FILING DATE: 1999-11-23
; PRIOR APPLICATION NUMBER: 60/110,152
; PRIOR FILING DATE: 1998-11-25
; NUMBER OF SEQ ID NOS: 10
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 5
; LENGTH: 34
; TYPE: PRT
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: MOD_RES
; LOCATION: (1)
; OTHER INFORMATION: Desamino Ala
US-10-361-928-5

Query Match 67.6%; Score 23; DB 12; Length 34;
Best Local Similarity 100.0%; Pred. No. 1.1e-16;
Matches 23; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 12 GKHLNSMERVEWLRKKLQDVHNF 34
|||
Db 12 GKHLNSMERVEWLRKKLQDVHNF 34

RESULT 16

US-10-361-928-8

; Sequence 8, Application US/10361928
; Publication No. US20030144209A1
; GENERAL INFORMATION:
; APPLICANT: BRINGHURST, F. RICHARD
; APPLICANT: TAKASU, HISASHI
; APPLICANT: GARDELLA, THOMAS J.
; TITLE OF INVENTION: AMINO-TERMINAL MODIFIED PARATHYROID HORMONE (PTH)
; TITLE OF INVENTION: ANALOGS
; FILE REFERENCE: 0609.4630002
; CURRENT APPLICATION NUMBER: US/10/361,928
; CURRENT FILING DATE: 2003-02-11
; PRIOR APPLICATION NUMBER: 09/447,800
; PRIOR FILING DATE: 1999-11-23
; PRIOR APPLICATION NUMBER: 60/110,152
; PRIOR FILING DATE: 1998-11-25
; NUMBER OF SEQ ID NOS: 10
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 8
; LENGTH: 34
; TYPE: PRT
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: MOD_RES
; LOCATION: (1)
; OTHER INFORMATION: Desamino Ser
US-10-361-928-8

Query Match 67.6%; Score 23; DB 12; Length 34;
Best Local Similarity 100.0%; Pred. No. 1.1e-16;
Matches 23; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 12 GKHLNSMERVEWLRKKLQDVHNF 34
| | | | | | | | | | | | | | | | | |
Db 12 GKHLNSMERVEWLRKKLQDVHNF 34

RESULT 17

US-10-340-484-15

; Sequence 15, Application US/10340484
; Publication No. US20030171288A1
; GENERAL INFORMATION:
; APPLICANT: Stewart, Andrew F.
; TITLE OF INVENTION: Treatment of Bone Disorders with Skelatal Anabolic
; TITLE OF INVENTION: Drugs
; FILE REFERENCE: 25200-501
; CURRENT APPLICATION NUMBER: US/10/340,484
; CURRENT FILING DATE: 2003-01-10
; PRIOR APPLICATION NUMBER: 60/347,215
; PRIOR FILING DATE: 2002-01-10
; PRIOR APPLICATION NUMBER: 60/353,296
; PRIOR FILING DATE: 2002-02-01
; PRIOR APPLICATION NUMBER: 60/368,955
; PRIOR FILING DATE: 2002-03-28
; PRIOR APPLICATION NUMBER: 60/379,125
; PRIOR FILING DATE: 2002-05-08
; NUMBER OF SEQ ID NOS: 27
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 15
; LENGTH: 34
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-340-484-15

Query Match 67.6%; Score 23; DB 12; Length 34;
Best Local Similarity 100.0%; Pred. No. 1.1e-16;
Matches 23; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 12 GKHLNSMERVEWLRKKLQDVHNF 34
| | | | | | | | | | | | | | | | | |
Db 12 GKHLNSMERVEWLRKKLQDVHNF 34

RESULT 18

US-10-340-484-16

; Sequence 16, Application US/10340484
; Publication No. US20030171288A1
; GENERAL INFORMATION:
; APPLICANT: Stewart, Andrew F.
; TITLE OF INVENTION: Treatment of Bone Disorders with Skelatal Anabolic
; TITLE OF INVENTION: Drugs
; FILE REFERENCE: 25200-501
; CURRENT APPLICATION NUMBER: US/10/340,484
; CURRENT FILING DATE: 2003-01-10
; PRIOR APPLICATION NUMBER: 60/347,215
; PRIOR FILING DATE: 2002-01-10
; PRIOR APPLICATION NUMBER: 60/353,296
; PRIOR FILING DATE: 2002-02-01

; PRIOR APPLICATION NUMBER: 60/368,955
; PRIOR FILING DATE: 2002-03-28
; PRIOR APPLICATION NUMBER: 60/379,125
; PRIOR FILING DATE: 2002-05-08
; NUMBER OF SEQ ID NOS: 27
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 16
; LENGTH: 34
; TYPE: PRT
; ORGANISM: Macaca fascicularis
US-10-340-484-16

Query Match 67.6%; Score 23; DB 12; Length 34;
Best Local Similarity 100.0%; Pred. No. 1.1e-16;
Matches 23; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 12 GKHLNSMERVEWLRKKLQDVHNF 34
| | | | | | | | | | | | | | | | | | | | | |
Db 12 GKHLNSMERVEWLRKKLQDVHNF 34

RESULT 19

US-10-016-403-5

; Sequence 5, Application US/10016403
; Publication No. US20020107505A1
; GENERAL INFORMATION:
; APPLICANT: Holladay, Leslie A.
; TITLE OF INVENTION: MODIFICATION OF POLYPEPTIDE DRUGS TO
; INCREASE ELECTROTRANSPORT FLUX
; NUMBER OF SEQUENCES: 10
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Stroud, Stroud, Willink, Thompson & Howard
; STREET: 25 West Main Street
; CITY: Madison
; STATE: WI
; COUNTRY: USA
; ZIP: 53701-2236
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/10/016,403
; FILING DATE: 10-Dec-2001
; CLASSIFICATION: <Unknown>
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/466,610
; FILING DATE: 1995-JUN-06
; ATTORNEY/AGENT INFORMATION:
; NAME: Frenchick, Grady J.
; REGISTRATION NUMBER: 29,018
; REFERENCE/DOCKET NUMBER: 8734.28
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 608-257-2281
; TELEFAX: 608-257-7643
; INFORMATION FOR SEQ ID NO: 5:

```

; SEQUENCE CHARACTERISTICS:
;   LENGTH: 34 amino acids
;   TYPE: amino acid
;   TOPOLOGY: linear
; FEATURE:
;   NAME/KEY: Peptide
;   LOCATION: 1..34
;   OTHER INFORMATION: /note= "parathyroid hormone"
; SEQUENCE DESCRIPTION: SEQ ID NO: 5:
US-10-016-403-5

```

```

Query Match          67.6%; Score 23; DB 14; Length 34;
Best Local Similarity 100.0%; Pred. No. 1.1e-16;
Matches 23; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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```

Qy      12 GKHLNSMERVEWLRKKLQDVHNF 34
        |||||
Db      12 GKHLNSMERVEWLRKKLQDVHNF 34

```

RESULT 20

US-10-016-403-6

```

; Sequence 6, Application US/10016403
; Publication No. US20020107505A1
; GENERAL INFORMATION:
;   APPLICANT: Holladay, Leslie A.
;   TITLE OF INVENTION: MODIFICATION OF POLYPEPTIDE DRUGS TO
;                       INCREASE ELECTROTRANSPORT FLUX
;   NUMBER OF SEQUENCES: 10
;   CORRESPONDENCE ADDRESS:
;       ADDRESSEE: Stroud, Stroud, Willink, Thompson & Howard
;       STREET: 25 West Main Street
;       CITY: Madison
;       STATE: WI
;       COUNTRY: USA
;       ZIP: 53701-2236
;   COMPUTER READABLE FORM:
;       MEDIUM TYPE: Floppy disk
;       COMPUTER: IBM PC compatible
;       OPERATING SYSTEM: PC-DOS/MS-DOS
;       SOFTWARE: PatentIn Release #1.0, Version #1.25
;   CURRENT APPLICATION DATA:
;       APPLICATION NUMBER: US/10/016,403
;       FILING DATE: 10-Dec-2001
;       CLASSIFICATION: <Unknown>
;   PRIOR APPLICATION DATA:
;       APPLICATION NUMBER: 08/466,610
;       FILING DATE: 1995-JUN-06
;   ATTORNEY/AGENT INFORMATION:
;       NAME: Frenchick, Grady J.
;       REGISTRATION NUMBER: 29,018
;       REFERENCE/DOCKET NUMBER: 8734.28
;   TELECOMMUNICATION INFORMATION:
;       TELEPHONE: 608-257-2281
;       TELEFAX: 608-257-7643
; INFORMATION FOR SEQ ID NO: 6:
; SEQUENCE CHARACTERISTICS:

```

; LENGTH: 34 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; FEATURE:
; NAME/KEY: Peptide
; LOCATION: 1..34
; OTHER INFORMATION: /note= "modified parathyroid
; hormone"
; SEQUENCE DESCRIPTION: SEQ ID NO: 6:
US-10-016-403-6

Query Match 67.6%; Score 23; DB 14; Length 34;
Best Local Similarity 100.0%; Pred. No. 1.1e-16;
Matches 23; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 12 GKHLNSMERVEWLRKKLQDVHNF 34
 |||||
Db 12 GKHLNSMERVEWLRKKLQDVHNF 34

RESULT 21

US-10-097-079-1

; Sequence 1, Application US/10097079
; Publication No. US20020132973A1
; GENERAL INFORMATION:
; APPLICANT: Condon, Stephen M.
; Morize, Isabelle
; TITLE OF INVENTION: PEPTIDE PARATHYROID HORMONE ANALOGS
; NUMBER OF SEQUENCES: 88
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Rhone-Poulenc Rorer Inc.
; STREET: 500 Arcola Road, Mailstop 3C43
; CITY: Collegeville
; STATE: PA
; COUNTRY: USA
; ZIP: 19426
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/10/097,079
; FILING DATE: 13-Mar-2002
; CLASSIFICATION: <Unknown>
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 09/228,990
; FILING DATE: <Unknown>
; APPLICATION NUMBER: US 60/046,472
; FILING DATE: 14-MAY-1997
; ATTORNEY/AGENT INFORMATION:
; NAME: Martin Esq., Michael B.
; REGISTRATION NUMBER: 37,521
; REFERENCE/DOCKET NUMBER: A2678B-WO
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (610) 454-2793
; TELEFAX: (610) 454-3808

```

; INFORMATION FOR SEQ ID NO: 1:
;   SEQUENCE CHARACTERISTICS:
;       LENGTH: 34 amino acids
;       TYPE: amino acid
;       STRANDEDNESS: <Unknown>
;       TOPOLOGY: No. US20020132973A1 Relevant
;   MOLECULE TYPE: peptide
;   FRAGMENT TYPE: N-terminal
;   SEQUENCE DESCRIPTION: SEQ ID NO: 1:
US-10-097-079-1

```

```

Query Match          67.6%; Score 23; DB 14; Length 34;
Best Local Similarity 100.0%; Pred. No. 1.1e-16;
Matches    23; Conservative    0; Mismatches    0; Indels    0; Gaps    0;

```

```

Qy      12 GKHLNSMERVEWLRKKLQDVHNF 34
        ||||||||||||||||||||
Db      12 GKHLNSMERVEWLRKKLQDVHNF 34

```

```

RESULT 22
US-09-843-221A-15
; Sequence 15, Application US/09843221A
; Publication No. US20030039654A1
; GENERAL INFORMATION:
;   APPLICANT: KOSTENUIK, PAUL
;   APPLICANT: LIU, CHUAN-FA
;   APPLICANT: LACEY, DAVID LEE
;   TITLE OF INVENTION: MODULATORS OF RECEPTORS FOR PARATHYROID HORMONE AND
PARATHYROID HORMONE-
;   TITLE OF INVENTION: RELATED PROTEIN
;   FILE REFERENCE: A-665B
;   CURRENT APPLICATION NUMBER: US/09/843,221A
;   CURRENT FILING DATE: 2001-04-26
;   PRIOR APPLICATION NUMBER: 60/266,673
;   PRIOR FILING DATE: 2001-02-06
;   PRIOR APPLICATION NUMBER: 60/214,860
;   PRIOR FILING DATE: 2000-06-28
;   PRIOR APPLICATION NUMBER: 60/200,053
;   PRIOR FILING DATE: 2000-04-27
;   NUMBER OF SEQ ID NOS: 170
;   SOFTWARE: PatentIn version 3.1
; SEQ ID NO 15
;   LENGTH: 37
;   TYPE: PRT
;   ORGANISM: Homo sapiens
US-09-843-221A-15

```

```

Query Match          67.6%; Score 23; DB 11; Length 37;
Best Local Similarity 100.0%; Pred. No. 1.2e-16;
Matches    23; Conservative    0; Mismatches    0; Indels    0; Gaps    0;

```

```

Qy      12 GKHLNSMERVEWLRKKLQDVHNF 34
        ||||||||||||||||||||
Db      11 GKHLNSMERVEWLRKKLQDVHNF 33

```

RESULT 23

US-10-168-185-9

; Sequence 9, Application US/10168185
 ; Publication No. US20030175802A1
 ; GENERAL INFORMATION:
 ; APPLICANT: Armbruster, Franz Paul
 ; APPLICANT: Missbichler, Albert
 ; APPLICANT: Schmidt-Gayk, Heinrich
 ; APPLICANT: Roth, Heinz-Jurgen
 ; TITLE OF INVENTION: Method for Determining Parathormone
 ; TITLE OF INVENTION: Activity in a Human Sample
 ; FILE REFERENCE: HLZ-004US
 ; CURRENT APPLICATION NUMBER: US/10/168,185
 ; CURRENT FILING DATE: 2002-06-17
 ; PRIOR APPLICATION NUMBER: PCT/EP00/12911
 ; PRIOR FILING DATE: 2000-12-18
 ; PRIOR APPLICATION NUMBER: DE 19961350
 ; PRIOR FILING DATE: 1999-12-17
 ; NUMBER OF SEQ ID NOS: 11
 ; SOFTWARE: FastSEQ for Windows Version 4.0
 ; SEQ ID NO 9
 ; LENGTH: 37
 ; TYPE: PRT
 ; ORGANISM: Homo sapiens

US-10-168-185-9

Query Match 67.6%; Score 23; DB 12; Length 37;
 Best Local Similarity 100.0%; Pred. No. 1.2e-16;
 Matches 23; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 12 GKHLNSMERVEWLRKKLQDVHNF 34
 |||||
 Db 12 GKHLNSMERVEWLRKKLQDVHNF 34

RESULT 24

US-09-169-786-4

; Sequence 4, Application US/09169786B
 ; Patent No. US20020025929A1
 ; GENERAL INFORMATION:
 ; APPLICANT: Sato, Masahiko
 ; TITLE OF INVENTION: METHOD OF BUILDING AND MAINTAINING BONE
 ; FILE REFERENCE: X-11480
 ; CURRENT APPLICATION NUMBER: US/09/169,786B
 ; CURRENT FILING DATE: 1998-10-09
 ; EARLIER APPLICATION NUMBER: US 60/061,800
 ; EARLIER FILING DATE: 1997-10-14
 ; NUMBER OF SEQ ID NOS: 12
 ; SOFTWARE: PatentIn Ver. 2.0
 ; SEQ ID NO 4
 ; LENGTH: 38
 ; TYPE: PRT
 ; ORGANISM: Homo sapiens

US-09-169-786-4

Query Match 67.6%; Score 23; DB 9; Length 38;
 Best Local Similarity 100.0%; Pred. No. 1.2e-16;


```
; PRIOR APPLICATION NUMBER: US 09/128,401
; PRIOR FILING DATE: 1998-08-03
; PRIOR APPLICATION NUMBER: US 08/625,586
; PRIOR FILING DATE: 1996-03-28
; PRIOR APPLICATION NUMBER: US 08/232,849
; PRIOR FILING DATE: 1994-04-25
; PRIOR APPLICATION NUMBER: US 07/953,397
; PRIOR FILING DATE: 1992-09-29
; NUMBER OF SEQ ID NOS: 1
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 1
;   LENGTH: 38
;   TYPE: PRT
;   ORGANISM: Artificial Sequence
;   FEATURE:
;   OTHER INFORMATION: parathyroid hormone (PTH) fragment molecules
US-10-245-707-1
```

```
Query Match          67.6%; Score 23; DB 12; Length 38;
Best Local Similarity 100.0%; Pred. No. 1.2e-16;
Matches    23; Conservative    0; Mismatches    0; Indels    0; Gaps    0;
```

```
Qy      12 GKHLNSMERVEWLRKKLQDVHNF 34
          |||||
Db      12 GKHLNSMERVEWLRKKLQDVHNF 34
```

RESULT 27

US-10-361-928-3

```
; Sequence 3, Application US/10361928
; Publication No. US20030144209A1
; GENERAL INFORMATION:
; APPLICANT: BRINGHURST, F. RICHARD
; APPLICANT: TAKASU, HISASHI
; APPLICANT: GARDELLA, THOMAS J.
; TITLE OF INVENTION: AMINO-TERMINAL MODIFIED PARATHYROID HORMONE (PTH)
; TITLE OF INVENTION: ANALOGS
; FILE REFERENCE: 0609.4630002
; CURRENT APPLICATION NUMBER: US/10/361,928
; CURRENT FILING DATE: 2003-02-11
; PRIOR APPLICATION NUMBER: 09/447,800
; PRIOR FILING DATE: 1999-11-23
; PRIOR APPLICATION NUMBER: 60/110,152
; PRIOR FILING DATE: 1998-11-25
; NUMBER OF SEQ ID NOS: 10
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 3
;   LENGTH: 33
;   TYPE: PRT
;   ORGANISM: Homo sapiens
;   FEATURE:
;   NAME/KEY: MOD_RES
;   LOCATION: (1)
;   OTHER INFORMATION: Desamino Gly
US-10-361-928-3
```

```
Query Match          64.7%; Score 22; DB 12; Length 33;
```

Best Local Similarity 100.0%; Pred. No. 1.2e-15;
Matches 22; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 12 GKHLNSMERVEWLRKKLQDVHN 33
|||||
Db 12 GKHLNSMERVEWLRKKLQDVHN 33

RESULT 28

US-10-361-928-6

; Sequence 6, Application US/10361928
; Publication No. US20030144209A1
; GENERAL INFORMATION:
; APPLICANT: BRINGHURST, F. RICHARD
; APPLICANT: TAKASU, HISASHI
; APPLICANT: GARDELLA, THOMAS J.
; TITLE OF INVENTION: AMINO-TERMINAL MODIFIED PARATHYROID HORMONE (PTH)
; TITLE OF INVENTION: ANALOGS
; FILE REFERENCE: 0609.4630002
; CURRENT APPLICATION NUMBER: US/10/361,928
; CURRENT FILING DATE: 2003-02-11
; PRIOR APPLICATION NUMBER: 09/447,800
; PRIOR FILING DATE: 1999-11-23
; PRIOR APPLICATION NUMBER: 60/110,152
; PRIOR FILING DATE: 1998-11-25
; NUMBER OF SEQ ID NOS: 10
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 6
; LENGTH: 33
; TYPE: PRT
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: MOD_RES
; LOCATION: (1)
; OTHER INFORMATION: Desamino Ala
US-10-361-928-6

Query Match 64.7%; Score 22; DB 12; Length 33;
Best Local Similarity 100.0%; Pred. No. 1.2e-15;
Matches 22; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 12 GKHLNSMERVEWLRKKLQDVHN 33
|||||
Db 12 GKHLNSMERVEWLRKKLQDVHN 33

RESULT 29

US-10-361-928-9

; Sequence 9, Application US/10361928
; Publication No. US20030144209A1
; GENERAL INFORMATION:
; APPLICANT: BRINGHURST, F. RICHARD
; APPLICANT: TAKASU, HISASHI
; APPLICANT: GARDELLA, THOMAS J.
; TITLE OF INVENTION: AMINO-TERMINAL MODIFIED PARATHYROID HORMONE (PTH)
; TITLE OF INVENTION: ANALOGS
; FILE REFERENCE: 0609.4630002

RESULT 31

US-09-169-786-2

; Sequence 2, Application US/09169786B
 ; Patent No. US20020025929A1
 ; GENERAL INFORMATION:
 ; APPLICANT: Sato, Masahiko
 ; TITLE OF INVENTION: METHOD OF BUILDING AND MAINTAINING BONE
 ; FILE REFERENCE: X-11480
 ; CURRENT APPLICATION NUMBER: US/09/169,786B
 ; CURRENT FILING DATE: 1998-10-09
 ; EARLIER APPLICATION NUMBER: US 60/061,800
 ; EARLIER FILING DATE: 1997-10-14
 ; NUMBER OF SEQ ID NOS: 12
 ; SOFTWARE: PatentIn Ver. 2.0
 ; SEQ ID NO 2
 ; LENGTH: 31
 ; TYPE: PRT
 ; ORGANISM: Homo sapiens

US-09-169-786-2

Query Match 58.8%; Score 20; DB 9; Length 31;
 Best Local Similarity 100.0%; Pred. No. 1.3e-13;
 Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 12 GKHLNSMERVEWLRKKLQDV 31
 |||||
 Db 12 GKHLNSMERVEWLRKKLQDV 31

RESULT 32

US-09-843-221A-27

; Sequence 27, Application US/09843221A
 ; Publication No. US20030039654A1
 ; GENERAL INFORMATION:
 ; APPLICANT: KOSTENUIK, PAUL
 ; APPLICANT: LIU, CHUAN-FA
 ; APPLICANT: LACEY, DAVID LEE
 ; TITLE OF INVENTION: MODULATORS OF RECEPTORS FOR PARATHYROID HORMONE AND
 PARATHYROID HORMONE-
 ; TITLE OF INVENTION: RELATED PROTEIN
 ; FILE REFERENCE: A-665B
 ; CURRENT APPLICATION NUMBER: US/09/843,221A
 ; CURRENT FILING DATE: 2001-04-26
 ; PRIOR APPLICATION NUMBER: 60/266,673
 ; PRIOR FILING DATE: 2001-02-06
 ; PRIOR APPLICATION NUMBER: 60/214,860
 ; PRIOR FILING DATE: 2000-06-28
 ; PRIOR APPLICATION NUMBER: 60/200,053
 ; PRIOR FILING DATE: 2000-04-27
 ; NUMBER OF SEQ ID NOS: 170
 ; SOFTWARE: PatentIn version 3.1
 ; SEQ ID NO 27
 ; LENGTH: 31
 ; TYPE: PRT
 ; ORGANISM: Homo sapiens

US-09-843-221A-27

Query Match 58.8%; Score 20; DB 11; Length 31;
Best Local Similarity 100.0%; Pred. No. 1.3e-13;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 12 GKHLNSMERVEWLRKKLQDV 31
 |||||
Db 12 GKHLNSMERVEWLRKKLQDV 31

RESULT 33

US-09-843-221A-165

; Sequence 165, Application US/09843221A
; Publication No. US20030039654A1
; GENERAL INFORMATION:
; APPLICANT: KOSTENUIK, PAUL
; APPLICANT: LIU, CHUAN-FA
; APPLICANT: LACEY, DAVID LEE
; TITLE OF INVENTION: MODULATORS OF RECEPTORS FOR PARATHYROID HORMONE AND
PARATHYROID HORMONE-
; TITLE OF INVENTION: RELATED PROTEIN
; FILE REFERENCE: A-665B
; CURRENT APPLICATION NUMBER: US/09/843,221A
; CURRENT FILING DATE: 2001-04-26
; PRIOR APPLICATION NUMBER: 60/266,673
; PRIOR FILING DATE: 2001-02-06
; PRIOR APPLICATION NUMBER: 60/214,860
; PRIOR FILING DATE: 2000-06-28
; PRIOR APPLICATION NUMBER: 60/200,053
; PRIOR FILING DATE: 2000-04-27
; NUMBER OF SEQ ID NOS: 170
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 165
; LENGTH: 31
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Preferred embodiments - PTH
; NAME/KEY: misc_feature
; LOCATION: (31)..(31)
; OTHER INFORMATION: Optional linker and Fc domain attached at the C-terminus
US-09-843-221A-165

Query Match 58.8%; Score 20; DB 11; Length 31;
Best Local Similarity 100.0%; Pred. No. 1.3e-13;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 12 GKHLNSMERVEWLRKKLQDV 31
 |||||
Db 12 GKHLNSMERVEWLRKKLQDV 31

RESULT 34

US-09-843-221A-39

; Sequence 39, Application US/09843221A
; Publication No. US20030039654A1

```
; GENERAL INFORMATION:
; APPLICANT: KOSTENUIK, PAUL
; APPLICANT: LIU, CHUAN-FA
; APPLICANT: LACEY, DAVID LEE
; TITLE OF INVENTION: MODULATORS OF RECEPTORS FOR PARATHYROID HORMONE AND
PARATHYROID HORMONE-
; TITLE OF INVENTION: RELATED PROTEIN
; FILE REFERENCE: A-665B
; CURRENT APPLICATION NUMBER: US/09/843,221A
; CURRENT FILING DATE: 2001-04-26
; PRIOR APPLICATION NUMBER: 60/266,673
; PRIOR FILING DATE: 2001-02-06
; PRIOR APPLICATION NUMBER: 60/214,860
; PRIOR FILING DATE: 2000-06-28
; PRIOR APPLICATION NUMBER: 60/200,053
; PRIOR FILING DATE: 2000-04-27
; NUMBER OF SEQ ID NOS: 170
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 39
; LENGTH: 30
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-843-221A-39
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```
Query Match          55.9%; Score 19; DB 11; Length 30;
Best Local Similarity 100.0%; Pred. No. 1.3e-12;
Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
```

```
QY      12 GKHLNSMERVEWLRKKLQD 30
        |||||
Db       12 GKHLNSMERVEWLRKKLQD 30
```

RESULT 35

```
US-09-843-221A-40
; Sequence 40, Application US/09843221A
; Publication No. US20030039654A1
; GENERAL INFORMATION:
; APPLICANT: KOSTENUIK, PAUL
; APPLICANT: LIU, CHUAN-FA
; APPLICANT: LACEY, DAVID LEE
; TITLE OF INVENTION: MODULATORS OF RECEPTORS FOR PARATHYROID HORMONE AND
PARATHYROID HORMONE-
; TITLE OF INVENTION: RELATED PROTEIN
; FILE REFERENCE: A-665B
; CURRENT APPLICATION NUMBER: US/09/843,221A
; CURRENT FILING DATE: 2001-04-26
; PRIOR APPLICATION NUMBER: 60/266,673
; PRIOR FILING DATE: 2001-02-06
; PRIOR APPLICATION NUMBER: 60/214,860
; PRIOR FILING DATE: 2000-06-28
; PRIOR APPLICATION NUMBER: 60/200,053
; PRIOR FILING DATE: 2000-04-27
; NUMBER OF SEQ ID NOS: 170
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 40
; LENGTH: 30
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; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: modified human PTH
US-09-843-221A-40

Query Match 55.9%; Score 19; DB 11; Length 30;
Best Local Similarity 100.0%; Pred. No. 1.3e-12;
Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 12 GKHLNSMERVEWLRKKLQD 30
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Db 12 GKHLNSMERVEWLRKKLQD 30

RESULT 36

US-09-843-221A-43
; Sequence 43, Application US/09843221A
; Publication No. US20030039654A1
; GENERAL INFORMATION:
; APPLICANT: KOSTENUIK, PAUL
; APPLICANT: LIU, CHUAN-FA
; APPLICANT: LACEY, DAVID LEE
; TITLE OF INVENTION: MODULATORS OF RECEPTORS FOR PARATHYROID HORMONE AND
PARATHYROID HORMONE-
; TITLE OF INVENTION: RELATED PROTEIN
; FILE REFERENCE: A-665B
; CURRENT APPLICATION NUMBER: US/09/843,221A
; CURRENT FILING DATE: 2001-04-26
; PRIOR APPLICATION NUMBER: 60/266,673
; PRIOR FILING DATE: 2001-02-06
; PRIOR APPLICATION NUMBER: 60/214,860
; PRIOR FILING DATE: 2000-06-28
; PRIOR APPLICATION NUMBER: 60/200,053
; PRIOR FILING DATE: 2000-04-27
; NUMBER OF SEQ ID NOS: 170
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 43
; LENGTH: 30
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: modified human PTH
US-09-843-221A-43

Query Match 55.9%; Score 19; DB 11; Length 30;
Best Local Similarity 100.0%; Pred. No. 1.3e-12;
Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 12 GKHLNSMERVEWLRKKLQD 30
| | | | | | | | | | | | | | | | | | | |
Db 12 GKHLNSMERVEWLRKKLQD 30

RESULT 37

US-09-843-221A-166
; Sequence 166, Application US/09843221A

; Publication No. US20030039654A1
; GENERAL INFORMATION:
; APPLICANT: KOSTENUIK, PAUL
; APPLICANT: LIU, CHUAN-FA
; APPLICANT: LACEY, DAVID LEE
; TITLE OF INVENTION: MODULATORS OF RECEPTORS FOR PARATHYROID HORMONE AND
PARATHYROID HORMONE-
; TITLE OF INVENTION: RELATED PROTEIN
; FILE REFERENCE: A-665B
; CURRENT APPLICATION NUMBER: US/09/843,221A
; CURRENT FILING DATE: 2001-04-26
; PRIOR APPLICATION NUMBER: 60/266,673
; PRIOR FILING DATE: 2001-02-06
; PRIOR APPLICATION NUMBER: 60/214,860
; PRIOR FILING DATE: 2000-06-28
; PRIOR APPLICATION NUMBER: 60/200,053
; PRIOR FILING DATE: 2000-04-27
; NUMBER OF SEQ ID NOS: 170
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 166
; LENGTH: 30
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Preferred embodiments - PTH
; NAME/KEY: misc_feature
; LOCATION: (30)..(30)
; OTHER INFORMATION: Optional linker and Fc domain attached at the C-terminus
US-09-843-221A-166

Query Match 55.9%; Score 19; DB 11; Length 30;
Best Local Similarity 100.0%; Pred. No. 1.3e-12;
Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 12 GKHLNSMERVEWLRKKLQD 30
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Db 12 GKHLNSMERVEWLRKKLQD 30

RESULT 38
US-09-843-221A-34
; Sequence 34, Application US/09843221A
; Publication No. US20030039654A1
; GENERAL INFORMATION:
; APPLICANT: KOSTENUIK, PAUL
; APPLICANT: LIU, CHUAN-FA
; APPLICANT: LACEY, DAVID LEE
; TITLE OF INVENTION: MODULATORS OF RECEPTORS FOR PARATHYROID HORMONE AND
PARATHYROID HORMONE-
; TITLE OF INVENTION: RELATED PROTEIN
; FILE REFERENCE: A-665B
; CURRENT APPLICATION NUMBER: US/09/843,221A
; CURRENT FILING DATE: 2001-04-26
; PRIOR APPLICATION NUMBER: 60/266,673
; PRIOR FILING DATE: 2001-02-06
; PRIOR APPLICATION NUMBER: 60/214,860
; PRIOR FILING DATE: 2000-06-28

US-09-843-221A-167

US-09-843-221A-167

Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Db 12 GKHLNSMERVEWLRKKLO 29

Job time : 23.8785 secs

GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: January 14, 2004, 10:28:19 ; Search time 25.4206 Seconds
(without alignments)
345.145 Million cell updates/sec

Title: US-09-843-221A-163
Perfect score: 34
Sequence: 1 SVSEIQLMHNKGKHLNSMERVEWLRKKLQDVHNF 34

Scoring table: OLIGO
Gapop 60.0 , Gapext 60.0

Searched: 830525 seqs, 258052604 residues

Word size : 0

Total number of hits satisfying chosen parameters: 13497

Minimum DB seq length: 28
Maximum DB seq length: 40

Post-processing: Listing first 1000 summaries

Database : SPTREMBL_23:*
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2: sp_bacteria:*
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6: sp_mammal:*
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10: sp_plant:*
11: sp_rodent:*
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13: sp_vertibrate:*
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15: sp_rvirus:*
16: sp_bacteriap:*
17: sp_archeap:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

| Result | % | Query | | | | | |
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| 2 | 9 | 26.5 | 31 | 11 | Q91Y91 | Q91y91 peromyscus |
| 3 | 5 | 14.7 | 34 | 5 | O17148 | O17148 echinococcu |
| 4 | 5 | 14.7 | 34 | 16 | Q97K50 | Q97k50 clostridium |
| 5 | 5 | 14.7 | 34 | 17 | Q9HR65 | Q9hr65 halobacteri |
| 6 | 5 | 14.7 | 35 | 11 | Q8BTB9 | Q8btb9 mus musculu |
| 7 | 5 | 14.7 | 35 | 16 | Q97RG6 | Q97rg6 streptococc |
| 8 | 4 | 11.8 | 28 | 10 | O24285 | O24285 pinus radia |
| 9 | 4 | 11.8 | 29 | 2 | Q49148 | Q49148 methylobact |
| 10 | 4 | 11.8 | 29 | 4 | Q9UCL2 | Q9ucl2 homo sapien |
| 11 | 4 | 11.8 | 29 | 5 | Q25603 | Q25603 onchocerca |
| 12 | 4 | 11.8 | 29 | 8 | Q9TI61 | Q9ti61 allosyncarp |
| 13 | 4 | 11.8 | 29 | 13 | O13043 | O13043 scylliorhinu |
| 14 | 4 | 11.8 | 30 | 4 | Q9UBV5 | Q9ubv5 homo sapien |
| 15 | 4 | 11.8 | 30 | 16 | Q8DZP7 | Q8dzp7 streptococc |
| 16 | 4 | 11.8 | 31 | 1 | Q55314 | Q55314 sulfolobus |
| 17 | 4 | 11.8 | 31 | 4 | Q8NEI8 | Q8nei8 homo sapien |
| 18 | 4 | 11.8 | 31 | 16 | O50669 | O50669 borrelia bu |
| 19 | 4 | 11.8 | 31 | 16 | Q8EIW8 | Q8eiw8 shewanella |
| 20 | 4 | 11.8 | 32 | 11 | Q9QZQ2 | Q9qzq2 mus musculu |
| 21 | 4 | 11.8 | 32 | 17 | Q9HSZ0 | Q9hsz0 halobacteri |
| 22 | 4 | 11.8 | 33 | 5 | Q95SD4 | Q95sd4 drosophila |
| 23 | 4 | 11.8 | 33 | 16 | Q9PKX3 | Q9pkx3 chlamydia m |
| 24 | 4 | 11.8 | 34 | 2 | Q9ZG81 | Q9zg81 chlamydia t |
| 25 | 4 | 11.8 | 34 | 2 | Q8GFK2 | Q8gfk2 staphylococ |
| 26 | 4 | 11.8 | 34 | 11 | Q8C4P4 | Q8c4p4 mus musculu |
| 27 | 4 | 11.8 | 34 | 13 | Q90ZJ4 | Q90zj4 gallus gall |
| 28 | 4 | 11.8 | 34 | 16 | Q98FK5 | Q98fk5 rhizobium l |
| 29 | 4 | 11.8 | 35 | 4 | Q15421 | Q15421 homo sapien |
| 30 | 4 | 11.8 | 35 | 12 | Q8V6J8 | Q8v6j8 halovirus h |
| 31 | 4 | 11.8 | 35 | 16 | Q9KQG4 | Q9kqg4 vibrio chol |
| 32 | 4 | 11.8 | 35 | 16 | Q8F102 | Q8f102 leptospira |
| 33 | 4 | 11.8 | 36 | 2 | Q53920 | Q53920 streptomyce |
| 34 | 4 | 11.8 | 36 | 2 | O68941 | O68941 rhodospiril |
| 35 | 4 | 11.8 | 36 | 4 | Q8WXW8 | Q8wxw8 homo sapien |
| 36 | 4 | 11.8 | 36 | 10 | Q9SJ63 | Q9sj63 arabidopsis |
| 37 | 4 | 11.8 | 36 | 12 | Q9PXD1 | Q9pxd1 hepatitis c |
| 38 | 4 | 11.8 | 36 | 12 | Q91D77 | Q91d77 ttv-like mi |
| 39 | 4 | 11.8 | 36 | 13 | Q9YHT9 | Q9yht9 brachydanio |
| 40 | 4 | 11.8 | 36 | 16 | Q97S91 | Q97s91 streptococc |
| 41 | 4 | 11.8 | 37 | 2 | Q8KYJ0 | Q8kyj0 bacillus an |
| 42 | 4 | 11.8 | 37 | 5 | Q9N2L2 | Q9n2l2 caenorhabdi |
| 43 | 4 | 11.8 | 37 | 10 | Q39942 | Q39942 helianthus |
| 44 | 4 | 11.8 | 37 | 13 | Q8AWW8 | Q8aww8 oncorhynchu |
| 45 | 4 | 11.8 | 37 | 16 | Q8F6U2 | Q8f6u2 leptospira |
| 46 | 4 | 11.8 | 37 | 16 | Q8F5H3 | Q8f5h3 leptospira |
| 47 | 4 | 11.8 | 37 | 16 | Q8F419 | Q8f419 leptospira |
| 48 | 4 | 11.8 | 37 | 16 | Q8EXV9 | Q8exv9 leptospira |
| 49 | 4 | 11.8 | 38 | 2 | Q8KWH7 | Q8kwh7 lactobacill |
| 50 | 4 | 11.8 | 38 | 5 | Q9NBE3 | Q9nbe3 chironomus |
| 51 | 4 | 11.8 | 38 | 5 | Q9NBE5 | Q9nbe5 chironomus |
| 52 | 4 | 11.8 | 38 | 5 | Q9NBE8 | Q9nbe8 chironomus |
| 53 | 4 | 11.8 | 38 | 5 | Q9NBE4 | Q9nbe4 chironomus |
| 54 | 4 | 11.8 | 38 | 5 | Q9NBE7 | Q9nbe7 chironomus |
| 55 | 4 | 11.8 | 38 | 11 | O35918 | O35918 rattus norv |
| 56 | 4 | 11.8 | 38 | 11 | Q91VC8 | Q91vc8 mus musculu |
| 57 | 4 | 11.8 | 38 | 13 | Q8AWW9 | Q8aww9 oncorhynchu |

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| 58 | 4 | 11.8 | 38 | 16 | Q8E0D2 | Q8e0d2 streptococc |
| 59 | 4 | 11.8 | 39 | 2 | Q8GPO8 | Q8gpo8 pseudomonas |
| 60 | 4 | 11.8 | 39 | 12 | Q68847 | Q68847 hepatitis c |
| 61 | 4 | 11.8 | 39 | 12 | Q68845 | Q68845 hepatitis c |
| 62 | 4 | 11.8 | 39 | 12 | Q68846 | Q68846 hepatitis c |
| 63 | 4 | 11.8 | 39 | 13 | Q90776 | Q90776 gallus gall |
| 64 | 4 | 11.8 | 39 | 16 | Q9KYH4 | Q9kyh4 streptomyce |
| 65 | 4 | 11.8 | 39 | 16 | Q8F0C7 | Q8f0c7 leptospira |
| 66 | 4 | 11.8 | 40 | 2 | Q8GCS7 | Q8gcs7 eubacterium |
| 67 | 4 | 11.8 | 40 | 4 | Q9UE56 | Q9ue56 homo sapien |
| 68 | 4 | 11.8 | 40 | 5 | Q9NFH5 | Q9nfh5 plasmodium |
| 69 | 4 | 11.8 | 40 | 6 | Q9N1X0 | Q9nlx0 equus cabal |
| 70 | 4 | 11.8 | 40 | 6 | Q29283 | Q29283 sus scrofa |
| 71 | 4 | 11.8 | 40 | 12 | Q91JZ7 | Q91jz7 hepatitis c |
| 72 | 3 | 8.8 | 28 | 2 | Q01303 | Q01303 treponema p |
| 73 | 3 | 8.8 | 28 | 2 | Q05574 | Q05574 prochloroth |
| 74 | 3 | 8.8 | 28 | 2 | Q9ZB83 | Q9zb83 vibrio angu |
| 75 | 3 | 8.8 | 28 | 3 | Q8TGN3 | Q8tgn3 saccharomyc |
| 76 | 3 | 8.8 | 28 | 3 | Q8TGT8 | Q8tgt8 saccharomyc |
| 77 | 3 | 8.8 | 28 | 4 | Q96SD9 | Q96sd9 homo sapien |
| 78 | 3 | 8.8 | 28 | 4 | Q16326 | Q16326 homo sapien |
| 79 | 3 | 8.8 | 28 | 4 | Q96EU0 | Q96eu0 homo sapien |
| 80 | 3 | 8.8 | 28 | 4 | O75980 | O75980 homo sapien |
| 81 | 3 | 8.8 | 28 | 4 | O95737 | O95737 homo sapien |
| 82 | 3 | 8.8 | 28 | 5 | Q8MUW0 | Q8muw0 schistosoma |
| 83 | 3 | 8.8 | 28 | 5 | Q8MPY2 | Q8mpy2 caenorhabdi |
| 84 | 3 | 8.8 | 28 | 5 | Q9BJE4 | Q9bje4 paupopus sp |
| 85 | 3 | 8.8 | 28 | 6 | O62821 | O62821 bubalus bub |
| 86 | 3 | 8.8 | 28 | 6 | Q9XS89 | Q9xs89 equus cabal |
| 87 | 3 | 8.8 | 28 | 8 | Q8WBC8 | Q8wbc8 cucurbita e |
| 88 | 3 | 8.8 | 28 | 8 | Q9TIE9 | Q9tie9 centella er |
| 89 | 3 | 8.8 | 28 | 8 | Q9TIE8 | Q9tie8 centella as |
| 90 | 3 | 8.8 | 28 | 8 | Q9MR96 | Q9mr96 crocodylus |
| 91 | 3 | 8.8 | 28 | 8 | Q9TIE6 | Q9tie6 centella hi |
| 92 | 3 | 8.8 | 28 | 8 | Q9ZYS4 | Q9zys4 leishmania |
| 93 | 3 | 8.8 | 28 | 8 | Q9MR94 | Q9mr94 chelonia my |
| 94 | 3 | 8.8 | 28 | 8 | Q9TIE7 | Q9tie7 centella tr |
| 95 | 3 | 8.8 | 28 | 8 | Q8HS23 | Q8hs23 pisum sativ |
| 96 | 3 | 8.8 | 28 | 8 | Q8HS11 | Q8hs11 spathiphyll |
| 97 | 3 | 8.8 | 28 | 8 | Q8HS07 | Q8hs07 welwitschia |
| 98 | 3 | 8.8 | 28 | 8 | Q8HKF0 | Q8hkf0 rhipicephal |
| 99 | 3 | 8.8 | 28 | 9 | Q9AZJ9 | Q9azj9 bacterioph |
| 100 | 3 | 8.8 | 28 | 9 | Q38269 | Q38269 bacterioph |
| 101 | 3 | 8.8 | 28 | 10 | Q8S526 | Q8s526 ipomoea bat |
| 102 | 3 | 8.8 | 28 | 10 | Q8W232 | Q8w232 zea mays (m |
| 103 | 3 | 8.8 | 28 | 10 | Q9LMD6 | Q9lmd6 arabidopsis |
| 104 | 3 | 8.8 | 28 | 11 | Q9ESI4 | Q9esi4 petromus ty |
| 105 | 3 | 8.8 | 28 | 11 | Q9ESI5 | Q9esi5 thryonomys |
| 106 | 3 | 8.8 | 28 | 11 | Q9ESI6 | Q9esi6 hystrix afr |
| 107 | 3 | 8.8 | 28 | 11 | Q99PL9 | Q99pl9 mus musculu |
| 108 | 3 | 8.8 | 28 | 11 | Q9ESI2 | Q9esi2 cryptomys h |
| 109 | 3 | 8.8 | 28 | 11 | Q9EP60 | Q9ep60 heliophobi |
| 110 | 3 | 8.8 | 28 | 11 | Q9ESI0 | Q9esi0 cryptomys s |
| 111 | 3 | 8.8 | 28 | 11 | Q91XP0 | Q91xp0 rattus norv |
| 112 | 3 | 8.8 | 28 | 11 | P70651 | P70651 mus sp. bet |
| 113 | 3 | 8.8 | 28 | 11 | Q9EP59 | Q9ep59 georychus c |
| 114 | 3 | 8.8 | 28 | 11 | Q9ESI1 | Q9esi1 cryptomys d |

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| 115 | 3 | 8.8 | 28 | 11 | P97914 | P97914 | rattus norv |
| 116 | 3 | 8.8 | 28 | 11 | Q9EP61 | Q9ep61 | heteroceph |
| 117 | 3 | 8.8 | 28 | 11 | Q9ESH8 | Q9esh8 | bathyergus |
| 118 | 3 | 8.8 | 28 | 11 | Q9ESH9 | Q9esh9 | bathyergus |
| 119 | 3 | 8.8 | 28 | 11 | Q9QXB4 | Q9qxb4 | mus musculu |
| 120 | 3 | 8.8 | 28 | 11 | Q9ESI3 | Q9esi3 | cryptomys h |
| 121 | 3 | 8.8 | 28 | 12 | Q68087 | Q68087 | hepatitis c |
| 122 | 3 | 8.8 | 28 | 12 | Q67786 | Q67786 | human adeno |
| 123 | 3 | 8.8 | 28 | 12 | Q68095 | Q68095 | hepatitis c |
| 124 | 3 | 8.8 | 28 | 12 | Q68097 | Q68097 | hepatitis c |
| 125 | 3 | 8.8 | 28 | 12 | Q68092 | Q68092 | hepatitis c |
| 126 | 3 | 8.8 | 28 | 12 | Q68091 | Q68091 | hepatitis c |
| 127 | 3 | 8.8 | 28 | 12 | Q68093 | Q68093 | hepatitis c |
| 128 | 3 | 8.8 | 28 | 12 | Q68099 | Q68099 | hepatitis c |
| 129 | 3 | 8.8 | 28 | 12 | Q68096 | Q68096 | hepatitis c |
| 130 | 3 | 8.8 | 28 | 12 | Q68098 | Q68098 | hepatitis c |
| 131 | 3 | 8.8 | 28 | 12 | Q83181 | Q83181 | cauliflower |
| 132 | 3 | 8.8 | 28 | 12 | Q68086 | Q68086 | hepatitis c |
| 133 | 3 | 8.8 | 28 | 12 | Q68552 | Q68552 | hepatitis c |
| 134 | 3 | 8.8 | 28 | 12 | Q68094 | Q68094 | hepatitis c |
| 135 | 3 | 8.8 | 28 | 12 | Q9WNI4 | Q9wni4 | tt virus. o |
| 136 | 3 | 8.8 | 28 | 13 | Q9PRE8 | Q9pre8 | oryzias lat |
| 137 | 3 | 8.8 | 28 | 13 | Q9PRI9 | Q9pri9 | amia calva |
| 138 | 3 | 8.8 | 28 | 13 | Q9PRN8 | Q9prn8 | carassius a |
| 139 | 3 | 8.8 | 28 | 15 | O71346 | O71346 | human endog |
| 140 | 3 | 8.8 | 28 | 15 | Q9QEY3 | Q9qey3 | human immun |
| 141 | 3 | 8.8 | 28 | 16 | Q8X415 | Q8x415 | escherichia |
| 142 | 3 | 8.8 | 28 | 16 | Q8NVB8 | Q8nvb8 | staphylococ |
| 143 | 3 | 8.8 | 28 | 16 | Q8ENT7 | Q8ent7 | oceanobacil |
| 144 | 3 | 8.8 | 28 | 16 | Q8CK95 | Q8ck95 | yersinia pe |
| 145 | 3 | 8.8 | 29 | 2 | Q9ZGG4 | Q9zgg4 | heliobacill |
| 146 | 3 | 8.8 | 29 | 2 | Q54200 | Q54200 | streptomyce |
| 147 | 3 | 8.8 | 29 | 2 | Q9X3E3 | Q9x3e3 | prochloroco |
| 148 | 3 | 8.8 | 29 | 2 | Q9X3J9 | Q9x3j9 | prochloroco |
| 149 | 3 | 8.8 | 29 | 2 | Q47650 | Q47650 | escherichia |
| 150 | 3 | 8.8 | 29 | 2 | Q9AKV1 | Q9akv1 | neisseria g |
| 151 | 3 | 8.8 | 29 | 2 | Q9R511 | Q9r511 | bacillus su |
| 152 | 3 | 8.8 | 29 | 2 | Q8GL27 | Q8gl27 | borrelia bu |
| 153 | 3 | 8.8 | 29 | 3 | P78747 | P78747 | saccharomyc |
| 154 | 3 | 8.8 | 29 | 3 | Q8TGQ5 | Q8tgq5 | saccharomyc |
| 155 | 3 | 8.8 | 29 | 4 | Q9Y3G1 | Q9y3g1 | homo sapien |
| 156 | 3 | 8.8 | 29 | 4 | Q9H2A1 | Q9h2a1 | homo sapien |
| 157 | 3 | 8.8 | 29 | 4 | Q9UN87 | Q9un87 | homo sapien |
| 158 | 3 | 8.8 | 29 | 4 | Q9UDJ9 | Q9udj9 | homo sapien |
| 159 | 3 | 8.8 | 29 | 4 | Q9H465 | Q9h465 | homo sapien |
| 160 | 3 | 8.8 | 29 | 4 | Q8NEF6 | Q8nef6 | homo sapien |
| 161 | 3 | 8.8 | 29 | 4 | Q8TDW8 | Q8tdw8 | homo sapien |
| 162 | 3 | 8.8 | 29 | 4 | Q96IR5 | Q96ir5 | homo sapien |
| 163 | 3 | 8.8 | 29 | 4 | Q9BSQ3 | Q9bsq3 | homo sapien |
| 164 | 3 | 8.8 | 29 | 5 | Q95VB2 | Q95vb2 | spirometra |
| 165 | 3 | 8.8 | 29 | 5 | Q95NF4 | Q95nf4 | drosophila |
| 166 | 3 | 8.8 | 29 | 5 | Q24683 | Q24683 | dugesia tig |
| 167 | 3 | 8.8 | 29 | 6 | Q95MD3 | Q95md3 | bos taurus |
| 168 | 3 | 8.8 | 29 | 6 | Q9TRG5 | Q9trg5 | sus scrofa |
| 169 | 3 | 8.8 | 29 | 8 | Q8WBB9 | Q8wbb9 | cucurbita f |
| 170 | 3 | 8.8 | 29 | 8 | Q9TI57 | Q9ti57 | corymbia pa |
| 171 | 3 | 8.8 | 29 | 8 | Q8W7W7 | Q8w7w7 | cucurbita p |

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| 172 | 3 | 8.8 | 29 | 8 | Q9GF70 | Q9gf70 trochodendr |
| 173 | 3 | 8.8 | 29 | 8 | Q8W7W4 | Q8w7w4 cucurbita a |
| 174 | 3 | 8.8 | 29 | 8 | Q8W7W6 | Q8w7w6 cucurbita p |
| 175 | 3 | 8.8 | 29 | 8 | Q8WBC1 | Q8wbc1 cucurbita o |
| 176 | 3 | 8.8 | 29 | 8 | Q9B5Z6 | Q9b5z6 pseudostylo |
| 177 | 3 | 8.8 | 29 | 8 | Q8W7W5 | Q8w7w5 cucurbita p |
| 178 | 3 | 8.8 | 29 | 8 | Q9B938 | Q9b938 eupristina |
| 179 | 3 | 8.8 | 29 | 8 | Q9G370 | Q9g370 draco blanf |
| 180 | 3 | 8.8 | 29 | 8 | Q8WBD0 | Q8wbd0 cucurbita a |
| 181 | 3 | 8.8 | 29 | 8 | Q8WBB6 | Q8wbb6 citrullus l |
| 182 | 3 | 8.8 | 29 | 8 | Q8W7W9 | Q8w7w9 cucurbita f |
| 183 | 3 | 8.8 | 29 | 8 | Q8W7W8 | Q8w7w8 cucurbita m |
| 184 | 3 | 8.8 | 29 | 8 | Q8HS21 | Q8hs21 rheum x cul |
| 185 | 3 | 8.8 | 29 | 9 | Q9FZX6 | Q9fzx6 bacteriopha |
| 186 | 3 | 8.8 | 29 | 10 | Q9SC62 | Q9sc62 picea abies |
| 187 | 3 | 8.8 | 29 | 10 | Q9SC58 | Q9sc58 picea abies |
| 188 | 3 | 8.8 | 29 | 10 | Q9FUS3 | Q9fus3 physcomitre |
| 189 | 3 | 8.8 | 29 | 10 | Q9SC57 | Q9sc57 picea abies |
| 190 | 3 | 8.8 | 29 | 10 | P82196 | P82196 spinacia ol |
| 191 | 3 | 8.8 | 29 | 11 | Q9JK05 | Q9jk05 mus musculu |
| 192 | 3 | 8.8 | 29 | 11 | Q9Z2C0 | Q9z2c0 mus musculu |
| 193 | 3 | 8.8 | 29 | 11 | Q921Z6 | Q921z6 mus musculu |
| 194 | 3 | 8.8 | 29 | 11 | Q9Z2C1 | Q9z2c1 mus musculu |
| 195 | 3 | 8.8 | 29 | 11 | O70564 | O70564 mus musculu |
| 196 | 3 | 8.8 | 29 | 11 | Q9QY65 | Q9qy65 mus musculu |
| 197 | 3 | 8.8 | 29 | 11 | Q62300 | Q62300 mus musculu |
| 198 | 3 | 8.8 | 29 | 11 | O08980 | O08980 mus musculu |
| 199 | 3 | 8.8 | 29 | 11 | Q8CGM8 | Q8cgm8 mus musculu |
| 200 | 3 | 8.8 | 29 | 12 | Q91HB1 | Q91hb1 porcine cir |
| 201 | 3 | 8.8 | 29 | 12 | O92646 | O92646 hepatitis e |
| 202 | 3 | 8.8 | 29 | 12 | Q919A5 | Q919a5 porcine rep |
| 203 | 3 | 8.8 | 29 | 12 | Q919A7 | Q919a7 porcine rep |
| 204 | 3 | 8.8 | 29 | 12 | Q86872 | Q86872 cauliflower |
| 205 | 3 | 8.8 | 29 | 12 | O92648 | O92648 hepatitis e |
| 206 | 3 | 8.8 | 29 | 12 | O56835 | O56835 vibrio chol |
| 207 | 3 | 8.8 | 29 | 13 | Q8AYR0 | Q8ayr0 oryzias lat |
| 208 | 3 | 8.8 | 29 | 13 | Q8AWC2 | Q8awc2 gallus gall |
| 209 | 3 | 8.8 | 29 | 15 | O72001 | O72001 human endog |
| 210 | 3 | 8.8 | 29 | 15 | O71342 | O71342 human endog |
| 211 | 3 | 8.8 | 29 | 15 | O71339 | O71339 human endog |
| 212 | 3 | 8.8 | 29 | 15 | O71347 | O71347 human endog |
| 213 | 3 | 8.8 | 29 | 15 | O71340 | O71340 human endog |
| 214 | 3 | 8.8 | 29 | 15 | O71343 | O71343 human endog |
| 215 | 3 | 8.8 | 29 | 15 | Q9IQJ8 | Q9iqj8 human immun |
| 216 | 3 | 8.8 | 29 | 15 | O71991 | O71991 human endog |
| 217 | 3 | 8.8 | 29 | 15 | Q9IQJ1 | Q9iqj1 human immun |
| 218 | 3 | 8.8 | 29 | 15 | O71994 | O71994 human endog |
| 219 | 3 | 8.8 | 29 | 15 | O71341 | O71341 human endog |
| 220 | 3 | 8.8 | 29 | 15 | O71345 | O71345 human endog |
| 221 | 3 | 8.8 | 29 | 15 | O71336 | O71336 human endog |
| 222 | 3 | 8.8 | 29 | 15 | O71344 | O71344 human endog |
| 223 | 3 | 8.8 | 29 | 15 | O71338 | O71338 human endog |
| 224 | 3 | 8.8 | 29 | 15 | O71992 | O71992 human endog |
| 225 | 3 | 8.8 | 29 | 15 | O71337 | O71337 human endog |
| 226 | 3 | 8.8 | 29 | 15 | Q9IQJ9 | Q9iqj9 human immun |
| 227 | 3 | 8.8 | 29 | 15 | O71997 | O71997 human endog |
| 228 | 3 | 8.8 | 29 | 15 | O71335 | O71335 human endog |

| | | | | | | |
|----------------------|-----|---|-----|----|----|--------|
| Q8x419 escherichia | 229 | 3 | 8.8 | 29 | 16 | Q8X419 |
| Q8q0h5 methanosarc | 230 | 3 | 8.8 | 29 | 17 | Q8Q0H5 |
| Q9jp75 salmonella | 231 | 3 | 8.8 | 30 | 2 | Q9JP75 |
| Q9l8w9 streptomyc | 232 | 3 | 8.8 | 30 | 2 | Q9L8W9 |
| Q9l8x1 streptomyc | 233 | 3 | 8.8 | 30 | 2 | Q9L8X1 |
| Q9r4z6 clostridium | 234 | 3 | 8.8 | 30 | 2 | Q9R4Z6 |
| Q9r4j2 helicobacte | 235 | 3 | 8.8 | 30 | 2 | Q9REI5 |
| Q8vuw9 staphylococ | 236 | 3 | 8.8 | 30 | 2 | Q9R4J2 |
| Q9r4i5 mycoplasma | 237 | 3 | 8.8 | 30 | 2 | Q8VUW9 |
| Q9r4a9 clostridium | 238 | 3 | 8.8 | 30 | 2 | Q9R4I5 |
| Q9r5q3 leuconostoc | 239 | 3 | 8.8 | 30 | 2 | Q9R4A9 |
| Q45966 coxiella bu | 240 | 3 | 8.8 | 30 | 2 | Q9R5Q3 |
| Q9r5c4 comamonas | 241 | 3 | 8.8 | 30 | 2 | Q45966 |
| Q9s014 borrelia bu | 242 | 3 | 8.8 | 30 | 2 | Q9R5C4 |
| Q9r4i6 mycoplasma | 243 | 3 | 8.8 | 30 | 2 | Q9S014 |
| Q9r4a8 clostridium | 244 | 3 | 8.8 | 30 | 2 | Q9R4I6 |
| Q9rere enterobacte | 245 | 3 | 8.8 | 30 | 2 | Q9R4A8 |
| Q9p817 candida alb | 246 | 3 | 8.8 | 30 | 2 | Q9RER6 |
| Q9p817 candida alb | 247 | 3 | 8.8 | 30 | 3 | Q9P817 |
| Q9urb0 candida alb | 248 | 3 | 8.8 | 30 | 3 | Q9URB0 |
| Q8j172 trichoderma | 249 | 3 | 8.8 | 30 | 3 | Q8J172 |
| Q8j171 hypocrea li | 250 | 3 | 8.8 | 30 | 3 | Q8J171 |
| Q16330 homo sapien | 251 | 3 | 8.8 | 30 | 4 | Q16330 |
| Q9uca9 homo sapien | 252 | 3 | 8.8 | 30 | 4 | Q9UCA9 |
| Q95595 homo sapien | 253 | 3 | 8.8 | 30 | 4 | Q95595 |
| P78460 homo sapien | 254 | 3 | 8.8 | 30 | 4 | P78460 |
| Q8n563 homo sapien | 255 | 3 | 8.8 | 30 | 4 | Q8N563 |
| Q9hbg2 homo sapien | 256 | 3 | 8.8 | 30 | 4 | Q9HBG2 |
| Q9bzn2 homo sapien | 257 | 3 | 8.8 | 30 | 4 | Q9BZN2 |
| P78542 homo sapien | 258 | 3 | 8.8 | 30 | 4 | P78542 |
| Q9twh7 ancylostoma | 259 | 3 | 8.8 | 30 | 5 | Q9TWH7 |
| Q968n1 tritrichomo | 260 | 3 | 8.8 | 30 | 5 | Q968N1 |
| P82214 bombyx mori | 261 | 3 | 8.8 | 30 | 5 | P82214 |
| Q9bdk1 bos taurus | 262 | 3 | 8.8 | 30 | 6 | Q9BDK1 |
| Q9tTF9 ateles delz | 263 | 3 | 8.8 | 30 | 6 | Q9TTF9 |
| Q8w7l1 cucurbita m | 264 | 3 | 8.8 | 30 | 8 | Q8W7L1 |
| Q8w7k9 cucurbita p | 265 | 3 | 8.8 | 30 | 8 | Q8W7K9 |
| Q8w7h8 cucurbita a | 266 | 3 | 8.8 | 30 | 8 | Q8W7H8 |
| Q8wbc2 cucurbita o | 267 | 3 | 8.8 | 30 | 8 | Q8WBC2 |
| Q8w7k8 cucurbita p | 268 | 3 | 8.8 | 30 | 8 | Q8W7K8 |
| Q8w7h6 cucurbita m | 269 | 3 | 8.8 | 30 | 8 | Q8W7H6 |
| Q8wbc4 cucurbita p | 270 | 3 | 8.8 | 30 | 8 | Q8WBC4 |
| Q8w7l2 cucurbita a | 271 | 3 | 8.8 | 30 | 8 | Q8W7L2 |
| Q8wbc6 cucurbita a | 272 | 3 | 8.8 | 30 | 8 | Q8WBC6 |
| Q8wbb7 sechium edu | 273 | 3 | 8.8 | 30 | 8 | Q8WBB7 |
| Q99328 meloidogyne | 274 | 3 | 8.8 | 30 | 8 | Q99328 |
| Q8w7h7 cucurbita e | 275 | 3 | 8.8 | 30 | 8 | Q8W7H7 |
| Q8wbc0 cucurbita f | 276 | 3 | 8.8 | 30 | 8 | Q8WBC0 |
| Q8w7l0 cucurbita p | 277 | 3 | 8.8 | 30 | 8 | Q8W7L0 |
| Q9ti56 eucalyptus | 278 | 3 | 8.8 | 30 | 8 | Q9TI56 |
| Q8hkg1 rhizidicaphal | 279 | 3 | 8.8 | 30 | 8 | Q8HKG1 |
| Q8w674 enterobacte | 280 | 3 | 8.8 | 30 | 9 | Q8W674 |
| Q9s8t2 cicer ariet | 281 | 3 | 8.8 | 30 | 10 | Q9S8T2 |
| 023933 flavaria tr | 282 | 3 | 8.8 | 30 | 10 | 023933 |
| Q9fusi physcomitre | 283 | 3 | 8.8 | 30 | 10 | Q9FUS1 |
| Q8rudi zea mays (m | 284 | 3 | 8.8 | 30 | 10 | Q8RUD1 |
| Q93wy2 oryza sativ | 285 | 3 | 8.8 | 30 | 10 | Q93WY2 |

| | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
|--------|-------------|--------|-------------|--------|-------------|--------|-----------|--------|-------------|--------|-----------|--------|------------|--------|-------------|--------|-------------|--------|-------------|--------|-------------|--------|-------------|--------|-------------|-------|-------------|--------|-------------|--------|-------------|--------|-------------|--------|-------------|---------|-------------|--------|-------------|--------|-------------|--------|-------------|--------|------------|-------|-------------|--------|-------------|--------|-------------|--------|-------------|--------|-------------|--------|-------------|--------|-------------|--------|-------------|--------|-------------|--------|------------|--------|-------------|---------|-------------|--------|-------------|--------|-------------|--------|-------------|--------|-------------|--------|-------------|--------|-------------|--------|-------------|--------|-------------|--------|-------------|--------|-------------|--------|--------------|--------|-------------|--------|------------|--------|-------------|--------|-------------|--------|-------------|--------|-------------|--------|-------------|--------|-------------|--------|-------------|---------|-------------|--------|-------------|----|----|--------|--|----|----|--------|--|----|----|--------|--|----|---|--------|--|----|---|--------|--|----|---|--------|--|----|---|--------|--|----|---|--------|--|----|---|--------|--|----|---|--------|--|----|---|--------|--|----|---|--------|--|----|---|--------|--|----|---|--------|--|----|---|--------|--|----|---|--------|--|----|---|--------|--|----|---|--------|--|----|---|--------|--|----|---|--------|--|----|---|--------|--|----|---|--------|--|
| 063885 | mus sp. cys | 088549 | mesocricetu | 08vdl1 | mus musculu | 09qv18 | ratus sp. | 09qv14 | mus sp. col | 09qv19 | ratus sp. | 010753 | ratus norv | 08br32 | mus musculu | 091hb7 | tt virus. o | 091hc4 | tt virus. o | 091jv5 | norwalk vir | 086870 | cauliflower | 091hc3 | tt virus. o | 091k3 | hepatitis e | 091hc0 | tt virus. o | 042551 | brachydanio | 098ue7 | xenopus lae | 09prw0 | struthio ca | 09prt00 | oncorhynchu | 086599 | human endog | 0991p5 | human immun | 050822 | borrelia bu | 09x0w9 | thermotoga | 09p53 | campylobact | 09ku55 | vibrio chol | 09kt75 | vibrio chol | 09ksa7 | vibrio chol | 09jsq6 | neisseria m | 097sy9 | streptococc | 097sx5 | streptococc | 09k1w7 | chlamydia p | 08u566 | agrobacteri | 08kes5 | chlorobium | 08glr1 | brucella su | 08ftzx9 | brucella su | 08cu88 | staphylococ | 08zzf0 | pyrobaculum | 08zvl0 | pyrobaculum | 09s619 | prochloroco | 08kyk0 | bacillus an | 09jmv2 | escherichia | 09x3c3 | prochloroco | 068825 | pseudomonas | 09kh08 | thermus aqu | 047323 | escherichia | 09thf9 | actinetobact | 08ky19 | bacillus an | 08rts5 | uncultured | 08l3d3 | colwellia m | 093pel | yersinia ps | 094120 | saccharomyc | 096a45 | homo sapien | 09uea9 | homo sapien | 08wyf5 | homo sapien | 08n5x3 | homo sapien | 09bxxm4 | homo sapien | 09udes | homo sapien | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
| 286 | | 30 | 11 | 063885 | | 30 | 11 | 090v14 | | 30 | 11 | 090v19 | | 30 | 11 | 08BR32 | | 30 | 12 | 091HC4 | | 30 | 12 | 091HC3 | | 30 | 12 | 09WTK3 | | 30 | 12 | 091HC0 | | 30 | 13 | 042551 | | 30 | 13 | 098UE7 | | 30 | 13 | 09PRW0 | | 30 | 13 | 09PT00 | | 30 | 15 | 086599 | | 30 | 15 | 0991P5 | | 30 | 16 | 050822 | | 30 | 16 | 09XW09 | | 30 | 16 | 09PP53 | | 30 | 16 | 09KU55 | | 30 | 16 | 09KT75 | | 30 | 16 | 09KSA7 | | 30 | 16 | 09JSQ6 | | 30 | 16 | 097SY9 | | 30 | 16 | 097SX5 | | 30 | 16 | 09K1W7 | | 30 | 16 | 08U566 | | 30 | 16 | 08KE55 | | 30 | 16 | 08G1R1 | | 30 | 16 | 08FZX9 | | 30 | 16 | 08CU88 | | 30 | 17 | 08ZZF0 | | 30 | 17 | 08ZVL0 | | 31 | 2 | 09S619 | | 31 | 2 | 08KYK0 | | 31 | 2 | 09JMV2 | | 31 | 2 | 09X3C3 | | 31 | 2 | 068825 | | 31 | 2 | 09KH08 | | 31 | 2 | 047323 | | 31 | 2 | 09RHF9 | | 31 | 2 | 08KY19 | | 31 | 2 | 08RTS5 | | 31 | 2 | 08L3D3 | | 31 | 2 | 093PE1 | | 31 | 3 | 094120 | | 31 | 4 | 096A45 | | 31 | 4 | 09UEA9 | | 31 | 4 | 08WYF5 | | 31 | 4 | 08N5X3 | | 31 | 4 | 09BXM4 | | 31 | 4 | 09UDES | |
| 287 | | 30 | 11 | 088549 | | 30 | 11 | 08VDL1 | | 30 | 11 | 08VDL1 | | 30 | 11 | 08BR32 | | 30 | 12 | 091HC4 | | 30 | 12 | 091HC3 | | 30 | 12 | 09WTK3 | | 30 | 12 | 091HC0 | | 30 | 13 | 042551 | | 30 | 13 | 098UE7 | | 30 | 13 | 09PRW0 | | 30 | 13 | 09PT00 | | 30 | 15 | 086599 | | 30 | 15 | 0991P5 | | 30 | 16 | 050822 | | 30 | 16 | 09XW09 | | 30 | 16 | 09PP53 | | 30 | 16 | 09KU55 | | 30 | 16 | 09KT75 | | 30 | 16 | 09KSA7 | | 30 | 16 | 09JSQ6 | | 30 | 16 | 097SY9 | | 30 | 16 | 097SX5 | | 30 | 16 | 09K1W7 | | 30 | 16 | 08U566 | | 30 | 16 | 08KE55 | | 30 | 16 | 08G1R1 | | 30 | 16 | 08FZX9 | | 30 | 16 | 08CU88 | | 30 | 17 | 08ZZF0 | | 30 | 17 | 08ZVL0 | | 31 | 2 | 09S619 | | 31 | 2 | 08KYK0 | | 31 | 2 | 09JMV2 | | 31 | 2 | 09X3C3 | | 31 | 2 | 068825 | | 31 | 2 | 09KH08 | | 31 | 2 | 047323 | | 31 | 2 | 09RHF9 | | 31 | 2 | 08KY19 | | 31 | 2 | 08RTS5 | | 31 | 2 | 08L3D3 | | 31 | 2 | 093PE1 | | 31 | 3 | 094120 | | 31 | 4 | 096A45 | | 31 | 4 | 09UEA9 | | 31 | 4 | 08WYF5 | | 31 | 4 | 08N5X3 | | 31 | 4 | 09BXM4 | | 31 | 4 | 09UDES | |
| 288 | | 30 | 11 | 088549 | | 30 | 11 | 08VDL1 | | 30 | 11 | 08VDL1 | | 30 | 11 | 08BR32 | | 30 | 12 | 091HC4 | | 30 | 12 | 091HC3 | | 30 | 12 | 09WTK3 | | 30 | 12 | 091HC0 | | 30 | 13 | 042551 | | 30 | 13 | 098UE7 | | 30 | 13 | 09PRW0 | | 30 | 13 | 09PT00 | | 30 | 15 | 086599 | | 30 | 15 | 0991P5 | | 30 | 16 | 050822 | | 30 | 16 | 09XW09 | | 30 | 16 | 09PP53 | | 30 | 16 | 09KU55 | | 30 | 16 | 09KT75 | | 30 | 16 | 09KSA7 | | 30 | 16 | 09JSQ6 | | 30 | 16 | 097SY9 | | 30 | 16 | 097SX5 | | 30 | 16 | 09K1W7 | | 30 | 16 | 08U566 | | 30 | 16 | 08KE55 | | 30 | 16 | 08G1R1 | | 30 | 16 | 08FZX9 | | 30 | 16 | 08CU88 | | 30 | 17 | 08ZZF0 | | 30 | 17 | 08ZVL0 | | 31 | 2 | 09S619 | | 31 | 2 | 08KYK0 | | 31 | 2 | 09JMV2 | | 31 | 2 | 09X3C3 | | 31 | 2 | 068825 | | 31 | 2 | 09KH08 | | 31 | 2 | 047323 | | 31 | 2 | 09RHF9 | | 31 | 2 | 08KY19 | | 31 | 2 | 08RTS5 | | 31 | 2 | 08L3D3 | | 31 | 2 | 093PE1 | | 31 | 3 | 094120 | | 31 | 4 | 096A45 | | 31 | 4 | 09UEA9 | | 31 | 4 | 08WYF5 | | 31 | 4 | 08N5X3 | | 31 | 4 | 09BXM4 | | 31 | 4 | 09UDES | |
| 289 | | 30 | 11 | 088549 | | 30 | 11 | 08VDL1 | | 30 | 11 | 08VDL1 | | 30 | 11 | 08BR32 | | 30 | 12 | 091HC4 | | 30 | 12 | 091HC3 | | 30 | 12 | 09WTK3 | | 30 | 12 | 091HC0 | | 30 | 13 | 042551 | | 30 | 13 | 098UE7 | | 30 | 13 | 09PRW0 | | 30 | 13 | 09PT00 | | 30 | 15 | 086599 | | 30 | 15 | 0991P5 | | 30 | 16 | 050822 | | 30 | 16 | 09XW09 | | 30 | 16 | 09PP53 | | 30 | 16 | 09KU55 | | 30 | 16 | 09KT75 | | 30 | 16 | 09KSA7 | | 30 | 16 | 09JSQ6 | | 30 | 16 | 097SY9 | | 30 | 16 | 097SX5 | | 30 | 16 | 09K1W7 | | 30 | 16 | 08U566 | | 30 | 16 | 08KE55 | | 30 | 16 | 08G1R1 | | 30 | 16 | 08FZX9 | | 30 | 16 | 08CU88 | | 30 | 17 | 08ZZF0 | | 30 | 17 | 08ZVL0 | | 31 | 2 | 09S619 | | 31 | 2 | 08KYK0 | | 31 | 2 | 09JMV2 | | 31 | 2 | 09X3C3 | | 31 | 2 | 068825 | | 31 | 2 | 09KH08 | | 31 | 2 | 047323 | | 31 | 2 | 09RHF9 | | 31 | 2 | 08KY19 | | 31 | 2 | 08RTS5 | | 31 | 2 | 08L3D3 | | 31 | 2 | 093PE1 | | 31 | 3 | 094120 | | 31 | 4 | 096A45 | | 31 | 4 | 09UEA9 | | 31 | 4 | 08WYF5 | | 31 | 4 | 08N5X3 | | 31 | 4 | 09BXM4 | | 31 | 4 | 09UDES | |
| 290 | | 30 | 11 | 088549 | | 30 | 11 | 08VDL1 | | 30 | 11 | 08VDL1 | | 30 | 11 | 08BR32 | | 30 | 12 | 091HC4 | | 30 | 12 | 091HC3 | | 30 | 12 | 09WTK3 | | 30 | 12 | 091HC0 | | 30 | 13 | 042551 | | 30 | 13 | 098UE7 | | 30 | 13 | 09PRW0 | | 30 | 13 | 09PT00 | | 30 | 15 | 086599 | | 30 | 15 | 0991P5 | | 30 | 16 | 050822 | | 30 | 16 | 09XW09 | | 30 | 16 | 09PP53 | | 30 | 16 | 09KU55 | | 30 | 16 | 09KT75 | | 30 | 16 | 09KSA7 | | 30 | 16 | 09JSQ6 | | 30 | 16 | 097SY9 | | 30 | 16 | 097SX5 | | 30 | 16 | 09K1W7 | | 30 | 16 | 08U566 | | 30 | 16 | 08KE55 | | 30 | 16 | 08G1R1 | | 30 | 16 | 08FZX9 | | 30 | 16 | 08CU88 | | 30 | 17 | 08ZZF0 | | 30 | 17 | 08ZVL0 | | 31 | 2 | 09S619 | | 31 | 2 | 08KYK0 | | 31 | 2 | 09JMV2 | | 31 | 2 | 09X3C3 | | 31 | 2 | 068825 | | 31 | 2 | 09KH08 | | 31 | 2 | 047323 | | 31 | 2 | 09RHF9 | | 31 | 2 | 08KY19 | | 31 | 2 | 08RTS5 | | 31 | 2 | 08L3D3 | | 31 | 2 | 093PE1 | | 31 | 3 | 094120 | | 31 | 4 | 096A45 | | 31 | 4 | 09UEA9 | | 31 | 4 | 08WYF5 | | 31 | 4 | 08N5X3 | | 31 | 4 | 09BXM4 | | 31 | 4 | 09UDES | |
| 291 | | 30 | 11 | 088549 | | 30 | 11 | 08VDL1 | | 30 | 11 | 08VDL1 | | 30 | 11 | 08BR32 | | 30 | 12 | 091HC4 | | 30 | 12 | 091HC3 | | 30 | 12 | 09WTK3 | | 30 | 12 | 091HC0 | | 30 | 13 | 042551 | | 30 | 13 | 098UE7 | | 30 | 13 | 09PRW0 | | 30 | 13 | 09PT00 | | 30 | 15 | 086599 | | 30 | 15 | 0991P5 | | 30 | 16 | 050822 | | 30 | 16 | 09XW09 | | 30 | 16 | 09PP53 | | 30 | 16 | 09KU55 | | 30 | 16 | 09KT75 | | 30 | 16 | 09KSA7 | | 30 | 16 | 09JSQ6 | | 30 | 16 | 097SY9 | | 30 | 16 | 097SX5 | | 30 | 16 | 09K1W7 | | 30 | 16 | 08U566 | | 30 | 16 | 08KE55 | | 30 | 16 | 08G1R1 | | 30 | 16 | 08FZX9 | | 30 | 16 | 08CU88 | | 30 | 17 | 08ZZF0 | | 30 | 17 | 08ZVL0 | | 31 | 2 | 09S619 | | 31 | 2 | 08KYK0 | | 31 | 2 | 09JMV2 | | 31 | 2 | 09X3C3 | | 31 | 2 | 068825 | | 31 | 2 | 09KH08 | | 31 | 2 | 047323 | | 31 | 2 | 09RHF9 | | 31 | 2 | 08KY19 | | 31 | 2 | 08RTS5 | | 31 | 2 | 08L3D3 | | 31 | 2 | 093PE1 | | 31 | 3 | 094120 | | 31 | 4 | 096A45 | | 31 | 4 | 09UEA9 | | 31 | 4 | 08WYF5 | | 31 | 4 | 08N5X3 | | 31 | 4 | 09BXM4 | | 31 | 4 | 09UDES | |
| 292 | | 30 | 11 | 088549 | | 30 | 11 | 08VDL1 | | 30 | 11 | 08VDL1 | | 30 | 11 | 08BR32 | | 30 | 12 | 091HC4 | | 30 | 12 | 091HC3 | | 30 | 12 | 09WTK3 | | 30 | 12 | 091HC0 | | 30 | 13 | 042551 | | 30 | 13 | 098UE7 | | 30 | 13 | 09PRW0 | | 30 | 13 | 09PT00 | | 30 | 15 | 086599 | | 30 | 15 | 0991P5 | | 30 | 16 | 050822 | | 30 | 16 | 09XW09 | | 30 | 16 | 09PP53 | | 30 | 16 | 09KU55 | | 30 | 16 | 09KT75 | | 30 | 16 | 09KSA7 | | 30 | 16 | 09JSQ6 | | 30 | 16 | 097SY9 | | 30 | 16 | 097SX5 | | 30 | 16 | 09K1W7 | | 30 | 16 | 08U566 | | 30 | 16 | 08KE55 | | 30 | 16 | 08G1R1 | | 30 | 16 | 08FZX9 | | 30 | 16 | 08CU88 | | 30 | 17 | 08ZZF0 | | 30 | 17 | 08ZVL0 | | 31 | 2 | 09S619 | | 31 | 2 | 08KYK0 | | 31 | 2 | 09JMV2 | | 31 | 2 | 09X3C3 | | 31 | 2 | 068825 | | 31 | 2 | 09KH08 | | 31 | 2 | 047323 | | 31 | 2 | 09RHF9 | | 31 | 2 | 08KY19 | | 31 | 2 | 08RTS5 | | 31 | 2 | 08L3D3 | | 31 | 2 | 093PE1 | | 31 | 3 | 094120 | | 31 | 4 | 096A45 | | 31 | 4 | 09UEA9 | | 31 | 4 | 08WYF5 | | 31 | 4 | 08N5X3 | | 31 | 4 | 09BXM4 | | 31 | 4 | 09UDES | |
| 293 | | 30 | 11 | 088549 | | 30 | 11 | 08VDL1 | | 30 | 11 | 08VDL1 | | 30 | 11 | 08BR32 | | 30 | 12 | 091HC4 | | 30 | 12 | 091HC3 | | 30 | 12 | 09WTK3 | | 30 | 12 | 091HC0 | | 30 | 13 | 042551 | | 30 | 13 | 098UE7 | | 30 | 13 | 09PRW0 | | 30 | 13 | 09PT00 | | 30 | 15 | 086599 | | 30 | 15 | 0991P5 | | 30 | 16 | 050822 | | 30 | 16 | 09XW09 | | 30 | 16 | 09PP53 | | 30 | 16 | 09KU55 | | 30 | 16 | 09KT75 | | 30 | 16 | 09KSA7 | | 30 | 16 | 09JSQ6 | | 30 | 16 | 097SY9 | | 30 | 16 | 097SX5 | | 30 | 16 | 09K1W7 | | 30 | 16 | 08U566 | | 30 | 16 | 08KE55 | | 30 | 16 | 08G1R1 | | 30 | 16 | 08FZX9 | | 30 | 16 | 08CU88 | | 30 | 17 | 08ZZF0 | | 30 | 17 | 08ZVL0 | | 31 | 2 | 09S619 | | 31 | 2 | 08KYK0 | | 31 | 2 | 09JMV2 | | 31 | 2 | 09X3C3 | | 31 | 2 | 068825 | | 31 | 2 | 09KH08 | | 31 | 2 | 047323 | | 31 | 2 | 09RHF9 | | 31 | 2 | 08KY19 | | 31 | 2 | 08RTS5 | | 31 | 2 | 08L3D3 | | 31 | 2 | 093PE1 | | 31 | 3 | 094120 | | 31 | 4 | 096A45 | | 31 | 4 | 09UEA9 | | 31 | 4 | 08WYF5 | | 31 | 4 | 08N5X3 | | | | | | | | | |

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|--------|-------------|----|----|-----|---|-----|
| Q81qV3 | drosophila | 31 | 5 | 8.8 | 3 | 343 |
| Q81EY3 | trypanosoma | 31 | 5 | 8.8 | 3 | 344 |
| Q9GLD6 | sus scrofa | 31 | 6 | 8.8 | 3 | 345 |
| Q8MIH5 | canis faml | 31 | 6 | 8.8 | 3 | 346 |
| Q776Z5 | bos taurus | 31 | 6 | 8.8 | 3 | 347 |
| Q951C0 | sus scrofa | 31 | 6 | 8.8 | 3 | 348 |
| Q9N1C8 | ovis aries | 31 | 6 | 8.8 | 3 | 349 |
| Q9XSB9 | ateles belz | 31 | 6 | 8.8 | 3 | 350 |
| Q97800 | bos taurus | 31 | 6 | 8.8 | 3 | 351 |
| Q29868 | homo sapien | 31 | 7 | 8.8 | 3 | 352 |
| Q9NMN2 | buto americ | 31 | 8 | 8.8 | 3 | 353 |
| Q80011 | enallagma a | 31 | 8 | 8.8 | 3 | 354 |
| Q34922 | limulus pol | 31 | 8 | 8.8 | 3 | 355 |
| Q8WEJ4 | gnetum gnet | 31 | 8 | 8.8 | 3 | 356 |
| Q8M9Y3 | chaetosphae | 31 | 8 | 8.8 | 3 | 357 |
| Q9NM12 | torrentophr | 31 | 8 | 8.8 | 3 | 358 |
| Q9MS78 | phacus acum | 31 | 8 | 8.8 | 3 | 359 |
| Q9NM13 | torrentophr | 31 | 8 | 8.8 | 3 | 360 |
| Q38499 | bacterioph | 31 | 9 | 8.8 | 3 | 361 |
| Q9XIT0 | glycine max | 31 | 10 | 8.8 | 3 | 362 |
| Q9QXB6 | mus musculu | 31 | 11 | 8.8 | 3 | 363 |
| Q99KK6 | mus musculu | 31 | 11 | 8.8 | 3 | 364 |
| Q922Z6 | mus musculu | 31 | 11 | 8.8 | 3 | 365 |
| Q8CGM7 | mus musculu | 31 | 11 | 8.8 | 3 | 366 |
| Q919E5 | human papil | 31 | 12 | 8.8 | 3 | 367 |
| Q919E4 | human papil | 31 | 12 | 8.8 | 3 | 368 |
| Q56713 | hepatitis c | 31 | 12 | 8.8 | 3 | 369 |
| Q919F7 | human papil | 31 | 12 | 8.8 | 3 | 370 |
| Q919E6 | human papil | 31 | 12 | 8.8 | 3 | 371 |
| Q56692 | hepatitis c | 31 | 12 | 8.8 | 3 | 372 |
| Q919F3 | human papil | 31 | 12 | 8.8 | 3 | 373 |
| Q56707 | hepatitis c | 31 | 12 | 8.8 | 3 | 374 |
| Q56687 | hepatitis c | 31 | 12 | 8.8 | 3 | 375 |
| Q919F8 | human papil | 31 | 12 | 8.8 | 3 | 376 |
| Q56691 | hepatitis c | 31 | 12 | 8.8 | 3 | 377 |
| Q919E1 | human papil | 31 | 12 | 8.8 | 3 | 378 |
| Q56701 | hepatitis c | 31 | 12 | 8.8 | 3 | 379 |
| Q56694 | hepatitis c | 31 | 12 | 8.8 | 3 | 380 |
| Q919D9 | human papil | 31 | 12 | 8.8 | 3 | 381 |
| Q919F6 | human papil | 31 | 12 | 8.8 | 3 | 382 |
| Q919E3 | human papil | 31 | 12 | 8.8 | 3 | 383 |
| Q56712 | hepatitis c | 31 | 12 | 8.8 | 3 | 384 |
| Q919E8 | human papil | 31 | 12 | 8.8 | 3 | 385 |
| Q56710 | hepatitis c | 31 | 12 | 8.8 | 3 | 386 |
| Q56688 | hepatitis c | 31 | 12 | 8.8 | 3 | 387 |
| Q56696 | hepatitis c | 31 | 12 | 8.8 | 3 | 388 |
| Q56695 | hepatitis c | 31 | 12 | 8.8 | 3 | 389 |
| Q56698 | hepatitis c | 31 | 12 | 8.8 | 3 | 390 |
| Q56702 | hepatitis c | 31 | 12 | 8.8 | 3 | 391 |
| Q56703 | hepatitis c | 31 | 12 | 8.8 | 3 | 392 |
| Q56697 | hepatitis c | 31 | 12 | 8.8 | 3 | 393 |
| Q919F0 | human papil | 31 | 12 | 8.8 | 3 | 394 |
| Q56709 | hepatitis c | 31 | 12 | 8.8 | 3 | 395 |
| Q919F4 | human papil | 31 | 12 | 8.8 | 3 | 396 |
| Q56689 | hepatitis c | 31 | 12 | 8.8 | 3 | 397 |
| Q919F2 | human papil | 31 | 12 | 8.8 | 3 | 398 |
| Q919F1 | human papil | 31 | 12 | 8.8 | 3 | 399 |

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|--------|-------------|-----|----|----|--------|
| 400 | 3 | 8.8 | 31 | 12 | 056711 |
| 401 | 3 | 8.8 | 31 | 12 | Q919E2 |
| 402 | 3 | 8.8 | 31 | 12 | Q919D8 |
| 403 | 3 | 8.8 | 31 | 12 | 056686 |
| 404 | 3 | 8.8 | 31 | 12 | Q9WMX5 |
| 405 | 3 | 8.8 | 31 | 12 | 056690 |
| 406 | 3 | 8.8 | 31 | 12 | Q919E9 |
| 407 | 3 | 8.8 | 31 | 12 | 056706 |
| 408 | 3 | 8.8 | 31 | 12 | 056700 |
| 409 | 3 | 8.8 | 31 | 12 | 056704 |
| 410 | 3 | 8.8 | 31 | 12 | Q919D7 |
| 411 | 3 | 8.8 | 31 | 12 | Q919F5 |
| 412 | 3 | 8.8 | 31 | 12 | 056693 |
| 413 | 3 | 8.8 | 31 | 12 | 056685 |
| 414 | 3 | 8.8 | 31 | 12 | 056708 |
| 415 | 3 | 8.8 | 31 | 12 | Q919E0 |
| 416 | 3 | 8.8 | 31 | 12 | 056705 |
| 417 | 3 | 8.8 | 31 | 12 | Q919E7 |
| 418 | 3 | 8.8 | 31 | 12 | Q914M9 |
| 419 | 3 | 8.8 | 31 | 12 | 056699 |
| 420 | 3 | 8.8 | 31 | 13 | 042540 |
| 421 | 3 | 8.8 | 31 | 13 | Q91763 |
| 422 | 3 | 8.8 | 31 | 13 | Q9P5U1 |
| 423 | 3 | 8.8 | 31 | 13 | Q91816 |
| 424 | 3 | 8.8 | 31 | 16 | 050709 |
| 425 | 3 | 8.8 | 31 | 16 | 050818 |
| 426 | 3 | 8.8 | 31 | 16 | 050858 |
| 427 | 3 | 8.8 | 31 | 16 | 051007 |
| 428 | 3 | 8.8 | 31 | 16 | Q9PGF2 |
| 429 | 3 | 8.8 | 31 | 16 | Q9PAW4 |
| 430 | 3 | 8.8 | 31 | 16 | Q9KVF3 |
| 431 | 3 | 8.8 | 31 | 16 | Q9KR17 |
| 432 | 3 | 8.8 | 31 | 16 | Q9K7A8 |
| 433 | 3 | 8.8 | 31 | 16 | Q97SZ9 |
| 434 | 3 | 8.8 | 31 | 16 | Q97SW8 |
| 435 | 3 | 8.8 | 31 | 16 | Q97QB7 |
| 436 | 3 | 8.8 | 31 | 16 | Q97CV6 |
| 437 | 3 | 8.8 | 31 | 16 | Q9K2A0 |
| 438 | 3 | 8.8 | 31 | 16 | Q9K236 |
| 439 | 3 | 8.8 | 31 | 16 | Q8U5M9 |
| 440 | 3 | 8.8 | 31 | 16 | Q8P9W1 |
| 441 | 3 | 8.8 | 31 | 16 | Q8KEV8 |
| 442 | 3 | 8.8 | 31 | 16 | Q8KCQ0 |
| 443 | 3 | 8.8 | 31 | 16 | Q8KCD4 |
| 444 | 3 | 8.8 | 31 | 16 | Q8KBJ8 |
| 445 | 3 | 8.8 | 31 | 16 | Q8EI77 |
| 446 | 3 | 8.8 | 31 | 16 | Q8EG38 |
| 447 | 3 | 8.8 | 31 | 16 | Q8E9Y5 |
| 448 | 3 | 8.8 | 31 | 16 | Q8E8G1 |
| 449 | 3 | 8.8 | 31 | 16 | Q8CTW3 |
| 450 | 3 | 8.8 | 31 | 16 | Q8CTA2 |
| 451 | 3 | 8.8 | 32 | 2 | Q9AJ41 |
| 452 | 3 | 8.8 | 32 | 2 | Q00491 |
| 453 | 3 | 8.8 | 32 | 2 | Q49249 |
| 454 | 3 | 8.8 | 32 | 2 | Q44499 |
| 455 | 3 | 8.8 | 32 | 2 | Q9S629 |
| 456 | 3 | 8.8 | 32 | 2 | Q8KYN3 |
| 056711 | hepatitis c | | | | |
| Q919e2 | human papil | | | | |
| Q919d8 | human papil | | | | |
| 056686 | hepatitis c | | | | |
| Q9wmx5 | human echov | | | | |
| 056690 | hepatitis c | | | | |
| Q919e9 | human papil | | | | |
| 056706 | hepatitis c | | | | |
| 056700 | hepatitis c | | | | |
| 056704 | hepatitis c | | | | |
| Q919d7 | human papil | | | | |
| Q919f5 | human papil | | | | |
| 056693 | hepatitis c | | | | |
| 056685 | hepatitis c | | | | |
| 056708 | hepatitis c | | | | |
| Q919e0 | human papil | | | | |
| 056705 | hepatitis c | | | | |
| Q919e7 | human papil | | | | |
| Q914m9 | sulfolobus | | | | |
| 056699 | hepatitis c | | | | |
| 042540 | brachydanio | | | | |
| Q91763 | xenopus lae | | | | |
| Q9p5u1 | xenopus lae | | | | |
| Q91816 | xenopus lae | | | | |
| 050709 | borrelia bu | | | | |
| 050818 | borrelia bu | | | | |
| 050858 | borrelia bu | | | | |
| 051007 | borrelia bu | | | | |
| Q9pgf2 | xylella fas | | | | |
| Q9paw4 | xylella fas | | | | |
| Q9kvt3 | vibrio chol | | | | |
| Q9kr17 | vibrio chol | | | | |
| Q9k7a8 | bacillus ha | | | | |
| Q97sz9 | streptococc | | | | |
| Q97sw8 | streptococc | | | | |
| Q97qb7 | streptococc | | | | |
| Q97cv6 | streptococc | | | | |
| Q9k2a0 | chlamydia p | | | | |
| Q9k236 | chlamydia p | | | | |
| Q8u5m9 | agrobacteri | | | | |
| Q8p9w1 | xanthomonas | | | | |
| Q8kev8 | chlorobium | | | | |
| Q8kcq0 | chlorobium | | | | |
| Q8kcd4 | chlorobium | | | | |
| Q8kbj8 | chlorobium | | | | |
| Q8ei77 | shewanella | | | | |
| Q8eg38 | shewanella | | | | |
| Q8e9y5 | shewanella | | | | |
| Q8e8g1 | shewanella | | | | |
| Q8ctw3 | staphylococ | | | | |
| Q8cta2 | staphylococ | | | | |
| Q9aj41 | buchnera ap | | | | |
| Q00491 | streptomyc | | | | |
| Q49249 | mycoplasma | | | | |
| Q44499 | anabaena va | | | | |
| Q9s629 | prochloroco | | | | |
| Q8kyn3 | bacillus an | | | | |

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|---------|-------------|---------|----|----|-----|---|-----|
| 044509 | azotobacter | 044509 | 32 | 2 | 8.8 | 3 | 457 |
| 045534 | bacillus su | 045534 | 32 | 2 | 8.8 | 3 | 458 |
| 08vn21 | kluyvera ci | 08VN21 | 32 | 2 | 8.8 | 3 | 459 |
| 09r5q7 | aeromonas h | 09R5Q7 | 32 | 2 | 8.8 | 3 | 460 |
| 08kym4 | bacillus an | 08KYM4 | 32 | 2 | 8.8 | 3 | 461 |
| 032493 | bacteroides | 032493 | 32 | 2 | 8.8 | 3 | 462 |
| 08vnt6 | enterobacte | 08VNT6 | 32 | 2 | 8.8 | 3 | 463 |
| 091373 | rhizobium l | 091373 | 32 | 2 | 8.8 | 3 | 464 |
| 08gf58 | zymomonas m | 08Gf58 | 32 | 2 | 8.8 | 3 | 465 |
| 001058 | kluyveromyc | 001058 | 32 | 3 | 8.8 | 3 | 466 |
| 08tgr3 | saccharomyc | 08TGT3 | 32 | 3 | 8.8 | 3 | 467 |
| 012900 | homo sapien | 012900 | 32 | 4 | 8.8 | 3 | 468 |
| 09ueb0 | homo sapien | 09UEB0 | 32 | 4 | 8.8 | 3 | 469 |
| 08tc25 | homo sapien | 08TC25 | 32 | 4 | 8.8 | 3 | 470 |
| 096gm7 | homo sapien | 096GM7 | 32 | 4 | 8.8 | 3 | 471 |
| 08tbq3 | homo sapien | 08TBQ3 | 32 | 4 | 8.8 | 3 | 472 |
| 096i20 | homo sapien | 096I20 | 32 | 4 | 8.8 | 3 | 473 |
| 09un69 | homo sapien | 09UN69 | 32 | 4 | 8.8 | 3 | 474 |
| 09uqv1 | homo sapien | 09UQV1 | 32 | 4 | 8.8 | 3 | 475 |
| 09gpd9 | drosophi1a | 09GPD9 | 32 | 5 | 8.8 | 3 | 476 |
| 08t382 | leishmania | 08T382 | 32 | 5 | 8.8 | 3 | 477 |
| 096634 | trypanosoma | 096634 | 32 | 5 | 8.8 | 3 | 478 |
| 09twr8 | procambarus | 09TWR8 | 32 | 5 | 8.8 | 3 | 479 |
| 018606 | branchiosto | 018606 | 32 | 5 | 8.8 | 3 | 480 |
| 08t757 | branchiosto | 08T757 | 32 | 5 | 8.8 | 3 | 481 |
| 09tr67 | sus scrofa | 09TR67 | 32 | 6 | 8.8 | 3 | 482 |
| 09tr69 | sus scrofa | 09TR69 | 32 | 6 | 8.8 | 3 | 483 |
| 09tse6 | oryctolagus | 09TSE6 | 32 | 6 | 8.8 | 3 | 484 |
| 08mj91 | macaca muli | 08MJ91 | 32 | 6 | 8.8 | 3 | 485 |
| 08snf1 | gallinago m | 08SNF1 | 32 | 7 | 8.8 | 3 | 486 |
| 019722 | homo sapien | 019722 | 32 | 7 | 8.8 | 3 | 487 |
| 036494 | farfantepen | 036494 | 32 | 8 | 8.8 | 3 | 488 |
| 08sl89 | euglena ste | 08SL89 | 32 | 8 | 8.8 | 3 | 489 |
| 09gft95 | cercidiphy1 | 09GFT95 | 32 | 8 | 8.8 | 3 | 490 |
| 031736 | beta vulgar | 031736 | 32 | 8 | 8.8 | 3 | 491 |
| 08sl87 | euglena vir | 08SL87 | 32 | 8 | 8.8 | 3 | 492 |
| 031735 | beta vulgar | 031735 | 32 | 8 | 8.8 | 3 | 493 |
| 09mm00 | buto andrew | 09MM00 | 32 | 8 | 8.8 | 3 | 494 |
| 09mnl0 | buto danate | 09MNL0 | 32 | 8 | 8.8 | 3 | 495 |
| 0951q4 | renilla ren | 0951Q4 | 32 | 8 | 8.8 | 3 | 496 |
| 09gft72 | saururus ce | 09GFT72 | 32 | 8 | 8.8 | 3 | 497 |
| 09mbu5 | chlamydia p | 09MBU5 | 32 | 9 | 8.8 | 3 | 498 |
| 08s527 | ipomoea bat | 08S527 | 32 | 10 | 8.8 | 3 | 499 |
| 08rxq5 | arabidopsis | 08RXQ5 | 32 | 10 | 8.8 | 3 | 500 |
| 040727 | oryza sativ | 040727 | 32 | 10 | 8.8 | 3 | 501 |
| 09j1ui | ratus norv | 09J1UI | 32 | 11 | 8.8 | 3 | 502 |
| 09r0e3 | mus musculu | 09R0E3 | 32 | 11 | 8.8 | 3 | 503 |
| 09qwm2 | mus musculu | 09QWM2 | 32 | 11 | 8.8 | 3 | 504 |
| 09qwb2 | ratus sp. | 09QWB2 | 32 | 11 | 8.8 | 3 | 505 |
| 09qxx1 | mus musculu | 09QXX1 | 32 | 11 | 8.8 | 3 | 506 |
| 08c2n8 | mus musculu | 08C2N8 | 32 | 11 | 8.8 | 3 | 507 |
| 09pxv2 | hepatitis b | 09PXV2 | 32 | 12 | 8.8 | 3 | 508 |
| 09wni5 | tt virus. o | 09WNI5 | 32 | 12 | 8.8 | 3 | 509 |
| 0914f9 | sulfolobus | 0914F9 | 32 | 12 | 8.8 | 3 | 510 |
| 08qyt4 | grapevine v | 08QYT4 | 32 | 12 | 8.8 | 3 | 511 |
| 08qyt7 | grapevine v | 08QYT7 | 32 | 12 | 8.8 | 3 | 512 |
| 066854 | foot-and-mo | 066854 | 32 | 12 | 8.8 | 3 | 513 |

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|--------|-------------|---------|-------------|--------|------------|--------|-------------|--------|------------|--------|-------------|--------|------------|--------|------------|--------|------------|--------|------------|--------|-------------|--------|-------------|--------|-------------|--------|-------------|--------|-------------|--------|-------------|--------|-------------|--------|-------------|---------|-------------|--------|-------------|--------|-------------|--------|-------------|--------|-------------|--------|-------------|--------|------------|--------|------------|--------|------------|--------|------------|--------|------------|--------|------------|--------|------------|--------|-------------|--------|-------------|--------|-------------|--------|-------------|--------|-------------|--------|-------------|--------|-------------|--------|-------------|--------|-------------|--------|-------------|--------|-------------|--------|------------|--------|-------------|--------|-------------|--------|-------------|--------|-------------|--------|-------------|--------|-------------|--------|-------------|--------|-------------|--------|-------------|--------|-------------|--------|-------------|--------|-------------|--------|-------------|--------|-------------|
| Q8qyu0 | grapevine v | Q8qy934 | shope fibro | Q8qg73 | oncorhynch | Q8qg72 | salmo salar | Q8qg71 | oncorhynch | Q9ps21 | carassius a | Q8qg84 | oncorhynch | Q8qg83 | oncorhynch | Q8qg82 | oncorhynch | Q8qg70 | salvelinus | 050706 | borrelia bu | 050851 | borrelia bu | 050865 | borrelia bu | 051003 | borrelia bu | Q9pgt0 | xylella fas | Q9kvt7 | vibrio chol | Q9kvt2 | vibrio chol | Q9kpn9 | vibrio chol | Q9kltf0 | vibrio chol | Q9k7b0 | bacillus ha | Q9a2h0 | caulobacter | Q98ab6 | rhizobium l | Q8x3v6 | escherichia | Q8p382 | xanthomonas | Q8kg49 | chlorobium | Q8kcz9 | chlorobium | Q8kcv3 | chlorobium | Q9k4g0 | streptomyc | Q8ej44 | shewanella | Q8ee22 | shewanella | Q8ead5 | shewanella | Q8cu60 | staphylococ | Q8ctr7 | staphylococ | Q8cre7 | staphylococ | Q8zzf7 | pyrobaculum | Q8kh96 | pseudomonas | Q9s624 | prochloporo | Q9r2m3 | prochloporo | Q9x3m5 | prochloporo | Q9s651 | streptococc | Q9k533 | listeria mo | Q9k370 | rhizobium l | Q9f2c4 | salmonella | Q8kg80 | vibrio chol | Q56414 | escherichia | Q9s622 | prochloporo | Q9k2v1 | rhizobium l | Q9f1f4 | enterococcu | P82583 | streptococc | Q8gl15 | borrelia bu | Q8tgr1 | saccharomyc | Q99950 | homo sapien | Q9uc33 | homo sapien | Q9up36 | homo sapien | Q15285 | homo sapien | Q9udi1 | homo sapien | Q8n4j9 | homo sapien |
| 514 | | 515 | | 516 | | 517 | | 518 | | 519 | | 520 | | 521 | | 522 | | 523 | | 524 | | 525 | | 526 | | 527 | | 528 | | 529 | | 530 | | 531 | | 532 | | 533 | | 534 | | 535 | | 536 | | 537 | | 538 | | 539 | | 540 | | 541 | | 542 | | 543 | | 544 | | 545 | | 546 | | 547 | | 548 | | 549 | | 550 | | 551 | | 552 | | 553 | | 554 | | 555 | | 556 | | 557 | | 558 | | 559 | | 560 | | 561 | | 562 | | 563 | | 564 | | 565 | | 566 | | 567 | | 568 | | 569 | | 570 | |

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|-----|--------|-------------|---|-----|----|----|--------|
| 571 | Q92668 | homo sapien | 3 | 8.8 | 33 | 4 | Q92668 |
| 572 | Q96TB2 | ten | 3 | 8.8 | 33 | 5 | Q96TB2 |
| 573 | Q96T93 | cryptospori | 3 | 8.8 | 33 | 5 | Q96T93 |
| 574 | Q26673 | ten | 3 | 8.8 | 33 | 5 | Q26673 |
| 575 | Q26672 | ten | 3 | 8.8 | 33 | 5 | Q26672 |
| 576 | Q9GTC2 | plasmodium | 3 | 8.8 | 33 | 5 | Q9GTC2 |
| 577 | Q9GTC2 | plasmodium | 3 | 8.8 | 33 | 5 | Q9GTC2 |
| 578 | Q9GTC3 | ten | 3 | 8.8 | 33 | 5 | Q9GTC3 |
| 579 | Q9GTA1 | ten | 3 | 8.8 | 33 | 5 | Q9GTA1 |
| 580 | Q17293 | ten | 3 | 8.8 | 33 | 5 | Q17293 |
| 581 | Q27310 | ten | 3 | 8.8 | 33 | 5 | Q27310 |
| 582 | Q9GTA9 | ten | 3 | 8.8 | 33 | 5 | Q9GTA9 |
| 583 | Q9GTA9 | ten | 3 | 8.8 | 33 | 5 | Q9GTA9 |
| 584 | Q9GTA2 | ten | 3 | 8.8 | 33 | 5 | Q9GTA2 |
| 585 | Q9VHD7 | ten | 3 | 8.8 | 33 | 5 | Q9VHD7 |
| 586 | Q18916 | ten | 3 | 8.8 | 33 | 6 | Q18916 |
| 587 | Q9TSX7 | ten | 3 | 8.8 | 33 | 6 | Q9TSX7 |
| 588 | Q95M05 | ten | 3 | 8.8 | 33 | 6 | Q95M05 |
| 589 | Q8MGU2 | ten | 3 | 8.8 | 33 | 7 | Q8MGU2 |
| 590 | Q8SNF0 | ten | 3 | 8.8 | 33 | 7 | Q8SNF0 |
| 591 | Q9BAC6 | ten | 3 | 8.8 | 33 | 8 | Q9BAC6 |
| 592 | Q8W9G0 | ten | 3 | 8.8 | 33 | 8 | Q8W9G0 |
| 593 | Q9BAC1 | ten | 3 | 8.8 | 33 | 8 | Q9BAC1 |
| 594 | Q9XNP3 | ten | 3 | 8.8 | 33 | 8 | Q9XNP3 |
| 595 | Q78857 | ten | 3 | 8.8 | 33 | 8 | Q78857 |
| 596 | Q9T2N1 | ten | 3 | 8.8 | 33 | 8 | Q9T2N1 |
| 597 | Q9BAC4 | ten | 3 | 8.8 | 33 | 8 | Q9BAC4 |
| 598 | Q8WEJ5 | ten | 3 | 8.8 | 33 | 8 | Q8WEJ5 |
| 599 | Q8HJH3 | ten | 3 | 8.8 | 33 | 8 | Q8HJH3 |
| 600 | Q8HS33 | ten | 3 | 8.8 | 33 | 8 | Q8HS33 |
| 601 | Q38588 | ten | 3 | 8.8 | 33 | 9 | Q38588 |
| 602 | Q38551 | ten | 3 | 8.8 | 33 | 9 | Q38551 |
| 603 | Q49775 | ten | 3 | 8.8 | 33 | 10 | Q49775 |
| 604 | Q9S8V5 | ten | 3 | 8.8 | 33 | 10 | Q9S8V5 |
| 605 | Q90085 | ten | 3 | 8.8 | 33 | 12 | Q90085 |
| 606 | Q91J04 | ten | 3 | 8.8 | 33 | 12 | Q91J04 |
| 607 | Q72996 | ten | 3 | 8.8 | 33 | 12 | Q72996 |
| 608 | Q91J14 | ten | 3 | 8.8 | 33 | 12 | Q91J14 |
| 609 | Q91J12 | ten | 3 | 8.8 | 33 | 12 | Q91J12 |
| 610 | Q91J15 | ten | 3 | 8.8 | 33 | 12 | Q91J15 |
| 611 | Q91J07 | ten | 3 | 8.8 | 33 | 12 | Q91J07 |
| 612 | Q72995 | ten | 3 | 8.8 | 33 | 12 | Q72995 |
| 613 | Q91J09 | ten | 3 | 8.8 | 33 | 12 | Q91J09 |
| 614 | Q86912 | ten | 3 | 8.8 | 33 | 12 | Q86912 |
| 615 | Q8V5G7 | ten | 3 | 8.8 | 33 | 12 | Q8V5G7 |
| 616 | Q91J08 | ten | 3 | 8.8 | 33 | 12 | Q91J08 |
| 617 | Q72997 | ten | 3 | 8.8 | 33 | 12 | Q72997 |
| 618 | Q83963 | ten | 3 | 8.8 | 33 | 12 | Q83963 |
| 619 | Q91J06 | ten | 3 | 8.8 | 33 | 12 | Q91J06 |
| 620 | Q72999 | ten | 3 | 8.8 | 33 | 12 | Q72999 |
| 621 | Q91J16 | ten | 3 | 8.8 | 33 | 12 | Q91J16 |
| 622 | Q72998 | ten | 3 | 8.8 | 33 | 12 | Q72998 |
| 623 | Q91J11 | ten | 3 | 8.8 | 33 | 12 | Q91J11 |
| 624 | Q72994 | ten | 3 | 8.8 | 33 | 12 | Q72994 |
| 625 | Q8V5H0 | ten | 3 | 8.8 | 33 | 12 | Q8V5H0 |
| 626 | Q91J13 | ten | 3 | 8.8 | 33 | 12 | Q91J13 |
| 627 | Q8V5G8 | ten | 3 | 8.8 | 33 | 12 | Q8V5G8 |

| Accession | Gene | Length | GC Content (%) | GC Skew |
|-----------|--------------------|--------|----------------|---------|
| 628 | 073007 hepatitis c | 12 | 8.8 | 33 |
| 629 | 091J10 tc virus. o | 12 | 8.8 | 33 |
| 630 | 091J17 tc virus. o | 12 | 8.8 | 33 |
| 631 | 069461 human herpe | 12 | 8.8 | 33 |
| 632 | 08V5G9 hepatitis c | 12 | 8.8 | 33 |
| 633 | 073004 hepatitis c | 12 | 8.8 | 33 |
| 634 | Q99138 avian influ | 12 | 8.8 | 33 |
| 635 | P82740 rana tempor | 13 | 8.8 | 33 |
| 636 | P82236 rana tempor | 13 | 8.8 | 33 |
| 637 | Q86107 stman sarc | 15 | 8.8 | 33 |
| 638 | Q9PA23 xylolla fas | 16 | 8.8 | 33 |
| 639 | Q9KML1 vibrio choi | 16 | 8.8 | 33 |
| 640 | Q97T91 streptococc | 16 | 8.8 | 33 |
| 641 | Q97PC1 streptococc | 16 | 8.8 | 33 |
| 642 | Q932N2 staphylococ | 16 | 8.8 | 33 |
| 643 | Q8ZKL2 salmonella | 16 | 8.8 | 33 |
| 644 | Q8Z1V4 salmonella | 16 | 8.8 | 33 |
| 645 | Q8XAJ9 escherichia | 16 | 8.8 | 33 |
| 646 | Q8U5M4 agrobacteri | 16 | 8.8 | 33 |
| 647 | Q8NUL1 staphylococ | 16 | 8.8 | 33 |
| 648 | Q8KG99 chlorobium | 16 | 8.8 | 33 |
| 649 | Q8KEJ7 chlorobium | 16 | 8.8 | 33 |
| 650 | Q8FZ67 brucella su | 16 | 8.8 | 33 |
| 651 | Q8FYR6 brucella su | 16 | 8.8 | 33 |
| 652 | Q8FY86 brucella su | 16 | 8.8 | 33 |
| 653 | Q8EJH6 shewanella | 16 | 8.8 | 33 |
| 654 | Q8EJ76 shewanella | 16 | 8.8 | 33 |
| 655 | Q8EGA9 shewanella | 16 | 8.8 | 33 |
| 656 | Q8EE59 shewanella | 16 | 8.8 | 33 |
| 657 | Q8EE42 shewanella | 16 | 8.8 | 33 |
| 658 | Q8EBW4 shewanella | 16 | 8.8 | 33 |
| 659 | Q8E1Y5 streptococc | 16 | 8.8 | 33 |
| 660 | Q8DWW3 streptococc | 16 | 8.8 | 33 |
| 661 | Q8CQY7 staphylococ | 16 | 8.8 | 33 |
| 662 | Q9HSX6 halobacteri | 17 | 8.8 | 33 |
| 663 | Q8U2X8 pyrococcus | 17 | 8.8 | 33 |
| 664 | Q54427 spiroplasma | 2 | 8.8 | 34 |
| 665 | Q9X3L6 prochloroco | 2 | 8.8 | 34 |
| 666 | Q9R5U1 campylobact | 2 | 8.8 | 34 |
| 667 | Q56234 thermus aqu | 2 | 8.8 | 34 |
| 668 | Q44208 pseudomonas | 2 | 8.8 | 34 |
| 669 | Q9X7J6 pseudomonas | 2 | 8.8 | 34 |
| 670 | O31061 pseudomonas | 2 | 8.8 | 34 |
| 671 | Q9R8A2 chlamydia t | 2 | 8.8 | 34 |
| 672 | Q8GJC8 campylobact | 2 | 8.8 | 34 |
| 673 | Q8G8C9 pseudomonas | 2 | 8.8 | 34 |
| 674 | Q00377 coccidioide | 3 | 8.8 | 34 |
| 675 | Q99910 homo sapien | 4 | 8.8 | 34 |
| 676 | Q9UQN9 homo sapien | 4 | 8.8 | 34 |
| 677 | Q9H3R8 homo sapien | 4 | 8.8 | 34 |
| 678 | Q9UI64 homo sapien | 4 | 8.8 | 34 |
| 679 | Q8W5I1 homo sapien | 4 | 8.8 | 34 |
| 680 | Q9HBG1 homo sapien | 4 | 8.8 | 34 |
| 681 | Q9BSP7 homo sapien | 4 | 8.8 | 34 |
| 682 | Q9H4L8 homo sapien | 4 | 8.8 | 34 |
| 683 | Q8NEQ3 homo sapien | 4 | 8.8 | 34 |
| 684 | Q15251 homo sapien | 4 | 8.8 | 34 |

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| Q8kde4 | chlorobium | 34 | 16 | 8.8 | 3 | 741 |
| Q8ke15 | chlorobium | 34 | 16 | 8.8 | 3 | 740 |
| Q8keq8 | chlorobium | 34 | 16 | 8.8 | 3 | 739 |
| Q8nvl0 | staphylococ | 34 | 16 | 8.8 | 3 | 738 |
| Q8nwf8 | staphylococ | 34 | 16 | 8.8 | 3 | 737 |
| Q8nwx3 | staphylococ | 34 | 16 | 8.8 | 3 | 736 |
| Q8ric7 | fusobacteri | 34 | 16 | 8.8 | 3 | 735 |
| Q8vly1 | mycobacteri | 34 | 16 | 8.8 | 3 | 734 |
| Q8u5v2 | agrobacteri | 34 | 16 | 8.8 | 3 | 733 |
| Q8x4v1 | escheria | 34 | 16 | 8.8 | 3 | 732 |
| Q9k2b9 | chlamydia p | 34 | 16 | 8.8 | 3 | 731 |
| Q97p16 | streptococc | 34 | 16 | 8.8 | 3 | 730 |
| Q97sf7 | streptococc | 34 | 16 | 8.8 | 3 | 729 |
| Q9jvp3 | neisseria m | 34 | 16 | 8.8 | 3 | 728 |
| Q9jy24 | neisseria m | 34 | 16 | 8.8 | 3 | 727 |
| Q9k7c6 | bacillus ha | 34 | 16 | 8.8 | 3 | 726 |
| Q9km63 | vibrio chol | 34 | 16 | 8.8 | 3 | 725 |
| Q9kpw9 | vibrio chol | 34 | 16 | 8.8 | 3 | 724 |
| Q9kra8 | vibrio chol | 34 | 16 | 8.8 | 3 | 723 |
| Q9pdd0 | xylella fas | 34 | 16 | 8.8 | 3 | 722 |
| Q9pfa5 | xylella fas | 34 | 16 | 8.8 | 3 | 721 |
| Q9pgf8 | xylella fas | 34 | 16 | 8.8 | 3 | 720 |
| Q9pgh3 | xylella fas | 34 | 16 | 8.8 | 3 | 719 |
| 050877 | borrelia bu | 34 | 16 | 8.8 | 3 | 718 |
| 050812 | borrelia bu | 34 | 16 | 8.8 | 3 | 717 |
| Q9w8y1 | chimpanzee | 34 | 15 | 8.8 | 3 | 716 |
| Q9wr32 | human immun | 34 | 15 | 8.8 | 3 | 715 |
| 040445 | human immun | 34 | 15 | 8.8 | 3 | 714 |
| Q8qgf7 | oncorhynch | 34 | 13 | 8.8 | 3 | 713 |
| Q8qgg1 | oncorhynch | 34 | 13 | 8.8 | 3 | 712 |
| Q9pre7 | oryzias lat | 34 | 13 | 8.8 | 3 | 711 |
| 042526 | scylliorhin | 34 | 13 | 8.8 | 3 | 710 |
| Q8qfm9 | oncorhynch | 34 | 13 | 8.8 | 3 | 709 |
| Q8qgg2 | oncorhynch | 34 | 13 | 8.8 | 3 | 708 |
| 013101 | ambystoma m | 34 | 13 | 8.8 | 3 | 707 |
| 042521 | scylliorhin | 34 | 13 | 8.8 | 3 | 706 |
| Q9dw68 | rat cytomeg | 34 | 12 | 8.8 | 3 | 705 |
| Q8vhl4 | rattus norv | 34 | 11 | 8.8 | 3 | 704 |
| Q64170 | mus sp. b-r | 34 | 11 | 8.8 | 3 | 703 |
| Q99kx7 | mus muscul | 34 | 11 | 8.8 | 3 | 702 |
| Q99km9 | mus muscul | 34 | 11 | 8.8 | 3 | 701 |
| Q9et72 | mus muscul | 34 | 11 | 8.8 | 3 | 700 |
| Q8r557 | mus muscul | 34 | 11 | 8.8 | 3 | 699 |
| Q923z1 | mus muscul | 34 | 11 | 8.8 | 3 | 698 |
| Q9sca3 | lycopersico | 34 | 10 | 8.8 | 3 | 697 |
| Q8vwl0 | paspalum no | 34 | 10 | 8.8 | 3 | 696 |
| Q8w2h0 | paspalum no | 34 | 10 | 8.8 | 3 | 695 |
| Q8hke1 | rhinicephal | 34 | 8 | 8.8 | 3 | 694 |
| Q8mca2 | phaseolus a | 34 | 8 | 8.8 | 3 | 693 |
| 079025 | enallagma v | 34 | 8 | 8.8 | 3 | 692 |
| P82908 | bos taurus | 34 | 6 | 8.8 | 3 | 691 |
| P79429 | capra hircu | 34 | 6 | 8.8 | 3 | 690 |
| Q8itd9 | schistosoma | 34 | 5 | 8.8 | 3 | 689 |
| Q8n063 | plasmodium | 34 | 5 | 8.8 | 3 | 688 |
| Q9gges | branchiosto | 34 | 5 | 8.8 | 3 | 687 |
| Q9bip7 | cooperia pu | 34 | 5 | 8.8 | 3 | 686 |
| Q9nqy9 | homo sapien | 34 | 4 | 8.8 | 3 | 685 |
| Q8KDE4 | | 34 | 16 | 8.8 | 3 | 741 |
| Q8KE15 | | 34 | 16 | 8.8 | 3 | 740 |
| Q8KEQ8 | | 34 | 16 | 8.8 | 3 | 739 |
| Q8NVL0 | | 34 | 16 | 8.8 | 3 | 738 |
| Q8NWF8 | | 34 | 16 | 8.8 | 3 | 737 |
| Q8NWX3 | | 34 | 16 | 8.8 | 3 | 736 |
| Q8RIC7 | | 34 | 16 | 8.8 | 3 | 735 |
| Q8VIY1 | | 34 | 16 | 8.8 | 3 | 734 |
| Q8U5V2 | | 34 | 16 | 8.8 | 3 | 733 |
| Q8X4V1 | | 34 | 16 | 8.8 | 3 | 732 |
| Q9K2B9 | | 34 | 16 | 8.8 | 3 | 731 |
| Q97P16 | | 34 | 16 | 8.8 | 3 | 730 |
| Q97SF7 | | 34 | 16 | 8.8 | 3 | 729 |
| Q9JVP3 | | 34 | 16 | 8.8 | 3 | 728 |
| Q9JY24 | | 34 | 16 | 8.8 | 3 | 727 |
| Q9K7C6 | | 34 | 16 | 8.8 | 3 | 726 |
| Q9KM63 | | 34 | 16 | 8.8 | 3 | 725 |
| Q9KPW9 | | 34 | 16 | 8.8 | 3 | 724 |
| Q9KRA8 | | 34 | 16 | 8.8 | 3 | 723 |
| Q9PDD0 | | 34 | 16 | 8.8 | 3 | 722 |
| Q9PFA5 | | 34 | 16 | 8.8 | 3 | 721 |
| Q9PGF8 | | 34 | 16 | 8.8 | 3 | 720 |
| Q9PGH3 | | 34 | 16 | 8.8 | 3 | 719 |
| 050877 | | 34 | 16 | 8.8 | 3 | 718 |
| 050812 | | 34 | 16 | 8.8 | 3 | 717 |
| Q9W8Y1 | | 34 | 15 | 8.8 | 3 | 716 |
| Q9WR32 | | 34 | 15 | 8.8 | 3 | 715 |
| 040445 | | 34 | 15 | 8.8 | 3 | 714 |
| Q8QGf7 | | 34 | 13 | 8.8 | 3 | 713 |
| Q8QGG1 | | 34 | 13 | 8.8 | 3 | 712 |
| Q9PRE7 | | 34 | 13 | 8.8 | 3 | 711 |
| 042526 | | 34 | 13 | 8.8 | 3 | 710 |
| Q8QFM9 | | 34 | 13 | 8.8 | 3 | 709 |
| Q8QGG2 | | 34 | 13 | 8.8 | 3 | 708 |
| 013101 | | 34 | 13 | 8.8 | 3 | 707 |
| 042521 | | 34 | 13 | 8.8 | 3 | 706 |
| Q9DW68 | | 34 | 12 | 8.8 | 3 | 705 |
| Q8VHL4 | | 34 | 11 | 8.8 | 3 | 704 |
| Q64170 | | 34 | 11 | 8.8 | 3 | 703 |
| Q99KX7 | | 34 | 11 | 8.8 | 3 | 702 |
| Q99KM9 | | 34 | 11 | 8.8 | 3 | 701 |
| Q9ET72 | | 34 | 11 | 8.8 | 3 | 700 |
| Q8R557 | | 34 | 11 | 8.8 | 3 | 699 |
| Q923Z1 | | 34 | 11 | 8.8 | 3 | 698 |
| Q9SCA3 | | 34 | 10 | 8.8 | 3 | 697 |
| Q8VWL0 | | 34 | 10 | 8.8 | 3 | 696 |
| Q8W2H0 | | 34 | 10 | 8.8 | 3 | 695 |
| Q8HKE1 | | 34 | 8 | 8.8 | 3 | 694 |
| Q8MCA2 | | 34 | 8 | 8.8 | 3 | 693 |
| 079025 | | 34 | 8 | 8.8 | 3 | 692 |
| P82908 | | 34 | 6 | 8.8 | 3 | 691 |
| P79429 | | 34 | 6 | 8.8 | 3 | 690 |
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| Q8N063 | | 34 | 5 | 8.8 | 3 | 688 |
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| Q9BIP7 | | 34 | 5 | 8.8 | 3 | 686 |
| Q9NQY9 | | 34 | 4 | 8.8 | 3 | 685 |

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| Q8g2q2 | brucella su | 34 | 16 | Q8G2Q2 | 8.8 | 3 | 742 |
| Q8f897 | leptosira | 34 | 16 | Q8F897 | 8.8 | 3 | 743 |
| Q8f830 | leptosira | 34 | 16 | Q8F830 | 8.8 | 3 | 744 |
| Q8f827 | leptosira | 34 | 16 | Q8F827 | 8.8 | 3 | 745 |
| Q8f5y7 | leptosira | 34 | 16 | Q8F5Y7 | 8.8 | 3 | 746 |
| Q8f0v9 | leptosira | 34 | 16 | Q8F0V9 | 8.8 | 3 | 747 |
| Q8ezr6 | leptosira | 34 | 16 | Q8EZR6 | 8.8 | 3 | 748 |
| Q8ez37 | leptosira | 34 | 16 | Q8EZ37 | 8.8 | 3 | 749 |
| Q8eyw8 | leptosira | 34 | 16 | Q8EYW8 | 8.8 | 3 | 750 |
| Q8eyg6 | leptosira | 34 | 16 | Q8EYG6 | 8.8 | 3 | 751 |
| Q8exh6 | leptosira | 34 | 16 | Q8EXH6 | 8.8 | 3 | 752 |
| Q8exa8 | leptosira | 34 | 16 | Q8EXA8 | 8.8 | 3 | 753 |
| Q8ej65 | shewanella | 34 | 16 | Q8EJ65 | 8.8 | 3 | 754 |
| Q8ei45 | shewanella | 34 | 16 | Q8EI45 | 8.8 | 3 | 755 |
| Q8ehu5 | shewanella | 34 | 16 | Q8EHU5 | 8.8 | 3 | 756 |
| Q8e8y3 | shewanella | 34 | 16 | Q8E8Y3 | 8.8 | 3 | 757 |
| Q8e8w3 | shewanella | 34 | 16 | Q8E8W3 | 8.8 | 3 | 758 |
| Q8ei73 | streptococ | 34 | 16 | Q8EI73 | 8.8 | 3 | 759 |
| Q8cry3 | staphylococ | 34 | 16 | Q8CRY3 | 8.8 | 3 | 760 |
| Q8u111 | pyrococcus | 34 | 17 | Q8U111 | 8.8 | 3 | 761 |
| Q9r624 | bacillus su | 35 | 2 | Q9R624 | 8.8 | 3 | 762 |
| Q9jp99 | neisseria m | 35 | 2 | Q9JP99 | 8.8 | 3 | 763 |
| Q9r625 | bacillus su | 35 | 2 | Q9R625 | 8.8 | 3 | 764 |
| Q9x3d6 | procholoroco | 35 | 2 | Q9X3D6 | 8.8 | 3 | 765 |
| Q9r5i3 | thermoanaer | 35 | 2 | Q9R5I3 | 8.8 | 3 | 766 |
| Q9fcx4 | clostridium | 35 | 2 | Q9FCX4 | 8.8 | 3 | 767 |
| Q9xbk0 | bacillus ce | 35 | 2 | Q9XBK0 | 8.8 | 3 | 768 |
| Q53564 | neisseria g | 35 | 2 | Q53564 | 8.8 | 3 | 769 |
| Q46537 | bacteroides | 35 | 2 | Q46537 | 8.8 | 3 | 770 |
| Q9zg35 | chlamydia t | 35 | 2 | Q9ZG35 | 8.8 | 3 | 771 |
| Q9rhg5 | bacillus ce | 35 | 2 | Q9RHG5 | 8.8 | 3 | 772 |
| Q9r4a1 | klebsiella | 35 | 2 | Q9R4A1 | 8.8 | 3 | 773 |
| Q8rk93 | clostridium | 35 | 2 | Q8RK93 | 8.8 | 3 | 774 |
| Q8riw2 | clostridium | 35 | 2 | Q8RIW2 | 8.8 | 3 | 775 |
| Q9r626 | bacillus su | 35 | 2 | Q9R626 | 8.8 | 3 | 776 |
| P81927 | lactobacill | 35 | 2 | P81927 | 8.8 | 3 | 777 |
| Q8gkz7 | borrelia bu | 35 | 2 | Q8GKZ7 | 8.8 | 3 | 778 |
| Q96ut3 | saccharomyc | 35 | 3 | Q96UT3 | 8.8 | 3 | 779 |
| Q9bvr9 | homo sapien | 35 | 4 | Q9BVR9 | 8.8 | 3 | 780 |
| Q13380 | homo sapien | 35 | 4 | Q13380 | 8.8 | 3 | 781 |
| Q13165 | homo sapien | 35 | 4 | Q13165 | 8.8 | 3 | 782 |
| Q96fg7 | homo sapien | 35 | 4 | Q96FG7 | 8.8 | 3 | 783 |
| Q13828 | homo sapien | 35 | 4 | Q13828 | 8.8 | 3 | 784 |
| Q13264 | homo sapien | 35 | 4 | Q13264 | 8.8 | 3 | 785 |
| Q9y634 | homo sapien | 35 | 4 | Q9Y634 | 8.8 | 3 | 786 |
| Q9bu09 | homo sapien | 35 | 4 | Q9BU09 | 8.8 | 3 | 787 |
| Q8iu77 | homo sapien | 35 | 4 | Q8IU77 | 8.8 | 3 | 788 |
| Q9u780 | boophilus a | 35 | 5 | Q9U780 | 8.8 | 3 | 789 |
| Q26372 | tribolium c | 35 | 5 | Q26372 | 8.8 | 3 | 790 |
| Q9bn11 | mesobuthus | 35 | 5 | Q9BN11 | 8.8 | 3 | 791 |
| Q9u782 | boophilus m | 35 | 5 | Q9U782 | 8.8 | 3 | 792 |
| Q9tvi7 | boophilus m | 35 | 5 | Q9TVI7 | 8.8 | 3 | 793 |
| Q9u783 | boophilus m | 35 | 5 | Q9U783 | 8.8 | 3 | 794 |
| Q9u784 | boophilus m | 35 | 5 | Q9U784 | 8.8 | 3 | 795 |
| Q9u781 | boophilus m | 35 | 5 | Q9U781 | 8.8 | 3 | 796 |
| Q8if21 | trypanosoma | 35 | 5 | Q8IF21 | 8.8 | 3 | 797 |
| Q95n74 | equus cabal | 35 | 6 | Q95N74 | 8.8 | 3 | 798 |

Q9mza7 sus scrofa
Q951q6 protopitium
Q8w7s9 colpomenia
Q9gff85 ginkgo bilob
Q8w7t0 petalonia b
Q8w7s8 petalonia f
Q8we70 miliaria ca
Q8w7s7 scytosiphon
Q9gff98 ceratophyll
Q94p82 corallium r
Q8we77 cymas circi
Q951s7 anthothela
Q951r1 narellia nut
Q951s1 corallium k
Q8w1i3 colpomenia
Q951r3 anthomurice
Q8w1h9 scytosiphon
Q8w1h5 hydroclathr
Q951s9 protodendro
Q8w1i1 scytosiphon
Q951q9 narellia sp.
Q951s4 paragorgia
Q951r5 corallium s
Q9spu2 arabidopsis
Q9mab1 arabidopsis
Q9zuw2 arabidopsis
Q9s9g9 lycopersico
P92971 arabidopsis
Q91v08 arabidopsis
Q91q64 arabidopsis
Q929297 brassica na
Q8rvj7 populus eur
Q9tfj84 arabidopsis
Q8gux4 picea maria
Q63397 ratius norv
Q9j1a4 mus musculu
Q60608 mus musculu
Q9qv30 rattus sp.
Q9quu2 mus sp. rho
Q922h5 mus musculu
Q99j15 mus musculu
Q8bk89 mus musculu
Q90151 bombyx mori
Q65380 banana bunc
Q83333 murine hepa
Q55549 measles vir
Q8bb50 human papil
Q90xb5 xenopus lae
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P83225 oxyurans s
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P83226 oxyurans s
Q75981 human immu
Q9j3s2 human immu
Q71950 human immu

Q9mza7 35 6 8.8
Q951Q6 35 8 8.8
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Q9Gf85 35 8 8.8
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Q8w7S8 35 8 8.8
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Q9QVU2 35 11 8.8
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Q99J15 35 11 8.8
Q8BK89 35 11 8.8
Q90151 35 12 8.8
Q65380 35 12 8.8
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P83229 35 13 8.8
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Q9J3S2 35 15 8.8
Q71950 35 15 8.8

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| Accession | Gene | Length | GC Content (%) | BLAST E-value |
|-----------|--------------|--------|----------------|---------------|
| Q91PY2 | human | 35 | 8.8 | 3 |
| Q80574 | human | 35 | 8.8 | 3 |
| Q80601 | human | 35 | 8.8 | 3 |
| Q8QDX6 | human | 35 | 8.8 | 3 |
| Q9QFA0 | human | 35 | 8.8 | 3 |
| Q9YM80 | human | 35 | 8.8 | 3 |
| Q8QDY0 | human | 35 | 8.8 | 3 |
| Q75970 | human | 35 | 8.8 | 3 |
| Q9YM96 | human | 35 | 8.8 | 3 |
| Q9YM22 | human | 35 | 8.8 | 3 |
| Q75990 | human | 35 | 8.8 | 3 |
| Q75989 | human | 35 | 8.8 | 3 |
| Q9YM67 | human | 35 | 8.8 | 3 |
| Q77250 | human | 35 | 8.8 | 3 |
| Q75955 | human | 35 | 8.8 | 3 |
| Q9YM95 | human | 35 | 8.8 | 3 |
| Q91PY4 | human | 35 | 8.8 | 3 |
| O07593 | bacillus su | 35 | 8.8 | 3 |
| Q9KR18 | vibrio chol | 35 | 8.8 | 3 |
| Q9KNU1 | vibrio chol | 35 | 8.8 | 3 |
| Q9JWX5 | neisseria m | 35 | 8.8 | 3 |
| Q9JV38 | neisseria m | 35 | 8.8 | 3 |
| Q9A427 | caulobacter | 35 | 8.8 | 3 |
| Q9TJ30 | streptococc | 35 | 8.8 | 3 |
| Q9K241 | chlamydia p | 35 | 8.8 | 3 |
| Q8XZB7 | ralsstonia s | 35 | 8.8 | 3 |
| Q8X4F4 | escherichia | 35 | 8.8 | 3 |
| Q8KCA6 | chlorobium | 35 | 8.8 | 3 |
| Q8G2D4 | brucella su | 35 | 8.8 | 3 |
| Q8F9H5 | leptospiira | 35 | 8.8 | 3 |
| Q8F8D4 | leptospiira | 35 | 8.8 | 3 |
| Q8FYH6 | leptospiira | 35 | 8.8 | 3 |
| Q8EGT2 | shewanella | 35 | 8.8 | 3 |
| Q8EGC0 | shewanella | 35 | 8.8 | 3 |
| Q8EG97 | shewanella | 35 | 8.8 | 3 |
| Q8EBP3 | shewanella | 35 | 8.8 | 3 |
| Q8B9Z1 | shewanella | 35 | 8.8 | 3 |
| Q8DUY1 | streptococc | 35 | 8.8 | 3 |
| Q9HMP1 | halobacteri | 35 | 8.8 | 3 |
| Q8ZX99 | pyrrobaculum | 35 | 8.8 | 3 |
| O06954 | salmoneila | 36 | 8.8 | 3 |
| Q8VTS7 | listeria in | 36 | 8.8 | 3 |
| Q9ZG79 | chlamydia t | 36 | 8.8 | 3 |
| Q9RHE3 | pediococcus | 36 | 8.8 | 3 |
| Q8VTS5 | listeria we | 36 | 8.8 | 3 |
| Q4437 | agrobacteri | 36 | 8.8 | 3 |
| Q91B55 | helicobacte | 36 | 8.8 | 3 |
| Q48507 | lactococcus | 36 | 8.8 | 3 |
| Q99094 | salmoneila | 36 | 8.8 | 3 |
| Q9S635 | prochiloro | 36 | 8.8 | 3 |
| Q8VTR8 | listeria iv | 36 | 8.8 | 3 |
| Q8VTS0 | listeria mo | 36 | 8.8 | 3 |
| Q8KYW1 | uncultured | 36 | 8.8 | 3 |
| Q56028 | salmoneila | 36 | 8.8 | 3 |
| Q9R4X9 | azotobacter | 36 | 8.8 | 3 |
| Q9X3G2 | prochiloro | 36 | 8.8 | 3 |

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| 913 | 086086 | 2 | 36 | 8.8 | 3 |
| 914 | Q9R536 | 2 | 36 | 8.8 | 3 |
| 915 | Q8GRH1 | 2 | 36 | 8.8 | 3 |
| 916 | Q96W36 | 3 | 36 | 8.8 | 3 |
| 917 | Q9UNV7 | 4 | 36 | 8.8 | 3 |
| 918 | Q9PIE9 | 4 | 36 | 8.8 | 3 |
| 919 | Q9UPB7 | 4 | 36 | 8.8 | 3 |
| 920 | Q9UML4 | 4 | 36 | 8.8 | 3 |
| 921 | Q8NE47 | 4 | 36 | 8.8 | 3 |
| 922 | Q9GSY9 | 5 | 36 | 8.8 | 3 |
| 923 | Q9NGN1 | 5 | 36 | 8.8 | 3 |
| 924 | Q27730 | 5 | 36 | 8.8 | 3 |
| 925 | Q9GNP3 | 5 | 36 | 8.8 | 3 |
| 926 | 001333 | 5 | 36 | 8.8 | 3 |
| 927 | Q25781 | 5 | 36 | 8.8 | 3 |
| 928 | Q8ISR7 | 5 | 36 | 8.8 | 3 |
| 929 | Q97889 | 6 | 36 | 8.8 | 3 |
| 930 | Q29059 | 6 | 36 | 8.8 | 3 |
| 931 | Q9XT44 | 6 | 36 | 8.8 | 3 |
| 932 | Q9N1C5 | 6 | 36 | 8.8 | 3 |
| 933 | Q97890 | 6 | 36 | 8.8 | 3 |
| 934 | P79428 | 6 | 36 | 8.8 | 3 |
| 935 | 063675 | 8 | 36 | 8.8 | 3 |
| 936 | Q9GFB1 | 8 | 36 | 8.8 | 3 |
| 937 | Q9TIE4 | 8 | 36 | 8.8 | 3 |
| 938 | Q9TIF1 | 8 | 36 | 8.8 | 3 |
| 939 | Q9GFA3 | 8 | 36 | 8.8 | 3 |
| 940 | Q9GFP7 | 8 | 36 | 8.8 | 3 |
| 941 | Q94VL4 | 8 | 36 | 8.8 | 3 |
| 942 | Q36303 | 8 | 36 | 8.8 | 3 |
| 943 | Q9TIF0 | 8 | 36 | 8.8 | 3 |
| 944 | Q94NY5 | 8 | 36 | 8.8 | 3 |
| 945 | Q9GFW6 | 8 | 36 | 8.8 | 3 |
| 946 | Q9MSP9 | 8 | 36 | 8.8 | 3 |
| 947 | Q9TIF3 | 8 | 36 | 8.8 | 3 |
| 948 | Q9GFW4 | 8 | 36 | 8.8 | 3 |
| 949 | Q9TIE2 | 8 | 36 | 8.8 | 3 |
| 950 | Q9TIF2 | 8 | 36 | 8.8 | 3 |
| 951 | Q9GFB9 | 8 | 36 | 8.8 | 3 |
| 952 | Q9MSR0 | 8 | 36 | 8.8 | 3 |
| 953 | 063650 | 8 | 36 | 8.8 | 3 |
| 954 | Q9TIE3 | 8 | 36 | 8.8 | 3 |
| 955 | Q9TIE5 | 8 | 36 | 8.8 | 3 |
| 956 | Q9GFA9 | 8 | 36 | 8.8 | 3 |
| 957 | Q8HS50 | 8 | 36 | 8.8 | 3 |
| 958 | Q8HS46 | 8 | 36 | 8.8 | 3 |
| 959 | Q8HS42 | 8 | 36 | 8.8 | 3 |
| 960 | Q8HS31 | 8 | 36 | 8.8 | 3 |
| 961 | Q8HS27 | 8 | 36 | 8.8 | 3 |
| 962 | Q8HS18 | 8 | 36 | 8.8 | 3 |
| 963 | Q8HKF5 | 8 | 36 | 8.8 | 3 |
| 964 | Q8HKC6 | 8 | 36 | 8.8 | 3 |
| 965 | Q38977 | 10 | 36 | 8.8 | 3 |
| 966 | Q8VY71 | 10 | 36 | 8.8 | 3 |
| 967 | Q42097 | 10 | 36 | 8.8 | 3 |
| 968 | Q9JMC0 | 11 | 36 | 8.8 | 3 |
| 969 | Q60937 | 11 | 36 | 8.8 | 3 |
| 086086 | shewanella | | | | |
| 09536 | sphingomona | | | | |
| Q8GRH1 | pectobacter | | | | |
| Q96W36 | ophiostoma | | | | |
| Q9UNV7 | homo sapien | | | | |
| Q9PIE9 | homo sapien | | | | |
| Q9UPB7 | homo sapien | | | | |
| Q9UML4 | homo sapien | | | | |
| Q8NE47 | homo sapien | | | | |
| Q9GSY9 | carcinus ma | | | | |
| Q9NGN1 | strongyloce | | | | |
| Q27730 | plasmodium | | | | |
| Q9GNP3 | caenorhabdi | | | | |
| 001333 | caenorhabdi | | | | |
| Q25781 | plasmodium | | | | |
| Q8ISR7 | spodoptera | | | | |
| Q97889 | pongo pygma | | | | |
| Q29059 | sus scrofa | | | | |
| Q9XT44 | pongo pygma | | | | |
| Q9N1C5 | bos taurus | | | | |
| Q97890 | pan troglod | | | | |
| P79428 | capra hircu | | | | |
| 063675 | emberiza pu | | | | |
| Q9GFB1 | gnetum gnet | | | | |
| Q9TIE4 | hydrocotyle | | | | |
| Q9TIF1 | bolax gummif | | | | |
| Q9GFA3 | cabomba car | | | | |
| Q9GFP7 | ceratophyll | | | | |
| Q94VL4 | salmo trutt | | | | |
| Q36303 | musa schizo | | | | |
| Q9TIF0 | klotschia | | | | |
| Q94NY5 | salmo salar | | | | |
| Q9GFW6 | lactoris fe | | | | |
| Q9MSP9 | nymphaea od | | | | |
| Q9TIF3 | eremocharis | | | | |
| Q9GFW4 | liriodendro | | | | |
| Q9TIE2 | aralia chin | | | | |
| Q9TIF2 | azorella tr | | | | |
| Q9GFB9 | drimys wint | | | | |
| Q9MSR0 | zamia furtu | | | | |
| 063650 | emberiza sc | | | | |
| Q9TIE3 | hydrocotyle | | | | |
| Q9TIE5 | xanthosia a | | | | |
| Q9GFA9 | acorus cala | | | | |
| Q8HS50 | ascarina lu | | | | |
| Q8HS46 | austrobaile | | | | |
| Q8HS42 | chloanthus | | | | |
| Q8HS31 | lilium supe | | | | |
| Q8HS27 | magnolia st | | | | |
| Q8HS18 | sagittaria | | | | |
| Q8HKF5 | rhizophal | | | | |
| Q8HKC6 | haemaphysal | | | | |
| Q38977 | arabidopsis | | | | |
| Q8VY71 | arabidopsis | | | | |
| Q42097 | arabidopsis | | | | |
| Q9JMC0 | ratus norv | | | | |
| Q60937 | mus musculu | | | | |

| | | | | | | |
|--------|-------------|----|----|-----|---|------|
| P97598 | rattus norv | 11 | 36 | 8.8 | 3 | 970 |
| Q91x80 | hepatitis b | 12 | 36 | 8.8 | 3 | 971 |
| Q9qgs6 | tanapox vir | 12 | 36 | 8.8 | 3 | 972 |
| Q91x82 | hepatitis b | 12 | 36 | 8.8 | 3 | 973 |
| Q90722 | calicivirus | 12 | 36 | 8.8 | 3 | 974 |
| Q83609 | myxoma viru | 12 | 36 | 8.8 | 3 | 975 |
| Q91cy3 | tt virus. o | 12 | 36 | 8.8 | 3 | 976 |
| Q8qg22 | simian viru | 12 | 36 | 8.8 | 3 | 977 |
| Q42264 | xenopus lae | 13 | 36 | 8.8 | 3 | 978 |
| Q9w695 | gallus gall | 13 | 36 | 8.8 | 3 | 979 |
| Q8qgs0 | gallus gall | 13 | 36 | 8.8 | 3 | 980 |
| Q76587 | human immun | 15 | 36 | 8.8 | 3 | 981 |
| Q80551 | human immun | 15 | 36 | 8.8 | 3 | 982 |
| Q9ynx9 | human immun | 15 | 36 | 8.8 | 3 | 983 |
| Q80550 | human immun | 15 | 36 | 8.8 | 3 | 984 |
| Q80553 | human immun | 15 | 36 | 8.8 | 3 | 985 |
| Q40258 | human immun | 15 | 36 | 8.8 | 3 | 986 |
| Q77664 | human immun | 15 | 36 | 8.8 | 3 | 987 |
| Q25389 | helicobacte | 16 | 36 | 8.8 | 3 | 988 |
| Q50679 | borrelia bu | 16 | 36 | 8.8 | 3 | 989 |
| Q50686 | borrelia bu | 16 | 36 | 8.8 | 3 | 990 |
| Q50969 | borrelia bu | 16 | 36 | 8.8 | 3 | 991 |
| Q9ktv5 | vibrio chol | 16 | 36 | 8.8 | 3 | 992 |
| Q9kxb3 | vibrio chol | 16 | 36 | 8.8 | 3 | 993 |
| Q9kq34 | vibrio chol | 16 | 36 | 8.8 | 3 | 994 |
| Q9kpr2 | vibrio chol | 16 | 36 | 8.8 | 3 | 995 |
| Q9kpg3 | vibrio chol | 16 | 36 | 8.8 | 3 | 996 |
| Q9k1w9 | vibrio chol | 16 | 36 | 8.8 | 3 | 997 |
| Q9k7g3 | bacillus ha | 16 | 36 | 8.8 | 3 | 998 |
| Q9jtw3 | neisseria m | 16 | 36 | 8.8 | 3 | 999 |
| Q8z1t4 | salmonella | 16 | 36 | 8.8 | 3 | 1000 |

ALIGNMENTS

RESULT 1

Q91Y90 ID Q91Y90 PRELIMINARY; PRT; 31 AA.

AC Q91Y90; (TREMBLrel. 19, Created)

DT 01-DEC-2001 (TREMBLrel. 19, Last sequence update)

DT 01-OCT-2002 (TREMBLrel. 22, Last annotation update)

DE Parathyroid hormone (Fragment).

GN PTH.

OS Peromyscus maniculatus (Deer mouse).

OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Sigmodontinae;

OC Peromyscus.

OX NCBI_TaxID=10042;

RN [1]

RP SEQUENCE FROM N.A.

RA Prince K.L., Dewey M.J.;

RL Submitted (MAY-2001) to the EMBL/GenBank/DBJ databases.

DR EMBL; AF382953; AAK63072.1; -

DR InterPro; IPR001415; Parathyrd_hrm.

DR InterPro; IPR003625; Pthyhorm_sub.

AC 017148;
 ID 017148
 017148
 RESULT 3

DB 14 VSEIQLMHN 22
 QY 2 VSEIQLMHN 10

Query Match 26.5%; Score 9; DB 11; Length 31;
 Best Local Similarity 100.0%; Pred. No. 0.013;
 Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

SQ SEQUENCE 31 AA; 3461 MW; A208B0E772B9B55B CRC64;
 FT NON_TER 31
 FT NON_TER 1
 DR PROSITE; PS00335; PARATHYROID; 1.
 DR Prodom; PD010687; Pthyrrhorm_sub; 1.
 DR Pfam; PF01279; Parathyroid; 1.
 DR InterPro; IPR003625; Pthyrrhorm_sub.
 DR InterPro; IPR001415; Parathyrd_hrm.
 DR EMBL; AF382952; AAK63071.1; -.
 RL Submitted (MAY-2001) to the EMBL/GenBank/DBJ databases.
 RA Prince K.L., Dewey M.J.;
 RP SEQUENCE FROM N.A.
 RN [1]
 OX NCBI_TaxID=42413;
 OC Peromyscus.
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Sigmodontinae;
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OS Peromyscus polionotus (Oldfield mouse).
 GN PTH.
 DE Parathyroid hormone (Fragment).
 DT 01-OCT-2002 (TrEMBLrel. 22, last annotation update)
 DT 01-DEC-2001 (TrEMBLrel. 19, last sequence update)
 DT 01-DEC-2001 (TrEMBLrel. 19, Created)
 AC Q91Y91;
 ID Q91Y91 PRELIMINARY; PRT; 31 AA.
 Q91Y91

RESULT 2

DB 14 VSEIQLMHN 22
 QY 2 VSEIQLMHN 10

Query Match 26.5%; Score 9; DB 11; Length 31;
 Best Local Similarity 100.0%; Pred. No. 0.013;
 Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

SQ SEQUENCE 31 AA; 3461 MW; A208B0E772B9B55B CRC64;
 FT NON_TER 31
 FT NON_TER 1
 DR PROSITE; PS00335; PARATHYROID; 1.
 DR Prodom; PD010687; Pthyrrhorm_sub; 1.
 DR Pfam; PF01279; Parathyroid; 1.

DT 01-JAN-1998 (TREMBlrel. 05, Created)
 DT 01-JAN-1998 (TREMBlrel. 05, Last sequence update)
 DT 01-DEC-2001 (TREMBlrel. 19, Last annotation update)
 DE Antigen B/1 (Fragment).
 GN AGB/1.
 OS Echinococcus vogeli.
 OC Eukaryota; Metazoa; Platyhelminthes; Cestoda; Eucestoda;
 OC Cyclophyllidae; Taeniidae; Echinococcus.
 OX NCBI_TaxID=6213;
 RN [1]
 RP SEQUENCE FROM N.A.
 RA Haag K.L., Zaha A., Gottstein B.;
 RT "E. vogeli AgB/1 coding sequence."
 RL Submitted (SEP-1997) to the EMBL/GenBank/DBJ databases.
 DR EMBL; AF024665; AAB81611.1; -.
 FT NON_TER 1
 FT NON_TER 34
 SQ SEQUENCE 34 AA; 3964 MW; 3BE894E129CF84F3 CRC64;
 Query Match 14.7%; Score 5; DB 5; Length 34;
 Best Local Similarity 100.0%; Pred. No. 2.9e+02;
 Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 24 LRKKL 28
 DB 15 LRKKL 19
 RESULT 4
 Q97K50
 ID Q97K50 PRELIMINARY; PRT; 34 AA.
 AC Q97K50;
 DT 01-OCT-2001 (TREMBlrel. 18, Created)
 DT 01-OCT-2001 (TREMBlrel. 18, Last sequence update)
 DT 01-OCT-2001 (TREMBlrel. 18, Last annotation update)
 DE Transcriptional regulator, AcrR family.
 GN CAC1071.
 OS Clostridium acetobutylicum.
 OC Bacteria; Firmicutes; Clostridia; Clostridiales; Clostridiaceae;
 OC Clostridium.
 OX NCBI_TaxID=1488;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=ATCC 824 / DSM 792 / VKM B-1787;
 RX MEDLINE=21359325; PubMed=11466286;
 RA Noelling J., Breton G., Omelchenko M.V., Makarova K.S., Zeng Q.,
 RA Gibson R., Lee H.M., Dubois J., Qiu D., Hitti J., Wolf Y.I.,
 RA Tatusov R.L., Sabathe F., Doucet-Stamm L., Soucaille P., Daly M.J.,
 RA Bennett G.N., Koonin E.V., Smith D.R.;
 RT "Genome sequence and comparative analysis of the solvent-producing
 bacterium Clostridium acetobutylicum."

RESULT 5
ID Q9HR65 PRELIMINARY; PRT; 34 AA.
AC Q9HR65
DT 01-MAR-2001 (TrEMBLrel. 16, Created)
DT 01-MAR-2001 (TrEMBLrel. 16, Last sequence update)
DT 01-MAR-2001 (TrEMBLrel. 16, Last annotation update)
DE Vng0840h.
GN VNG0840H.
OS Halobacterium sp. (strain NRC-1).
OC Archaea; Euryarchaeota; Halobacteria; Halobacteriales;
OC Halobacteriaceae; Halobacterium.
OX NCBI_TaxID=64091;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=20504483; PubMed=11016950;
RA Ng W.V., Kennedy S.P., Mahairas G.G., Bergquist B., Pan M.,
RA Shukla H.D., Lasky S.R., Baliga N.S., Thorsson V., Sbrogna J.,
RA Swartzell S., Weir D., Hall J., Dahl T.A., Welti R., Goo Y.A.,
RA Leitbauer B., Keller K., Cruz R., Danson M.J., Hough D.W.,
RA Maddocks D.G., Jablonski P.E., Krebs M.P., Angvine C.M., Dale H.,
RA Isenbarger T.A., Beck R.F., Pohlschroder M., Spudich J.L., Jung K.-H.,
RA Alam M., Freitas T., Hou S., Daniels C.J., Dennis P.P., Omer A.D.,
RA Ebhardt H., Lowe T.M., Liang P., Riley M., Hood L., Dassarma S.,
RT "Genome sequence of Halobacterium species NRC-1."
RL Proc. Natl. Acad. Sci. U.S.A. 97:12176-12181(2000).
DR EMBL; AE005025; AAG19293.1; -.
KW Complete proteome.
SQ SEQUENCE 34 AA; 3731 MW; BA957904338DCD45 CRC64;

Query Match 14.7%; Score 5; DB 16; Length 34;
Best Local Similarity 100.0%; Pred. No. 2.9e+02;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 SVSRI 5
DB 30 SVSRI 34

RESULT 6
ID Q8BTB9 PRELIMINARY; PRT; 35 AA.
AC Q8BTB9
DT 01-MAR-2001 (TrEMBLrel. 16, Created)
DT 01-MAR-2001 (TrEMBLrel. 16, Last sequence update)
DT 01-MAR-2001 (TrEMBLrel. 16, Last annotation update)
DE Vng0840h.
GN VNG0840H.
OS Halobacterium sp. (strain NRC-1).
OC Archaea; Euryarchaeota; Halobacteria; Halobacteriales;
OC Halobacteriaceae; Halobacterium.
OX NCBI_TaxID=64091;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=20504483; PubMed=11016950;
RA Ng W.V., Kennedy S.P., Mahairas G.G., Bergquist B., Pan M.,
RA Shukla H.D., Lasky S.R., Baliga N.S., Thorsson V., Sbrogna J.,
RA Swartzell S., Weir D., Hall J., Dahl T.A., Welti R., Goo Y.A.,
RA Leitbauer B., Keller K., Cruz R., Danson M.J., Hough D.W.,
RA Maddocks D.G., Jablonski P.E., Krebs M.P., Angvine C.M., Dale H.,
RA Isenbarger T.A., Beck R.F., Pohlschroder M., Spudich J.L., Jung K.-H.,
RA Alam M., Freitas T., Hou S., Daniels C.J., Dennis P.P., Omer A.D.,
RA Ebhardt H., Lowe T.M., Liang P., Riley M., Hood L., Dassarma S.,
RT "Genome sequence of Halobacterium species NRC-1."
RL Proc. Natl. Acad. Sci. U.S.A. 97:12176-12181(2000).
DR EMBL; AE005025; AAG19293.1; -.
KW Complete proteome.
SQ SEQUENCE 34 AA; 3731 MW; BA957904338DCD45 CRC64;

Query Match 14.7%; Score 5; DB 17; Length 34;
Best Local Similarity 100.0%; Pred. No. 2.9e+02;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 24 LRKTL 28
DB 26 LRKTL 30

RESULT 6
ID Q8BTB9 PRELIMINARY; PRT; 35 AA.
AC Q8BTB9

DT 01-MAR-2003 (TREMBLrel. 23, Created)
 DT 01-MAR-2003 (TREMBLrel. 23, Last sequence update)
 DT 01-MAR-2003 (TREMBLrel. 23, Last annotation update)
 DE Translin.
 OS Mus musculus (Mouse).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
 OX NCBI_TaxID=10090;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=C57BL/6J; TISSUE=Body;
 RX MEDLINE=22354683; PubMed=12466851;
 RA The FANTOM Consortium,
 RA the RIKEN Genome Exploration Research Group Phase I & II Team;
 RT "Analysis of the mouse transcriptome based on functional annotation of
 RT 60,770 full-length cDNAs.";
 RL Nature 420:563-573 (2002).
 DR EMBL; AK011220; BAC25325.1; -
 SQ SEQUENCE 35 AA; 3967 MW; F811566686390ECD8 CRC64;
 Query Match 14.7%; Score 5; DB 11; Length 35;
 Best Local Similarity 100.0%; Pred. No. 3e+02;
 Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 SVSEI 5
 DB 2 SVSEI 6
 RESULT 7
 ID Q97RG6 PRELIMINARY; PRT; 35 AA.
 AC Q97RG6;
 DT 01-OCT-2001 (TREMBLrel. 18, Created)
 DT 01-OCT-2001 (TREMBLrel. 18, Last sequence update)
 DT 01-DEC-2001 (TREMBLrel. 19, Last annotation update)
 DE Hypothetical protein SP0853.
 GN SP0853.
 OS Streptococcus pneumoniae.
 OC Bacteria; Firmicutes; Lactobacillales; Streptococcaceae;
 OC Streptococcus.
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=TIGR4;
 RX MEDLINE=21357209; PubMed=11463916;
 RA Tetelin H., Nelson K.E., Paulsen I.T., Eissen J.A., Read T.D.,
 RA Peterson S., Heidelberg J., DeBoy R.T., Haft D.H., Dodson R.J.,
 RA Durkin A.S., Gwinn M., Kolonay J.F., Nelson W.C., Peterson J.D.,
 RA Umayam L.A., White O., Salzberg S.L., Lewis M.R., Radune D.,
 RA Holtzapple E., Khouri H., Wolf A.M., Uterback T.R., Hansen C.L.,
 RA McDonald L.A., Feldblyum T.V., Angiuoli S., Dickinson T., Hickey E.K.,
 RA Holt I.E., Loftus B.J., Yang F., Smith H.O., Venter J.C.,
 RA Dougherty B.A., Morrison D.A., Hollingshead S.K., Fraser C.M.;
 RT "Complete genome sequence of a virulent isolate of Streptococcus
 RT pneumoniae.";
 RL Science 293:498-506 (2001).

DR EMBL; AE007391; AAK74982.1; -
 DR TIGR; SP0853; -
 KW Hypothetical protein; Complete proteome.
 SQ SEQUENCE 35 AA; 4276 MW; 6B8813CC028D6C7B CRC64;
 Query Match 14.7%; Score 5; DB 16; Length 35;
 Best Local Similarity 100.0%; Pred. No. 3e+02;
 Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 26 KKLQD 30
 |||||
 DB 30 KKLQD 34

RESULT 8

ID 024285 PRELIMINARY; PRT; 28 AA.
 AC 024285;
 DT 01-JAN-1998 (TREMBLrel. 05, Created)
 DT 01-JAN-1998 (TREMBLrel. 05, Last sequence update)
 DT 01-DEC-2001 (TREMBLrel. 19, Last annotation update)
 DE LFY protein (Fragment).
 GN LFY.
 OS Pinus radiata (Monterey pine).
 OC Eukaryota; Viridiplantae; Streptophyta; Tracheophyta;
 OC Spermatophyta; Coniferopsida; Coniferales; Pinaceae; Pinus.
 OX NCBI_TaxID=3347;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC TISSUE=Vegetative;
 RA Izquierdo L.Y., Vergara R.F., Alvarez-Buylla E.R.;
 RT "Partial characterization of Pinus radiata meristem identity homolog
 gene (LFY).";
 RL Submitted (AUG-1996) to the EMBL/GenBank/DBJ databases.
 DR EMBL; U66725; AAB06792.1; -
 FT NON_TER 1
 FT NON_TER 28
 SQ SEQUENCE 28 AA; 3376 MW; 1736738622B4EE74 CRC64;

Query Match 11.8%; Score 4; DB 10; Length 28;
 Best Local Similarity 100.0%; Pred. No. 3e+03;
 Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 24 LKK 27
 |||||
 DB 15 LKK 18

RESULT 9

ID Q49148 PRELIMINARY; PRT; 29 AA.
 AC Q49148;
 DT 01-NOV-1996 (TREMBLrel. 01, Created)
 DT 01-NOV-1996 (TREMBLrel. 01, Last sequence update)
 DT 01-NOV-1998 (TREMBLrel. 08, Last annotation update)
 DE PQQ biosynthesis polypeptide.
 GN PQQ.

```

OS Methyllobacterium extorquens.
OC Bacteria; Proteobacteria; Alphaproteobacteria; Rhizobiales;
OC Methyllobacteriaceae; Methyllobacterium.
OX NCBI_TaxID=408;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=AM1;
RX MEDLINE=94179111; PubMed=8132470;
RA Morris C.J., Biville F., Turin E., Lee E., Ellermann K., Fan W.H.,
RA Ramamoorthy R., Springer A.L., Lidstrom M.E.;
RT "Isolation, phenotypic characterization, and complementation analysis
RT of mutants of Methyllobacterium extorquens AML unable to synthesize
RT pyrroloquinoline quinone and sequences of pqd, pqg, and pqc.";
RT J. Bacteriol. 176:1746-1755(1994).
DR EMBL; L25889; AAA17878.1; -
SEQUENCE 29 AA; 3222 MW; B4831562CF76973C CRC64;
SQ

Query Match 11.8%; Score 4; DB 2; Length 29;
Best Local Similarity 100.0%; Pred. No. 3.1e+03;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 VSEI 5
DB 8 VSEI 11

RESULT 10
Q9UCL2
ID Q9UCL2 PRELIMINARY; PRT; 29 AA.
AC Q9UCL2;
DT 01-MAY-2000 (TrEMBLrel. 13, Created)
DT 01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
DT 01-MAR-2003 (TrEMBLrel. 23, Last annotation update)
DE Renal intestinal-type alkaline phosphatase (Fragment).
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE.
RX MEDLINE=93092315; PubMed=1458595;
RA Nishihara Y., Hayashi Y., Adachi T., Koyama I., Stigbrand T.,
RA Hirano K.;
RT "Chemical nature of intestinal-type alkaline phosphatase in human
RT kidney.";
RT Clin. Chem. 38:2539-2542(1992).
DR InterPro; IPR001952; Alk_phosphatse.
DR Prodom; PD001868; Alk_phosphatse; 1.
SEQUENCE 29 AA; 3250 MW; 30501BB7BBEAD8D0 CRC64;
SQ

Query Match 11.8%; Score 4; DB 4; Length 29;
Best Local Similarity 100.0%; Pred. No. 3.1e+03;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 26 KKLQ 29
DB 23 KKLQ 26

```

RESULT 11

Q25603

ID Q25603 PRELIMINARY; PRT; 29 AA.

AC Q25603;

DT 01-NOV-1996 (TRMBLrel. 01, Created)

DT 01-NOV-1996 (TRMBLrel. 01, Last sequence update)

DT 01-DEC-2001 (TRMBLrel. 19, Last annotation update)

DE Tubulin.

OS Onchocerca volvulus.

OC Eukaryota; Metazoa; Nematoda; Chromadorea; Spirurida; Filarioidea;

OC Onchocercidae; Onchocerca.

OX NCBI_TaxID=6282;

RN [1]

RP SEQUENCE FROM N.A.

RA Chandrashekar R., Curtis K.C., Weil G.J.;

RT "Onchocerca volvulus cDNA clone.";

RL Submitted (SEP-1994) to the EMBL/GenBank/DBJ databases.

DR EMBL; U15095; AAA50364.1; -.

SQ SEQUENCE 29 AA; 3539 MW; B917126A923EF884 CRC64;

Query Match 11.8%; Score 4; DB 5; Length 29;

Best Local Similarity 100.0%; Pred. No. 3.1e+03;

Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 VSEI 5

DB 4 VSEI 7

RESULT 12

Q9TI61

ID Q9TI61 PRELIMINARY; PRT; 29 AA.

AC Q9TI61;

DT 01-MAY-2000 (TRMBLrel. 13, Created)

DT 01-MAY-2000 (TRMBLrel. 13, Last sequence update)

DT 01-MAY-2000 (TRMBLrel. 13, Last annotation update)

DE Photosystem Q(B) protein (Fragment).

GN PSBA.

OS Allosyncarpia ternata.

OG Chloroplast.

OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;

OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosidae;

OC eucots II; Myrtales; Myrtaceae; Allosyncarpia.

OX NCBI_TaxID=34307;

RN [1]

RP SEQUENCE FROM N.A.

RA Udovitch F., Ladiges P.Y.;

RT "Informativeness of nuclear and chloroplast DNA regions and the

RT phylogeny of the eucalypts and related genera (Myrtaceae).";

RL Submitted (SEP-1999) to the EMBL/GenBank/DBJ databases.

DR EMBL; AF190370; AAF15265.1; -.

KM Chloroplast.

FT NON TER 1

SQ SEQUENCE 29 AA; 3501 MW; 977D8E6E67E1D833 CRC64;

Query Match 11.8%; Score 4; DB 8; Length 29;
Best Local Similarity 100.0%; Pred. No. 3.1e+03;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 31 VHNF 34
DB 7 VHNF 10

RESULT 13

013043
ID 013043 PRELIMINARY; PRT; 29 AA.
AC 013043;
DT 01-JUL-1997 (TrEMBLrel. 04, Created)
DT 01-JUL-1997 (TrEMBLrel. 04, Last sequence update)
DT 01-JUN-2002 (TrEMBLrel. 21, Last annotation update)
DE Whn transcription factor (Fragment).
GN WHN.
OS Scyliorhinus canicula (Spotted dogfish) (Spotted catshark).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Chondrichthyes;
OC Elasmobranchii; Galeomorphii; Galeoidea; Carcharhiniformes;
OC Scyliorhinidae; Scyliorhinus.
OX NCBI_TaxID=7830;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=97268658; Pubmed=9108066;
RA Schlake T., Schorpp M., Nehls M., Boehm T.;
RT "The nude gene encodes a sequence-specific DNA binding protein with
RT homologs in organisms that lack an anticipatory immune system.";
RT Proc. Natl. Acad. Sci. U.S.A. 94:3842-3847(1997).
DR EMBL; Y11539; CAA72302.1; -.
DR InterPro; IPR001766; TF_Fork_head.
DR Pfam; PF00250; Fork_head; 1.
DR ProDom; PD000425; TF_Fork_head; 1.
FT NON_TER 1
FT NON_TER 29
SQ SEQUENCE 29 AA; 3243 MW; 62AE51F2BE7311E2 CRC64;

Query Match 11.8%; Score 4; DB 13; Length 29;
Best Local Similarity 100.0%; Pred. No. 3.1e+03;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 VSEI 5
DB 17 VSEI 20

RESULT 14

Q9UBV5
ID Q9UBV5 PRELIMINARY; PRT; 30 AA.
AC Q9UBV5;
DT 01-MAY-2000 (TrEMBLrel. 13, Created)
DT 01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
DT 01-MAR-2003 (TrEMBLrel. 23, Last annotation update)
DE Intestinal alkaline phosphatase (Fragment).
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

OC Mammalia; Euthera; Primates; Catarrhini; Homnidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE.
RX MEDLINE=93092315; PubMed=1458595;
RA Nishihara Y., Hayashi T., Adachi T., Koyama I., Stigbrand T.,
RA Hirano K.;
RT "Chemical nature of intestinal-type alkaline phosphatase in human
RT kidney.";
RL Clin. Chem. 38:2539-2542(1992).
DR InterPro; IPR001952; Aik_phosphatse.
DR ProDom; PD001868; Aik_phosphatse; 1.
SQ SEQUENCE 30 AA; 3349 MW; 30501BB7BBEB9BDE6 CRC64;
Query Match 11.8%; Score 4; DB 4; Length 30;
Best Local Similarity 100.0%; Pred. No. 3.1e+03;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 26 KKLQ 29
DB 24 KKLQ 27
RESULT 15
Q8DZP7
ID Q8DZP7 PRELIMINARY; PRT; 30 AA.
AC Q8DZP7;
DT 01-MAR-2003 (TrEMBLrel. 23, Created)
DT 01-MAR-2003 (TrEMBLrel. 23, Last sequence update)
DT 01-MAR-2003 (TrEMBLrel. 23, Last annotation update)
DE Hypothetical protein.
GN SAG1053.
OS Streptococcus agalactiae (serotype V).
OC Bacteria; Firmicutes; Lactobacillales; Streptococcaceae;
OC Streptococcus.
OX NCBI_TaxID=216466;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=2603 V/R / Serotype V;
RX MEDLINE=22222988; PubMed=12200547;
RA Tetelin H., Masiagnani V., Cieslewicz M.J., Eisen J.A., Peterson S.,
RA Wessels M.R., Paulsen I.T., Nelson K.E., Margarit I., Read T.D.,
RA Madoff L.C., Wolf A.M., Beanan M.J., Brinkac L.M., Daugherty S.C.,
RA DeBoy R.T., Durkin A.S., Kolonay J.F., Madupu R., Lewis M.R.,
RA Radune D., Fedorova N.B., Scanlan D., Khouri H., Mulligan S.,
RA Carty H.A., Cline R.T., Van Aken S.E., Gill J., Scarselli M., Mora M.,
RA Iacobini E.T., Brettoni C., Galli G., Mariani M., Vegni F., Malone D.,
RA Rinaudo D., Rappuoli R., Telford J.L., Kasper D.L., Grandi G.,
RA Fraser C.M.;
RT "Complete genome sequence and comparative genomic analysis of an
RT emerging human pathogen, serotype V Streptococcus agalactiae.";
RL Proc. Natl. Acad. Sci. U.S.A. 99:12391-12396(2002).
DR EMBL; AF014240; AAM99934.1; -.
DR TIGR; SAG1053; -.
KW Hypothetical protein; Complete proteome.
SQ SEQUENCE 30 AA; 3492 MW; 8BC8F7525007AE91 CRC64;

Query Match 11.8%; Score 4; DB 16; Length 30;
Best Local Similarity 100.0%; Pred. No. 3.1e+03;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 26 KKLQ 29
DB 23 KKLQ 26

RESULT 16

Q55314 ID Q55314 PRELIMINARY; PRT; 31 AA.
AC Q55314;
DT 01-NOV-1996 (TRMBLrel. 01, Created)
DT 01-NOV-1996 (TRMBLrel. 01, Last sequence update)
DT 01-DEC-2001 (TRMBLrel. 19, Last annotation update)
DE Urf2 protein (Fragment).

OS Sulfolobus solfataricus.
OC Archaea; Crenarchaeota; Thermoprotei; Sulfolobales; Sulfolobaceae;
OC Sulfolobus.
OX NCBI_TaxID=2287;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=96085144; PubMed=8521845;
RA Jones C.E., Fleming T.M., Cowan D.A., Littlechild J.A., Piper P.W.;

RT "The phosphoglycerate kinase and glyceraldehyde-3-phosphate
dehydrogenase genes from the thermophilic archaeon Sulfolobus
solfataricus overlap by 8bp. Isolation, sequencing of the genes and
expression on Escherichia coli.";
RT Eur. J. Biochem. 233:800-808(1995).
RN [2]
RP SEQUENCE FROM N.A.
RX MEDLINE=94082761; PubMed=8259927;
RA Arcari P., Russo A.D., Iannicello G., Gallo M., Bocchini V.;

RT "Nucleotide sequence and molecular evolution of the gene coding for
glyceraldehyde-3-phosphate dehydrogenase in the thermacidophilic
archaeobacterium Sulfolobus solfataricus.";

RT Biochem. Genet. 31:241-251(1993).
DR EMBL; X80178; CAA56461.1; -.
FT NON TER 31
SQ SEQUENCE 31 AA; 3554 MW; 9A2538F911C7309A CRC64;

Query Match 11.8%; Score 4; DB 1; Length 31;
Best Local Similarity 100.0%; Pred. No. 3.2e+03;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 23 WLRK 26
DB 11 WLRK 14

RESULT 17

Q8NE18 ID Q8NE18 PRELIMINARY; PRT; 31 AA.
AC Q8NE18;
DT 01-OCT-2002 (TRMBLrel. 22, Created)

DT 01-OCT-2002 (TrEMBLrel. 22, Last sequence update)
 DT 01-OCT-2002 (TrEMBLrel. 22, Last annotation update)
 DE Hypothetical protein (Fragment).
 OS Homo sapiens (Human).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
 OX NCBI_TaxID=9606;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC TISSUE=Kidney;
 RA Strausberg R.;
 RL Submitted (JUN-2002) to the EMBL/GenBank/DBJ databases.
 DR EMBL; BC030993; AAH30993.1; -.
 KW Hypothetical protein.
 FT NON_TER 1
 SQ SEQUENCE 31 AA; 3437 MW; 72DCD0761839F7F7 CRC64;
 Query Match 11.8%; Score 4; DB 4; Length 31;
 Best Local Similarity 100.0%; Pred. No. 3.2e+03;
 Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 2 VSEI 5
 DB 18 VSEI 21
 RESULT 18
 ID 050669 PRELIMINARY; PRT; 31 AA.
 AC 050669;
 DT 01-JUN-1998 (TrEMBLrel. 06, Created)
 DT 01-JUN-1998 (TrEMBLrel. 06, Last sequence update)
 DT 01-MAR-2002 (TrEMBLrel. 20, Last annotation update)
 DE Hypothetical protein BBH11.
 GN BBH11.
 OS Borrelia burgdorferi (Lyme disease spirochete).
 OG Plasmid lp28-3.
 OC Bacteria; Spirochaetes; Spirochaetales; Spirochaetaceae; Borrelia.
 OX NCBI_TaxID=139;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=ATCC 35210 / B31;
 RX MEDLINE=98065943; PubMed=9403685;
 RA Fraser C.M., Casjens S., Huang W.M., Sutton G.G., Clayton R.A.,
 RA Lathigra R., White O., Ketchum K.A., Dodson R., Hickey E.K., Gwinn M.,
 RA Dougherty B., Tomb J.-F., Fleischmann R.D., Richardson D.,
 RA Peterson J., Kervlavage A.R., Quackenbush J., Salzberg S., Hanson M.,
 RA van Vugt R., Palmer N., Adams M.D., Gocayne J.D., Weidman J.,
 RA Uterback T., Matthey L., McDonald L., Artach P., Bowman C.,
 RA Garland S., Fujii C., Cotton M.D., Horst K., Roberts K., Hatch B.,
 RA Smith H.O., Venter J.C.;
 RT "Genomic sequence of a Lyme disease spirochaete, Borrelia
 RT burgdorferi.";
 RL Nature 390:580-586(1997).
 DR EMBL; AE000784; AAC66002.1; -.
 DR TIGR; BBH11; -.
 KW Hypothetical protein; Plasmid; Complete proteome.

SEQ SEQUENCE 31 AA; 3892 MW; 8C9F6B9E72D10FBA CRC64;

Query Match 11.8%; Score 4; DB 16; Length 31;

Best Local Similarity 100.0%; Pred. No. 3.2e+03;

Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 26 KKLQ 29

||||

DB 26 KKLQ 29

RESULT 19

Q8E1W8

ID Q8E1W8

PRELIMINARY; PRT; 31 AA.

AC Q8E1W8;

DT 01-MAR-2003 (TREMBlrel. 23, Created)

DT 01-MAR-2003 (TREMBlrel. 23, Last sequence update)

DT 01-MAR-2003 (TREMBlrel. 23, Last annotation update)

DE Hypothetical protein.

GN S00711.

OS *Shewanella oneidensis*.

OC Bacteria; Proteobacteria; Gammaproteobacteria; Alteromonadales;

OC Alteromonadaceae; *Shewanella*.

OX NCBI_TaxID=70863;

RN [1]

RP SEQUENCE FROM N.A.

RC STRAIN=MR-1;

RX MEDLINE=22297686; PubMed=12368813;

RA Heidelberg J.F., Paulsen I.T., Nelson K.E., Gaidos E.J., Nelson W.C.,

RA Read T.D., Eisen J.A., Seshadri R., Ward N., Methe B., Clayton R.A.,

RA Meyer T., Tsapin A., Scott J., Beaman M., Brinkac L., Daugherty S.,

RA DeBoy R.T., Dodson R.J., Durkin A.S., Haft D.H., Kolonay J.F.,

RA Madupu R., Peterson J.D., Umayam L.A., White O., Wolf A.M.,

RA Vamathevan J., Weidman J., Impraim M., Lee K., Berry K., Lee C.,

RA Mueller J., Khouri H., Gill J., Uterback T.R., McDonald L.A.,

RA Feldblyum T.V., Smith H.O., Venter J.C., Nelson K.H., Fraser C.M.,

RT "Genome sequence of the dissimilatory metal ion-reducing bacterium

RT *Shewanella oneidensis*."

RL Nat. Biotechnol. 20:1118-1123(2002).

DR EMBL; AE015517; AAN53789.1; -.

DR TIGR; S00711; -.

KW Hypothetical protein; Complete proteome.

SEQ SEQUENCE 31 AA; 3597 MW; 7C6C5D55CFF9CFFF CRC64;

Query Match 11.8%; Score 4; DB 16; Length 31;

Best Local Similarity 100.0%; Pred. No. 3.2e+03;

Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 8 MHNK 11

||||

DB 1 MHNK 4

RESULT 20

Q9QZQ2

ID Q9QZQ2

PRELIMINARY; PRT; 32 AA.

AC Q9QZQ2;

DT 01-MAY-2000 (TREMBLrel. 13, Created)
 DT 01-MAY-2000 (TREMBLrel. 13, Last sequence update)
 DT 01-OCT-2002 (TREMBLrel. 22, Last annotation update)
 DE Neurotensin receptor (Fragment).
 GN NTR OR NTR1.
 OS Mus musculus (Mouse).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
 OX NCBI_TaxID=10090;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=129;
 RX MEDLINE=99445567; PubMed=10514493;
 RA Tavares D., Tully K., Dobner P.R.;
 RT "Sequences required for induction of neurotensin receptor gene
 RT expression during neuronal differentiation of NIE-115 neuroblastoma
 RT cells.";
 RL J. Biol. Chem. 274:30066-30079(1999).
 DR EMBL; AF172326; AAD51806.1; -.
 DR MGD; MGI:97386; Ntrr.
 KW Receptor.
 FT NON_TER 32
 SQ SEQUENCE 32 AA; 3447 MW; 7F7EA4FA2CCF2EFB CRC64;
 Query Match 11.8%; Score 4; DB 11; Length 32;
 Best Local Similarity 100.0%; Pred. No. 3.3e+03;
 Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 14 HLNS 17
 DB 2 HLNS 5
 RESULT 21
 ID Q9HSZ0 PRELIMINARY; PRT; 32 AA.
 AC Q9HSZ0;
 DT 01-MAR-2001 (TREMBLrel. 16, Created)
 DT 01-MAR-2001 (TREMBLrel. 16, Last sequence update)
 DT 01-MAR-2001 (TREMBLrel. 16, Last annotation update)
 DE Vng0019h.
 GN VNG0019H.
 OS Halobacterium sp. (strain NRC-1).
 OC Archaea; Euryarchaeota; Halobacteria; Halobacteriales;
 OC Halobacteriaceae; Halobacterium.
 OX NCBI_TaxID=64091;
 RN [1]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=20504483; PubMed=11016950;
 RA Ng W.V., Kennedy S.P., Mahairas G.G., Bergquist B., Pan M.,
 RA Shukla H.D., Lasky S.R., Baliga N.S., Thorsson V., Sbrogna J.,
 RA Swartzell S., Weir D., Hall J., Dahl T.A., Welti R., Goo Y.A.,
 RA Leitbauer B., Keller K., Cruz R., Danson M.J., Hough D.W.,
 RA Maddocks D.G., Jablonski P.E., Krebs M.P., Angwine C.M., Dale H.,
 RA Isenbarger T.A., Peck R.F., Pohlschroder M., Spudich J.L., Jung K.-H.,
 RA Alam M., Freitas T., Hou S., Daniels C.J., Dennis P.P., Omer A.D.,
 RA Ebhardt H., Lowe T.M., Liang P., Riley M., Hood L., Dassarma S.;

| | |
|--|---|
| RT | "Genome sequence of Halobacterium species NRC-1." |
| RT | Proc. Natl. Acad. Sci. U.S.A. 97:12176-12181(2000). |
| DR | EMBL; AF004971; AAG18659.1; -. |
| KM | Complete proteome. |
| SEQ | SEQUENCE 32 AA; 3758 MW; 22D669246C97A817 CRC64; |
| QY | 27 KLD 30 |
| DB | 13 KLD 16 |
| <p>Query Match 11.8%; Score 4; DB 17; Length 32; Best Local Similarity 100.0%; Pred. No. 3.3e+03; Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;</p> | |
| RESULT 22 | |
| ID | Q95SD4 |
| AC | Q95SD4; |
| DT | 01-DEC-2001 (TrEMBLrel. 19, Created) |
| DT | 01-DEC-2001 (TrEMBLrel. 19, Last sequence update) |
| DT | 01-OCT-2002 (TrEMBLrel. 22, Last annotation update) |
| DE | GM02640p. |
| GN | BCDNA:GM02640. |
| OS | Drosophila melanogaster (Fruit fly). |
| OC | Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota; |
| OC | Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha; |
| OC | Ephydroidea; Drosophilidae; Drosophila. |
| OX | NCBI_TaxID=7227; |
| RN | [1] |
| RP | SEQUENCE FROM N.A. |
| RA | Stapleton M., Brokstein P., Hong L., Agbayani A., Carlson J., |
| RA | Champe M., Chavez C., Dorsett V., Farfan D., Frise E., George R., |
| RA | Gonzalez M., Guarin H., Li P., Liao G., Miranda A., Mungall C.J., |
| RA | Numoo J., Pacleb J., Paragas V., Park S., Phouanavong S., Wan K., |
| RA | Yu C., Lewis S.E., Rubin G.M., Celniker S., |
| RL | Submitted (OCT-2001) to the EMBL/GenBank/DBJ databases. |
| DR | EMBL; AY060847; AAL28395.1; -. |
| DR | flyBase; FBgn0047288; BCDNA:GM02640. |
| SEQ | SEQUENCE 33 AA; 3720 MW; 9C3FC1AEC9FBB4A7 CRC64; |
| QY | 26 KLD 29 |
| DB | 21 KLD 24 |
| RESULT 23 | |
| ID | Q9PKX3 |
| AC | Q9PKX3; |
| DT | 01-OCT-2000 (TrEMBLrel. 15, Created) |
| DT | 01-OCT-2000 (TrEMBLrel. 15, Last sequence update) |
| DT | 01-DEC-2001 (TrEMBLrel. 19, Last annotation update) |

Query Match 11.8%; Score 4; DB 2; Length 34;
 Best Local Similarity 100.0%; Pred. No. 3.5e+03;
 Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

DE Hypothetical protein TC0337.
 GN TC0337.
 OS Chlamydia muridarum.
 OC Bacteria; Chlamydiae; Chlamydiales; Chlamydiaceae; Chlamydia.
 OX NCBI_TaxID=83560;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=MOPN / Nigg;
 RX MEDLINE=20150255; PubMed=10684935;
 RA Read T.D., Brunham R.C., Shen C., Gill S.R., Heidelberg J.F.,
 RA White O., Hickey E.K., Peterson J., Utterback T., Berry K., Bass S.,
 RA Linher K., Weidman J., Khouri H., Craven B., Bowman C., Dodson R.,
 RA Gwin M., Nelson W., DeBoy R., Kolonay J., McClarty G., Salzberg S.L.,
 RA Eisen J., Fraser C.M.;
 RT "Genome sequences of Chlamydia trachomatis MOPN and Chlamydia
 RT pneumoniae AR39."
 RL Nucleic Acids Res. 28:1397-1406(2000).
 DR EMBL; AF002301; AAF39200.1; -.
 DR TIGR; TC0337; -.
 KW Hypothetical protein; Complete proteome.
 SQ SEQUENCE 33 AA; 4075 MW; 1E7C5AD9BA5371EC CRC64;

Query Match 11.8%; Score 4; DB 16; Length 33;
 Best Local Similarity 100.0%; Pred. No. 3.4e+03;
 Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

DE Hypothetical protein TC0337.
 GN TC0337.
 OS Chlamydia muridarum.
 OC Bacteria; Chlamydiae; Chlamydiales; Chlamydiaceae; Chlamydia.
 OX NCBI_TaxID=83560;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=MOPN / Nigg;
 RX MEDLINE=20150255; PubMed=10684935;
 RA Read T.D., Brunham R.C., Shen C., Gill S.R., Heidelberg J.F.,
 RA White O., Hickey E.K., Peterson J., Utterback T., Berry K., Bass S.,
 RA Linher K., Weidman J., Khouri H., Craven B., Bowman C., Dodson R.,
 RA Gwin M., Nelson W., DeBoy R., Kolonay J., McClarty G., Salzberg S.L.,
 RA Eisen J., Fraser C.M.;
 RT "Genome sequences of Chlamydia trachomatis MOPN and Chlamydia
 RT pneumoniae AR39."
 RL Nucleic Acids Res. 28:1397-1406(2000).
 DR EMBL; AF002301; AAF39200.1; -.
 DR TIGR; TC0337; -.
 KW Hypothetical protein; Complete proteome.
 SQ SEQUENCE 33 AA; 4075 MW; 1E7C5AD9BA5371EC CRC64;

Query Match 11.8%; Score 4; DB 2; Length 34;
 Best Local Similarity 100.0%; Pred. No. 3.5e+03;
 Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

DE Hypothetical protein TC0337.
 GN TC0337.
 OS Chlamydia muridarum.
 OC Bacteria; Chlamydiae; Chlamydiales; Chlamydiaceae; Chlamydia.
 OX NCBI_TaxID=813;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=L2 434B;
 RA Wang L., Steenburg S.D., Zheng Y., Larsen S.H.;
 RT "Gene identification of Chlamydia trachomatis by random DNA
 RT sequencing."
 RL Submitted (AUG-1998) to the EMBL/GenBank/DBJ databases.
 DR EMBL; AF087260; AAD04038.1; -.
 FT NON_TER 1
 FT NON_TER 34
 FT SEQUENCE 34 AA; 4186 MW; 3B38196393258A53 CRC64;

Query Match 11.8%; Score 4; DB 16; Length 33;
 Best Local Similarity 100.0%; Pred. No. 3.4e+03;
 Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

DE Hypothetical protein TC0337.
 GN TC0337.
 OS Chlamydia muridarum.
 OC Bacteria; Chlamydiae; Chlamydiales; Chlamydiaceae; Chlamydia.
 OX NCBI_TaxID=83560;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=MOPN / Nigg;
 RX MEDLINE=20150255; PubMed=10684935;
 RA Read T.D., Brunham R.C., Shen C., Gill S.R., Heidelberg J.F.,
 RA White O., Hickey E.K., Peterson J., Utterback T., Berry K., Bass S.,
 RA Linher K., Weidman J., Khouri H., Craven B., Bowman C., Dodson R.,
 RA Gwin M., Nelson W., DeBoy R., Kolonay J., McClarty G., Salzberg S.L.,
 RA Eisen J., Fraser C.M.;
 RT "Genome sequences of Chlamydia trachomatis MOPN and Chlamydia
 RT pneumoniae AR39."
 RL Nucleic Acids Res. 28:1397-1406(2000).
 DR EMBL; AF002301; AAF39200.1; -.
 DR TIGR; TC0337; -.
 KW Hypothetical protein; Complete proteome.
 SQ SEQUENCE 33 AA; 4075 MW; 1E7C5AD9BA5371EC CRC64;

QY 24 LRKK 27
DB 25 LRKK 28

RESULT 25

ID Q8GFK2 PRELIMINARY; PRT; 34 AA.
AC Q8GFK2;
DT 01-MAR-2003 (TREMBLrel. 23, Created)
DT 01-MAR-2003 (TREMBLrel. 23, Last sequence update)
DT 01-MAR-2003 (TREMBLrel. 23, Last annotation update)
DE ORF37.
OS Staphylococcus aureus.
OG plasmid EDINA plasmid.
OC Bacteria; Firmicutes; Bacillales; Staphylococcus.
OX NCBI_TaxID=1280;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=E-1;
RA Sugai M., Yamaguchi T., Hayashi T., Nakasone K., Takami H.;
RT "Complete nucleotide sequence of Staphylococcus aureus E-1 EDINA
plasmid.";
RL Submitted (JAN-2001) to the EMBL/GenBank/DBJ databases.
DR EMBL; AP003089; BAC54529.1; -.
KW plasmid.
SQ SEQUENCE 34 AA; 4138 MW; 88FBD773858BC6EE CRC64;

Query Match 11.8%; Score 4; DB 2; Length 34;

Best Local Similarity 100.0%; Pred. No. 3.5e+03;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 26 KKLQ 29
DB 6 KKLQ 9

RESULT 26

ID Q8C4P4 PRELIMINARY; PRT; 34 AA.
AC Q8C4P4;
DT 01-MAR-2003 (TREMBLrel. 23, Created)
DT 01-MAR-2003 (TREMBLrel. 23, Last sequence update)
DT 01-MAR-2003 (TREMBLrel. 23, Last annotation update)
DE Zinc finger homeodomain 4 (Fragment).
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=C57BL/6J; TISSUE=Head;
RX MEDLINE=22354683; PubMed=12466851;
RA The FANTOM Consortium,
RA the RIKEN Genome Exploration Research Group Phase I & II Team;
RT "Analysis of the mouse transcriptome based on functional annotation of

RT 60,770 full-length cDNAs.
 RL Nature 420:563-573 (2002).
 DR EMBL; AK081561; BAC38260.1; --
 FT NON_TER 1
 SQ SEQUENCE 34 AA; 3755 MW; EF41DCAF348467B0 CRC64;
 Query Match 11.8%; Score 4; DB 11; Length 34;
 Best Local Similarity 100.0%; Pred. No. 3.5e+03;
 Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 27 KKL 30
 DB 2 KKL 5

RESULT 27

ID Q90ZJ4 PRELIMINARY; PRT; 34 AA.
 AC Q90ZJ4;
 DT 01-DEC-2001 (TrEMBLrel. 19, Created)
 DT 01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
 DT 01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
 DE Platelet-derived growth factor A chain long form (Fragment).
 GN PDGF-A.
 OS Gallus gallus (Chicken).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Archosauria; Aves; Neognathae; Galliformes; Phasianidae; Phasianinae;
 OC Gallus.
 OX NCBI_TaxID=9031;
 RN [1]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=21363439; PubMed=11470524;
 RA Horiuchi H., Inoue T., Furusawa S., Matsuda H.;
 RT "Characterization and expression of three forms of cDNA encoding
 RT chicken platelet-derived growth factor-A chain."
 RL Gene 272:181-190 (2001).
 DR EMBL; AB031024; BAB62544.1; --
 FT NON_TER 1
 SQ SEQUENCE 34 AA; 3983 MW; FEF02F8A45B27DA5 CRC64;

Query Match 11.8%; Score 4; DB 13; Length 34;
 Best Local Similarity 100.0%; Pred. No. 3.5e+03;
 Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 25 RKL 28
 DB 28 RKL 31

RESULT 28

ID Q98FK5 PRELIMINARY; PRT; 34 AA.
 AC Q98FK5;
 DT 01-OCT-2001 (TrEMBLrel. 18, Created)
 DT 01-OCT-2001 (TrEMBLrel. 18, Last sequence update)
 DT 01-MAR-2002 (TrEMBLrel. 20, Last annotation update)
 DE Hypothetical protein msr3733.

Query Match 11.8%; Score 4; DB 4; Length 35;
Best Local Similarity 100.0%; Pred. No. 3.6e+03;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

GN MS3733.
OS Rhizobium loti (Mesorhizobium loti).
OC Bacteria; Proteobacteria; Alphaproteobacteria; Rhizobiales;
OC Phyllobacteriaceae; Mesorhizobium.
OX NCBI_TaxID=381;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=MAFF303099;
RX MEDLINE=21082930; PubMed=11214968;
RA Kaneko T., Nakamura Y., Sato S., Asamizu E., Kato T., Sasamoto S.,
Watanabe A., Idesawa K., Ishikawa A., Kawashima K., Kimura T.,
Kishida Y., Kiyokawa C., Kohara M., Matsumoto M., Matsumo A.,
Mochizuki Y., Nakayama S., Nakazaki N., Shimo S., Sugimoto M.,
Takeuchi C., Yamada M., Tabata S.;
RT "Complete genome structure of the nitrogen-fixing symbiotic bacterium
Mesorhizobium loti.";
RL DNA Res. 7:331-338(2000).
DR EMBL; AP003002; BAB50562.1; -
KW Hypothetical protein; Complete proteome.
SQ SEQUENCE 34 AA; 3804 MW; D6AAA82FECB590413 CRC64;

Query Match 11.8%; Score 4; DB 16; Length 34;
Best Local Similarity 100.0%; Pred. No. 3.5e+03;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 27 KLQD 30
DB 28 KLQD 31

ID Q15421 PRELIMINARY; PRT; 35 AA.
AC Q15421;
DT 01-NOV-1996 (TREMBLrel. 01, Created)
DT 01-NOV-1996 (TREMBLrel. 01, Last sequence update)
DT 01-NOV-1998 (TREMBLrel. 08, Last annotation update)
DE Stilian sarcoma associated virus (SSAV)-related pol region DNA
DE (Fragment).
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=87071681; PubMed=2431542;
RA Leib-Mosch C., Brack R., Werner T., Erle V., Hehlmann R.;
RT "Isolation of an SSAV-related endogenous sequence from Human DNA.";
RL Virology 155:666-677(1986).
DR EMBL; M14911; AAA36592.1; -
FT NON_TER 1
FT NON_TER 35
SQ SEQUENCE 35 AA; 3742 MW; 2F70B02EE0BC86DF CRC64;

QY 28 LQDV 31
DB 6 LQDV 9

RESULT 30

ID Q8V6J8 PRELIMINARY; PRT; 35 AA.
AC Q8V6J8;
DT 01-MAR-2002 (TREMBLrel. 20, Created)
DT 01-MAR-2002 (TREMBLrel. 20, Last sequence update)
DT 01-MAR-2002 (TREMBLrel. 20, Last annotation update)
DE Hypothetical 4.1 kDa protein.
OS Halovirus HF2.
OC Viruses; dsDNA viruses, no RNA stage; Caudovirales; Myoviridae.
RN [1]
RP SEQUENCE FROM N.A.
RA Tang S.-L., Fisher C., Ngui K., Nuttall S.D., Dyal-Smith M.L.;
RT "Sequence and transcription of halovirus HF2."
RL Submitted (JAN-2000) to the EMBL/GenBank/DBJ databases.
DR EMBL; AF222060; AAL55025.1; -.
KW Hypothetical protein.
SQ SEQUENCE 35 AA; 4115 MW; 2652C319622B9CE4 CRC64;

Query Match 11.8%; Score 4; DB 12; Length 35;
Best Local Similarity 100.0%; Pred. No. 3.6e+03;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 SVSE 4
DB 10 SVSE 13

RESULT 31

ID Q9KQG4 PRELIMINARY; PRT; 35 AA.
AC Q9KQG4;
DT 01-OCT-2000 (TREMBLrel. 15, Created)
DT 01-OCT-2000 (TREMBLrel. 15, Last sequence update)
DT 01-DEC-2001 (TREMBLrel. 19, Last annotation update)
DE Hypothetical protein VC2034.
GN VC2034.
OS Vibrio cholerae.
OC Bacteria; Proteobacteria; Gammaproteobacteria; Vibrionales;
OC Vibrionaceae; Vibrio.
OX NCBI_TaxID=666;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=E1 Tor N1691 / Serotype O1;
RX MEDLINE=20406833; PubMed=10952301;
RA Heidelberg J.F., Eisen J.A., Nelson W.C., Clayton R.A., Gwinn M.L.,
RA Dodson R.J., Haft D.H., Hickey E.K., Peterson J.D., Umayam L.A.,
RA Gill S.R., Nelson K.E., Read T.D., Tettelin H., Richardson D.,
RA Ermolaeva M.D., Vamathevan J., Bass S., Qin H., Dragoi I., Sellers P.,
RA McDonald L., Utterback T., Fleischmann R.D., Nierman W.C., White O.

RA Salzberg S.L., Smith H.O., Colwell R.R., Mekalanos J.J., Venter J.C.,

RA Fraser C.M.;

RT "DNA sequence of both chromosomes of the cholera pathogen *Vibrio*

RT cholerae.";

RT Nature 406:477-483 (2000).

DR EMBL; AF004278; AAF95182.1; -.

DR TIGR; VC2034; -.

KW Hypothetical protein; Complete proteome.

SEQUENCE 35 AA; 4181 MW; D185B6339A711D54 CRC64;

Query Match 11.8%; Score 4; DB 16; Length 35;

Best Local Similarity 100.0%; Pred. No. 3.6e+03;

Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 26 KKLQ 29

||||

DB 24 KKLQ 27

RESULT 32

Q8F102

ID Q8F102

PRELIMINARY; PRT; 35 AA.

AC Q8F102;

DT 01-MAR-2003 (TREMBLrel. 23, Created)

DT 01-MAR-2003 (TREMBLrel. 23, Last sequence update)

DT 01-MAR-2003 (TREMBLrel. 23, Last annotation update)

DE Hypothetical protein.

GN LA3339.

OS Leptospira interrogans.

OC Bacteria; Spirochaetales; Leptospiraceae; Leptospira.

OX NCBI_TaxID=173;

RN [1]

RP SEQUENCE FROM N.A.

RC STRAIN=56601 / Serogroup Icterohaemorrhagiae / Serovar lai;

RA Ren S.;

RL Submitted (MAR-2002) to the EMBL/GenBank/DBJ databases.

DR EMBL; AE011494; AAN50536.1; -.

KW Hypothetical protein; Complete proteome.

SEQUENCE 35 AA; 4253 MW; 0DDFEDFFB322E980B CRC64;

Query Match 11.8%; Score 4; DB 16; Length 35;

Best Local Similarity 100.0%; Pred. No. 3.6e+03;

Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 14 HLNS 17

||||

DB 3 HLNS 6

RESULT 33

Q53920

ID Q53920

PRELIMINARY; PRT; 36 AA.

AC Q53920;

DT 01-NOV-1996 (TREMBLrel. 01, Created)

DT 01-NOV-1996 (TREMBLrel. 01, Last sequence update)

DT 01-JUN-2002 (TREMBLrel. 21, Last annotation update)

DE OrfA protein (Fragment).

Query Match 11.8%; Score 4; DB 2; Length 36;
 Best Local Similarity 100.0%; Pred. No. 3.7e+03;
 Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

RESULT 34
 068941
 ID 068941 PRELIMINARY; PRT; 36 AA.
 AC 068941;
 DT 01-AUG-1998 (TREMBLrel. 07, Created)
 DT 01-AUG-1998 (TREMBLrel. 07, Last sequence update)
 DT 01-MAR-2002 (TREMBLrel. 20, Last annotation update)
 DE Dinitrogenase 3 beta subunit (Fragment).
 OS Rhodospirillum rubrum.
 OC Bacteria; Proteobacteria; Alphaproteobacteria; Rhodospirillales;
 OC Rhodospirillaceae; Rhodospirillum.
 OX NCBI_TaxID=1085;
 RN [1]
 RP SEQUENCE FROM N.A.
 RA Lovelless T.M., Bishop P.E.;
 RT "Identification of Genes Unique to Mo-Independent Nitrogenase Systems
 in Diverse Diazotrophs.";
 RL Submitted (APR-1998) to the EMBL/GenBank/DBJ databases.
 DR EMBL; AF058778; AAC14327.1; -
 DR InterPro; IPR000510; Oxred_nitrognasel.
 DR Pfam; PF00148; oxidored_nitro; 1.
 FT NON_TER 36
 SQ SEQUENCE 36 AA; 3957 MW; D94F46BCFPD437D97 CRC64;

Query Match 11.8%; Score 4; DB 2; Length 36;
 Best Local Similarity 100.0%; Pred. No. 3.7e+03;
 Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

ORFA.
 OS Streptomyces chrysomallus.
 OC Bacteria; Actinobacteria; Actinomycetales;
 OC Streptomycetaceae; Streptomycetaceae; Streptomyces.
 OX NCBI_TaxID=1899;
 RN [1]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=94341259; PubMed=8062824;
 RA Pahl A., Keller U.;
 RT "Streptomyces chrysomallus FKBP-33 is a novel immunophilin consisting
 of two FK506-binding domains with its gene transcriptionally coupled
 to the FKBP-12 gene.";
 RL EMBO J. 13:3472-3480(1994).
 DR EMBL; Z34523; CAA84281.1; -
 DR InterPro; IPR004347; DUF245.
 DR Pfam; PF03136; DUF245; 1.
 FT NON_TER 1
 SQ SEQUENCE 36 AA; 4121 MW; EBD470AAAF99A728E CRC64;

QY 24 LRKK 27
DB 5 LRKK 8

RESULT 35

ID Q8WXW8 PRELIMINARY; PRT; 36 AA.

AC Q8WXW8; DT 01-MAR-2002 (TrEMBLrel. 20, Created)

DT 01-MAR-2002 (TrEMBLrel. 20, Last sequence update)

DT 01-JUN-2002 (TrEMBLrel. 21, Last annotation update)

DE Urea transporter JK glycoprotein (Fragment).

GN JK.

OS Homo sapiens (Human).

OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

OC Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.

OX NCBI_TaxID=9606;

RN [1]

RP SEQUENCE FROM N.A.

RA Olsson M.L., Irshaid N.M., Eicher N.I., Poole J., Hustinx H.;

RT "Molecular Basis of the JK(a-b-) Phenotype in Non-Finnish European

RT Pedigrees.";

RL Br. J. Haematol. 0:0-0(2001).

DR EMBL; AF328890; AAL37474.1; -.

DR InterPro; IPR004937; Urea_transporter.

DR Pfam; PF03253; UT; 1.

FT NON_TER 1

SQ SEQUENCE 36 AA; 3989 MW; C3A6A964C2F41007 CRC64;

Query Match 11.8%; Score 4; DB 4; Length 36;

Best Local Similarity 100.0%; Pred. No. 3.7e+03;

Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 15 LNSM 18
DB 7 LNSM 10

RESULT 36

Q9SJ63

ID Q9SJ63 PRELIMINARY; PRT; 36 AA.

AC Q9SJ63;

DT 01-MAY-2000 (TrEMBLrel. 13, Created)

DT 01-MAY-2000 (TrEMBLrel. 13, Last sequence update)

DT 01-DEC-2001 (TrEMBLrel. 19, Last annotation update)

DE At2g35870 protein.

GN AT2G35870.

OS Arabidopsis thaliana (Mouse-ear cress).

OC Eukaryota; Viridiplantae; Streptophyta; Tracheophyta;

OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosidae;

OC eurosids II; Brassicales; Brassicaceae; Arabidopsids.

OX NCBI_TaxID=3702;

RN [1]

RP SEQUENCE FROM N.A.

RC STRAIN=cv. Columbia;

RX MEDLINE=20083487; PubMed=10617197;

Query Match 11.8%; Score 4; DB 10; Length 36;
Best Local Similarity 100.0%; Pred. No. 3.7e+03;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 26 KKLQ 29
DB 4 KKLQ 7

RESULT 37

Q9PXD1 ID Q9PXD1 PRELIMINARY; PRT; 36 AA.
AC Q9PXD1;
DT 01-MAY-2000 (TREMBLrel. 13, Created)
DT 01-MAY-2000 (TREMBLrel. 13, Last sequence update)
DT 01-DEC-2001 (TREMBLrel. 19, Last annotation update)
DE Genome polypeptide [Contains: envelope glycoprotein E2/NS1 (GP68)]
DE (Fragment).
OS Hepatitis C virus.
OC Viruses; ssRNA positive-strand viruses, no DNA stage; Flaviviridae;
OC Hepacivirus.
OX NCBI_TaxID=11103;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=96343121; PubMed=8750162;
RA Chayama K., Tsubota A., Arase Y., Saitoh S., Ikeda K., Matsumoto T.,
RA Hashimoto M., Kobayashi M., Kanda M., Morinaga T.;
RT "Genotype, slow decrease in virus titer during interferon treatment
RT and high degree of sequence variability of hypervariable region are
RT indicative of poor response to interferon treatment in patients with
RT chronic hepatitis type C."
RL J. Hepatol. 23:648-653(1995).
DR Interfero; IPR002531; HCV_NS1.
DR Pfam; PF01560; HCV_NS1; 1.
KM Coat protein; Envelope protein; Glycoprotein; Nonstructural protein;
KM Polypeptide; Transmembrane.
SQ SEQUENCE 36 AA; 3546 MW; 5BB7935A55048D34 CRC64;

Query Match 11.8%; Score 4; DB 12; Length 36;

RA Lin X., Kaul S., Rounsley S.D., Shea T.P., Benito M.-I., Town C.D.,
RA Fujii C.Y., Mason T.M., Bowman C.L., Barnstead M.E., Feldblum T.V.,
RA Buell C.R., Ketchum K.A., Lee J.J., Ronning C.M., Koo H., Moffat K.S.,
RA Cronin L.A., Shen M., VanAken S.B., Umayam L., Tallon L.J., Gill J.E.,
RA Adams M.D., Carrera A.J., Greasy T.H., Goodman H.M., Somerville C.R.,
RA Copenhaver G.P., Preuss D., Nierman W.C., White O., Eisen J.A.,
RA Salzberg S.L., Fraser C.M., Venter J.C.;
RT "Sequence and analysis of chromosome 2 of the plant Arabidopsis
RT thaliana."
RL Nature 402:761-768(1999).
RN [2]
RP SEQUENCE FROM N.A.
RC STRAIN=cv. Columbia;
RA Lin X.;
RL Submitted (MAR-2000) to the EMBL/GenBank/DBJ databases.
DR EMBL; AC007017; AAD21470.1; -.
SQ SEQUENCE 36 AA; 4358 MW; DC966779BBDB6B834 CRC64;

Best Local Similarity 100.0%; Pred. No. 3.7e+03; Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 5 IQLM 8
DB 33 IQLM 36

RESULT 38

ID Q91D77 PRELIMINARY; PRT; 36 AA.
AC Q91D77;

DT 01-DEC-2001 (TrEMBLrel. 19, Created)
DT 01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
DT 01-MAR-2003 (TrEMBLrel. 23, Last annotation update)
DE ORF2 hypothetical protein, isolate:HM0319 (Fragment).

OS TTV-like mini virus.
OC Viruses; ssDNA viruses; Circoviridae.

OX NCBI_TaxID=93678;
RN [1]

RP SEQUENCE FROM N.A.
RC STRAIN=HM0319;

RA Michitaka K., Matsubara H., Horike N., Kihana T., Yano M., Mori T.,
RA Onji M.;

RT "Existence of TT virus DNA and TTV-like mini virus DNA in infant cord
RT blood.";

RL Submitted (APR-2001) to the EMBL/GenBank/DBJ databases.
DR EMBL; AB059561; BAB69654.1; -

DR InterPro; IPR004118; TT_ORF2.
DR Pfam; PF02957; TT_ORF2; 1.

KW Hypothetical protein.
FT NON_TER 36

SQ SEQUENCE 36 AA; 4291 MW; 92145F475EA841F1 CRC64;

Query Match 11.8%; Score 4; DB 12; Length 36;
Best Local Similarity 100.0%; Pred. No. 3.7e+03;

Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 26 KKLQ 29
DB 14 KKLQ 17

RESULT 39

ID Q9YHT9 PRELIMINARY; PRT; 36 AA.
AC Q9YHT9;

DT 01-MAY-1999 (TrEMBLrel. 10, Created)
DT 01-MAY-1999 (TrEMBLrel. 10, Last sequence update)
DT 01-OCT-2002 (TrEMBLrel. 22, Last annotation update)
DE Synaposome-associated protein 25.2 (Fragment).

GN SNAP25B OR SNAP.
OS Brachydanio rerio (Zebrafish) (Danio rerio).

OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Actinopterygii; Neopterygii; Teleostei; Ostariophysi; Cypriniformes;
OC Cyprinidae; Danio.
OX NCBI_TaxID=7955;

RN [1]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=99057281; PubMed=9843147;
 RA Risinger C., Salaneck E., Soderberg C., Gates M., Postlethwait J.H.,
 RA Larhammar D.;
 RT "Cloning of two loci for synapse protein Snap25 in zebrafish:
 RT comparison of paralogous linkage groups suggests loss of one locus in
 RT the mammalian lineage.";
 RL J. Neurosci. Res. 54:563-573 (1998).
 DR EMBL; AF091596; AAC73006.1; -.
 DR ZFIN; ZDB-GENE-980526-392; snap25b.
 FT NON_TER 1
 FT NON_TER 36
 SQ SEQUENCE 36 AA; 4046 MW; E3434855F7BEC02F CRC64;
 Query Match 11.8%; Score 4; DB 13; Length 36;
 Best Local Similarity 100.0%; Pred. No. 3.7e+03;
 Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 19 ERVE 22
 DB 2 ERVE 5
 RESULT 40
 Q97S91
 ID Q97S91 PRELIMINARY; PRT; 36 AA.
 AC Q97S91;
 DT 01-OCT-2001 (TrEMBLrel. 18, Created)
 DT 01-OCT-2001 (TrEMBLrel. 18, Last sequence update)
 DT 01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
 DE Hypothetical protein SP0497.
 GN SP0497.
 OS Streptococcus pneumoniae.
 OC Bacteria; Firmicutes; Lactobacillales; Streptococcaceae;
 OC Streptococcus.
 OX NCBI_TaxID=1313;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=TIGR4;
 RX MEDLINE=21357209; PubMed=11463916;
 RA Tetelin H., Nelson K.E., Paulsen I.T., Eisen J.A., Read T.D.,
 RA Peterson S., Heidelberg J., DeBoy R.T., Haft D.H., Dodson R.J.,
 RA Durkin A.S., Gwinn M., Kolonay J.F., Nelson W.C., Peterson J.D.,
 RA Umayam L.A., White O., Salzberg S.L., Lewis M.R., Radune D.,
 RA Holtzapple E., Khouri H., Wolf A.M., Utterback T.R., Hansen C.L.,
 RA McDonald L.A., Feldblyum T.V., Angiuoli S., Dickinson T., Hickey E.K.,
 RA Holt I.E., Loftus B.J., Yang F., Smith H.O., Venter J.C.,
 RA Dougherty B.A., Morrison D.A., Hollingshead S.K., Fraser C.M.;
 RT "Complete genome sequence of a virulent isolate of Streptococcus
 RT pneumoniae.";
 RL Science 293:498-506 (2001).
 DR EMBL; AE007361; AAK74655.1; -.
 DR TIGR; SP0497; -.
 KW Hypothetical protein; Complete proteome.
 SQ SEQUENCE 36 AA; 4282 MW; 749D427D078ACA76 CRC64;

Query Match 11.8%; Score 4; DB 16; Length 36;
Best Local Similarity 100.0%; Pred. No. 3.7e+03;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 26 KKLQ 29
||||
DB 10 KKLQ 13

Search completed: January 14, 2004, 10:41:52
Job time : 27.4206 secs

OM protein - protein search, using sw model

Run on: January 14, 2004, 10:28:19 ; Search time 5.61371 Seconds
(without alignments)
284.822 Million cell updates/sec

Title: US-09-843-221A-163

Perfect score: 34

Sequence: 1 SVSEIQLMHNNKGKHLNLSMERVEWLRKKLQDVHNF 34

Scoring table: OLIGO

Gapop 60.0 , Gapext 60.0

Searched: 127863 seqs, 47026705 residues

Word size : 0

Total number of hits satisfying chosen parameters: 1319

Minimum DB seq length: 28
Maximum DB seq length: 40

Post-processing: Listing first 1000 summaries

Database : SwissProt_41:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

| Result | No. | Score | Match | Length | ID | Description |
|--------|-----|-------|-------|--------|------------|--------------------|
| 1 | 5 | 14.7 | 33 | 1 | FABI RHASA | P81175 rhamdia sap |
| 2 | 4 | 11.8 | 29 | 1 | DMD RAT | P11530 rattus norv |
| 3 | 4 | 11.8 | 30 | 1 | PCG3_PACGO | P82416 pachycondyl |
| 4 | 4 | 11.8 | 39 | 1 | PSBY_SYNY3 | P73676 synechocyst |
| 5 | 4 | 11.8 | 39 | 1 | SRIC_SARPE | P08377 sarcophaga |
| 6 | 3 | 8.8 | 28 | 1 | CH60_MYCSM | P80673 mycobacteri |
| 7 | 3 | 8.8 | 28 | 1 | COXB_SOLTU | P80499 solanum tub |
| 8 | 3 | 8.8 | 28 | 1 | GUN_SCHCO | P81190 schizophyll |
| 9 | 3 | 8.8 | 28 | 1 | OMPA_YERPS | P38399 yersinia ps |
| 10 | 3 | 8.8 | 28 | 1 | PA2C_PSEPO | P20260 pseudochis |
| 11 | 3 | 8.8 | 28 | 1 | SCX2_BUTSI | P15230 buthus sind |
| 12 | 3 | 8.8 | 28 | 1 | SLP1_LEIQH | P80669 leirus qui |
| 13 | 3 | 8.8 | 28 | 1 | VIP_ALIMI | P48142 alligator m |
| 14 | 3 | 8.8 | 28 | 1 | VIP_RANRI | P81016 rana ridibu |
| 15 | 3 | 8.8 | 28 | 1 | VIP_SHEEP | P04565 ovis aries |
| 16 | 3 | 8.8 | 29 | 1 | CXOC_CONMA | P37300 conus magus |
| 17 | 3 | 8.8 | 29 | 1 | GATA_ALIMI | P47215 alligator m |

P47214 amia calva
P30802 gallus galli
P47213 oncorhynchus
P47216 rana ridibunda
P31234 ovis aries
P31297 chinchilla
P19371 desulfovibrio
P80267 solanum tuberosum
P82417 pachycondyla
P093639 methanosaeta
P80740 olea europaea
P81834 spinacia oleracea
P81079 desulfovibrio
P80279 phyllomedusa
P28733 bacteroides
P41521 anguilla anguilla
P11726 aeromonas hydrophila
P82415 pachycondyla
P83476 thrixopelma
P82037 uperoletia
P82038 uperoletia
Q04238 equisetum
P051473 borrelia burgdorferi
P046201 drosophila
P14661 sus scrofa
P56708 conus marmoreus
P82372 diptera
P15872 triticum aestivum
P81052 leuconostoc
Q53017 buchnera aphidivora
P41124 photorhabdus luminescens
P19877 homo sapiens
Q9bbr4 lotus japonicus
P12179 marchantia
Q9mun4 mesostigma
Q9tky9 nephroselmis
Q9cqd6 mus musculus
P42532 oryctolagus
P051762 borrelia burgdorferi
P28487 drosophila
P01264 oncorhynchus
P01265 oncorhynchus
P01262 anguilla japonica
P080296 bacteriophage phi12
P81078 desulfovibrio
P02343 synecdochystis
P55224 salmonella
P10293 cucurbita pepo
P07853 cucurbita maxima
P02875 dolichos axillaris
P07849 guillardia theta
P13064 desulfovibrio
P19589 pisum sativum
P49516 odontella
Q8s189 euglena steenbergii
Q8s187 euglena viridis
P39247 bacteriophage phi12

GAL1 AMICA
GAL1 CHICK
GAL1 ONCMY
GAL1 RANRI
GAL1 SHEEP
GAL1 CHIBR
GLUC CHIBR
IPYR DESVH
NUO1 SOLTU
PCG4 PACGO
RS7 METTE
SODC OLEEU
TL16 SPIOL
CY35 DESAC
DMS3 PHYSA
FTN BACFR
GLUM ANGAN
OTCC AERPU
PCG2 PACGO
TX2 THRP
UP61 UPEIN
UP62 UPEIN
VAA2 EQUAR
Y523 BORBU
A98A DEOME
CEC1 PIC
CXMA CONMR
DIUX DIPPU
H13 WHEAT
LCCB LEUME
LPL BUCRP
MALK PHOJU
NAP4 HUMAN
PETL LOTJA
PETL MARPO
PETL MESVI
PETL NEPOL
SARL MOUSE
SARL RABIT
Y822 BORBU
ADHR DROYA
CAT2 ONCKE
CAT3 ONCKI
CAT ANGJA
COA2 BPIFI
CY31 DESAC
DBH SYN1
RF21 SALEBN
ITR3 CUCPE
ITR4 CUCMA
LEC DOIAK
PETM GUITH
PHSS DESBN
PSBQ PEA
PSBT ODOI
PSBZ EUGST
PSBZ EUGVI
Y160 BPT4

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|-----|---|-----|----|---|--------------------|
| 75 | 3 | 8.8 | 32 | 1 | YCPG_MASIA |
| 76 | 3 | 8.8 | 33 | 1 | GLU2_ORENI |
| 77 | 3 | 8.8 | 33 | 1 | T1F_PARTE |
| 78 | 3 | 8.8 | 33 | 1 | YC12_EUGGR |
| 79 | 3 | 8.8 | 34 | 1 | DMS1_PHYSA |
| 80 | 3 | 8.8 | 34 | 1 | DMS2_PHYSA |
| 81 | 3 | 8.8 | 34 | 1 | GAST_CAPHI |
| 82 | 3 | 8.8 | 34 | 1 | GUNI_SCLSC |
| 83 | 3 | 8.8 | 34 | 1 | TX1_SCOGR |
| 84 | 3 | 8.8 | 35 | 1 | CECA_AEDAL |
| 85 | 3 | 8.8 | 35 | 1 | COPA_CANFA |
| 86 | 3 | 8.8 | 35 | 1 | CP12_PIG |
| 87 | 3 | 8.8 | 35 | 1 | GP58_BPSPI |
| 88 | 3 | 8.8 | 35 | 1 | HCYA_CHEDE |
| 89 | 3 | 8.8 | 35 | 1 | LECI_CYTSE |
| 90 | 3 | 8.8 | 35 | 1 | LEC3_ULFEU |
| 91 | 3 | 8.8 | 35 | 1 | PBP_ORGPS |
| 92 | 3 | 8.8 | 35 | 1 | PETG_CVACA |
| 93 | 3 | 8.8 | 35 | 1 | PSBT_MARPO |
| 94 | 3 | 8.8 | 35 | 1 | RL15_SYNP7 |
| 95 | 3 | 8.8 | 35 | 1 | SCCK_TITSE |
| 96 | 3 | 8.8 | 35 | 1 | SCX1_BUTSI |
| 97 | 3 | 8.8 | 35 | 1 | TMTX_MESTA |
| 98 | 3 | 8.8 | 35 | 1 | TX1_GRASP |
| 99 | 3 | 8.8 | 35 | 1 | TX1_THRPR |
| 100 | 3 | 8.8 | 35 | 1 | TX2_GRASP |
| 101 | 3 | 8.8 | 35 | 1 | VORB_METTM |
| 102 | 3 | 8.8 | 35 | 1 | Y210_HAEIN |
| 103 | 3 | 8.8 | 35 | 1 | YRKM_BACSU |
| 104 | 3 | 8.8 | 36 | 1 | ELH_THETS |
| 105 | 3 | 8.8 | 36 | 1 | NPF_ARTTR |
| 106 | 3 | 8.8 | 36 | 1 | OSTS_YEAST |
| 107 | 3 | 8.8 | 36 | 1 | PETM_SYNY3 |
| 108 | 3 | 8.8 | 36 | 1 | R18A_BOVIN |
| 109 | 3 | 8.8 | 36 | 1 | RET4_CHICK |
| 110 | 3 | 8.8 | 36 | 1 | RL6_HALCU |
| 111 | 3 | 8.8 | 36 | 1 | Y260_BACHD |
| 112 | 3 | 8.8 | 36 | 1 | Y609_ARCFU |
| 113 | 3 | 8.8 | 37 | 1 | DIVI_TENMO |
| 114 | 3 | 8.8 | 37 | 1 | LCONM_IACIA |
| 115 | 3 | 8.8 | 37 | 1 | PIP7_BOVIN |
| 116 | 3 | 8.8 | 37 | 1 | RK36_ODOSI |
| 117 | 3 | 8.8 | 37 | 1 | RL36_BACSU |
| 118 | 3 | 8.8 | 37 | 1 | RL36_CLOAB |
| 119 | 3 | 8.8 | 37 | 1 | RL36_LISMO |
| 120 | 3 | 8.8 | 37 | 1 | RL36_PASMU |
| 121 | 3 | 8.8 | 37 | 1 | RL36_STYAM |
| 122 | 3 | 8.8 | 37 | 1 | SCK1_MESTA |
| 123 | 3 | 8.8 | 37 | 1 | VGJ_BPPHX |
| 124 | 3 | 8.8 | 37 | 1 | Y63_BPT3 |
| 125 | 3 | 8.8 | 38 | 1 | CPRP_CANPG |
| 126 | 3 | 8.8 | 38 | 1 | NLT1_VITSX |
| 127 | 3 | 8.8 | 38 | 1 | NLT2_VITSX |
| 128 | 3 | 8.8 | 38 | 1 | OBP2_HYSCR |
| 129 | 3 | 8.8 | 38 | 1 | PYSA_METBA |
| 130 | 3 | 8.8 | 38 | 1 | RL36_CHLTE |
| 131 | 3 | 8.8 | 38 | 1 | RL36_ECOLI |
| 75 | 3 | 8.8 | 32 | 1 | P29735_mastigoclad |
| 76 | 3 | 8.8 | 33 | 1 | P81027_oreochromis |
| 77 | 3 | 8.8 | 33 | 1 | Q27172_paramectium |
| 78 | 3 | 8.8 | 33 | 1 | P31559_euglena gra |
| 79 | 3 | 8.8 | 34 | 1 | P24302_phyllomedus |
| 80 | 3 | 8.8 | 34 | 1 | P80278_phyllomedus |
| 81 | 3 | 8.8 | 34 | 1 | P04564_capra hircu |
| 82 | 3 | 8.8 | 34 | 1 | P21833_sclerotinia |
| 83 | 3 | 8.8 | 34 | 1 | P56855_scodra gris |
| 84 | 3 | 8.8 | 35 | 1 | P81417_aedes albop |
| 85 | 3 | 8.8 | 35 | 1 | P40765_canis famli |
| 86 | 3 | 8.8 | 35 | 1 | P80736_sus scrofa |
| 87 | 3 | 8.8 | 35 | 1 | O48412_bacterioph |
| 88 | 3 | 8.8 | 35 | 1 | P83173_cherax dest |
| 89 | 3 | 8.8 | 35 | 1 | P22970_cytisus ses |
| 90 | 3 | 8.8 | 35 | 1 | P23032_ulex europe |
| 91 | 3 | 8.8 | 35 | 1 | P34178_oryzia pseu |
| 92 | 3 | 8.8 | 35 | 1 | Q9T1q9_cyanidium c |
| 93 | 3 | 8.8 | 35 | 1 | P12182_marchantia |
| 94 | 3 | 8.8 | 35 | 1 | P31160_synochococc |
| 95 | 3 | 8.8 | 35 | 1 | P56219_titius serr |
| 96 | 3 | 8.8 | 35 | 1 | P15229_buthus sind |
| 97 | 3 | 8.8 | 35 | 1 | Q9bn12_mesobuthus |
| 98 | 3 | 8.8 | 35 | 1 | P56852_grammostola |
| 99 | 3 | 8.8 | 35 | 1 | P83480_thrixopelma |
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| 101 | 3 | 8.8 | 35 | 1 | P80908_methanobact |
| 102 | 3 | 8.8 | 35 | 1 | P43964_haemophilus |
| 103 | 3 | 8.8 | 35 | 1 | P54440_bacillus su |
| 104 | 3 | 8.8 | 36 | 1 | P80594_theromyzon |
| 105 | 3 | 8.8 | 36 | 1 | P41334_artioposthi |
| 106 | 3 | 8.8 | 36 | 1 | Q99380_saccharomyc |
| 107 | 3 | 8.8 | 36 | 1 | P74810_synochocyst |
| 108 | 3 | 8.8 | 36 | 1 | P82919_bos taurus |
| 109 | 3 | 8.8 | 36 | 1 | P30370_gallus gall |
| 110 | 3 | 8.8 | 36 | 1 | P05968_halobacteri |
| 111 | 3 | 8.8 | 36 | 1 | Q9kg53_bacillus ha |
| 112 | 3 | 8.8 | 36 | 1 | Q29646_archaeoglob |
| 113 | 3 | 8.8 | 37 | 1 | P56618_tenebrio mo |
| 114 | 3 | 8.8 | 37 | 1 | P83002_lactococcus |
| 115 | 3 | 8.8 | 37 | 1 | P21671_bos taurus |
| 116 | 3 | 8.8 | 37 | 1 | P49568_odontella s |
| 117 | 3 | 8.8 | 37 | 1 | P20278_bacillus su |
| 118 | 3 | 8.8 | 37 | 1 | Q97ek2_clostridium |
| 119 | 3 | 8.8 | 37 | 1 | Q927n0_listeria mo |
| 120 | 3 | 8.8 | 37 | 1 | P57942_pasteurella |
| 121 | 3 | 8.8 | 37 | 1 | Q99s42_staphylococ |
| 122 | 3 | 8.8 | 37 | 1 | P24663_mesobuthus |
| 123 | 3 | 8.8 | 37 | 1 | P03651_bacterioph |
| 124 | 3 | 8.8 | 37 | 1 | P20328_bacterioph |
| 125 | 3 | 8.8 | 38 | 1 | P81033_cancer pagu |
| 126 | 3 | 8.8 | 38 | 1 | P80275_vitis sp. (|
| 127 | 3 | 8.8 | 38 | 1 | P33556_vitis sp. (|
| 128 | 3 | 8.8 | 38 | 1 | P81648_hystrix cri |
| 129 | 3 | 8.8 | 38 | 1 | P80521_methanosarc |
| 130 | 3 | 8.8 | 38 | 1 | Q8kaj4_chlorobium |
| 131 | 3 | 8.8 | 38 | 1 | P21194_escherichia |

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| Q9hwt6 | pseudomonas | 38 | 1 | RT36 | PSEAE | 3 | 8.8 | 132 |
| Q9x1i6 | thermotoga | 38 | 1 | RT36 | THEMA | 3 | 8.8 | 133 |
| Q8zj91 | yersinia pe | 38 | 1 | RL36 | YERPE | 3 | 8.8 | 134 |
| P49168 | pinus conto | 38 | 1 | RL12 | PINCO | 3 | 8.8 | 135 |
| P55966 | leiturus qui | 38 | 1 | SCX8 | LEIQH | 3 | 8.8 | 136 |
| P43944 | haemophilus | 38 | 1 | Y114 | HAEIN | 3 | 8.8 | 137 |
| O28340 | archaeoglob | 38 | 1 | YJ39 | ARCFU | 3 | 8.8 | 138 |
| P83403 | glossina mo | 39 | 1 | CEC | GLOMR | 3 | 8.8 | 139 |
| P01195 | balaenopter | 39 | 1 | COLI | BALPH | 3 | 8.8 | 140 |
| P06297 | oryctolagus | 39 | 1 | COLI | RABIT | 3 | 8.8 | 141 |
| P01197 | squalus aca | 39 | 1 | COLI | SQUAC | 3 | 8.8 | 142 |
| P01196 | struthio ca | 39 | 1 | COLI | STRCA | 3 | 8.8 | 143 |
| P20394 | heloderma h | 39 | 1 | EXE3 | HELHO | 3 | 8.8 | 144 |
| P80349 | rattus norv | 39 | 1 | FUC3 | RAT | 3 | 8.8 | 145 |
| P81000 | spirulina s | 39 | 1 | GVPC | SPICC | 3 | 8.8 | 146 |
| P55897 | bufo bufo g | 39 | 1 | H2A | BUFFG | 3 | 8.8 | 147 |
| P36961 | lactococcus | 39 | 1 | LCGA | LACLA | 3 | 8.8 | 148 |
| P51197 | porphyra pu | 39 | 1 | PSBX | PORPU | 3 | 8.8 | 149 |
| P82009 | canis fami1 | 39 | 1 | SC62 | CANFA | 3 | 8.8 | 150 |
| P81188 | trachemys s | 40 | 1 | ALB1 | TRASG | 3 | 8.8 | 151 |
| P30946 | oryctolagus | 40 | 1 | HS9A | RABIT | 3 | 8.8 | 152 |
| P35141 | staphylococ | 40 | 1 | KAD | STACA | 3 | 8.8 | 153 |
| O31840 | bacillus su | 40 | 1 | PHRK | BACSU | 3 | 8.8 | 154 |
| P18189 | bacillus li | 40 | 1 | PRE | BACLI | 3 | 8.8 | 155 |
| P51416 | pisum sativ | 40 | 1 | RK33 | PEA | 3 | 8.8 | 156 |
| P27328 | lily sympto | 40 | 1 | RRPO | LSV | 3 | 8.8 | 157 |
| P01144 | phyllomedus | 40 | 1 | SAUV | PHYSA | 3 | 8.8 | 158 |
| P18312 | sarcophaga | 40 | 1 | SR1D | SARPE | 3 | 8.8 | 159 |
| P56531 | meleagris g | 40 | 1 | VIT | MEIGA | 3 | 8.8 | 160 |
| P32012 | streptomyce | 40 | 1 | YDRB | STRPE | 3 | 8.8 | 161 |
| P82611 | candida alb | 28 | 1 | ACON | CANAL | 2 | 5.9 | 162 |
| P33047 | oryctolagus | 28 | 1 | APC1 | RABIT | 2 | 5.9 | 163 |
| P80008 | nocardia gl | 28 | 1 | ARYC | NOCGL | 2 | 5.9 | 164 |
| P31722 | rattus norv | 28 | 1 | C1QC | RAT | 2 | 5.9 | 165 |
| P80568 | bacillus ce | 28 | 1 | ETX2 | BACCE | 2 | 5.9 | 166 |
| P02673 | canis fami1 | 28 | 1 | FIBA | CANFA | 2 | 5.9 | 167 |
| P21988 | treponema p | 28 | 1 | FLA1 | TREPH | 2 | 5.9 | 168 |
| P02865 | trititum mo | 28 | 1 | GDO | TRIMO | 2 | 5.9 | 169 |
| P31886 | alligator m | 28 | 1 | GRP | ALIMI | 2 | 5.9 | 170 |
| P20137 | gallus gall | 28 | 1 | GTS5 | CHICK | 2 | 5.9 | 171 |
| P80999 | oscillator | 28 | 1 | GVPC | OSGAG | 2 | 5.9 | 172 |
| P02864 | hordeum spo | 28 | 1 | HORC | HORSP | 2 | 5.9 | 173 |
| P82475 | vipera lebe | 28 | 1 | ICPF | VIPLE | 2 | 5.9 | 174 |
| P10296 | momordica c | 28 | 1 | IEL1 | MOMCH | 2 | 5.9 | 175 |
| P80911 | methanobact | 28 | 1 | IORB | METTM | 2 | 5.9 | 176 |
| P10295 | momordica c | 28 | 1 | ITR2 | MOMCH | 2 | 5.9 | 177 |
| P35628 | luffa cylin | 28 | 1 | ITR3 | LUFFCY | 2 | 5.9 | 178 |
| P30709 | momordica c | 28 | 1 | ITRA | MOMCH | 2 | 5.9 | 179 |
| P36230 | iris hollan | 28 | 1 | LECA | IRIHO | 2 | 5.9 | 180 |
| P22183 | escherichia | 28 | 1 | LPFS | ECOLI | 2 | 5.9 | 181 |
| P09149 | escherichia | 28 | 1 | LPL | ECOLI | 2 | 5.9 | 182 |
| Q8z9h9 | salmonella | 28 | 1 | LPL | SALTI | 2 | 5.9 | 183 |
| Q8z9h9 | salmonella | 28 | 1 | LPL | SALTY | 2 | 5.9 | 184 |
| P03062 | salmonella | 28 | 1 | LPW | SERMA | 2 | 5.9 | 185 |
| P03055 | serratia ma | 28 | 1 | MAA1 | RAT | 2 | 5.9 | 186 |
| P57113 | rattus norv | 28 | 1 | MCDP | MEGPE | 2 | 5.9 | 187 |
| P04567 | megabombus | 28 | 1 | NLT2 | WHEAT | 2 | 5.9 | 188 |
| P39085 | trititum ae | | | | | | | |

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|-----|---|-----|----|---|------------|--------|-------------|
| 189 | 2 | 5.9 | 28 | 1 | NXL1_BOUAN | P34074 | boulengerin |
| 190 | 2 | 5.9 | 28 | 1 | OBP1_HYSCR | P81647 | hystrix cri |
| 191 | 2 | 5.9 | 28 | 1 | ORND_PLAOR | P25513 | placobdella |
| 192 | 2 | 5.9 | 28 | 1 | OST1_CHICK | P80896 | gallus gall |
| 193 | 2 | 5.9 | 28 | 1 | PA22_MICNI | P21791 | micrurus ni |
| 194 | 2 | 5.9 | 28 | 1 | PA23_TRIST | P82894 | trimeresuru |
| 195 | 2 | 5.9 | 28 | 1 | PETL_CYAPA | P48102 | cyanophora |
| 196 | 2 | 5.9 | 28 | 1 | PHR_METTM | P58818 | methanobact |
| 197 | 2 | 5.9 | 28 | 1 | PHYB_ASPII | P81440 | aspergillus |
| 198 | 2 | 5.9 | 28 | 1 | PP71_HCMVT | P24429 | human cytom |
| 199 | 2 | 5.9 | 28 | 1 | PPOX_BOVIN | P56602 | bos taurus |
| 200 | 2 | 5.9 | 28 | 1 | RL5_HALCU | P05972 | halobacteri |
| 201 | 2 | 5.9 | 28 | 1 | RS19_PHYS1 | O66093 | phytoplasma |
| 202 | 2 | 5.9 | 28 | 1 | SCK2_ORTSC | P83244 | orthochirus |
| 203 | 2 | 5.9 | 28 | 1 | SMS2_ORENI | P81029 | oreochromis |
| 204 | 2 | 5.9 | 28 | 1 | TXO2_AGEAP | P15971 | agelenopsis |
| 205 | 2 | 5.9 | 28 | 1 | VG9_SPV4 | P11341 | spiroplasma |
| 206 | 2 | 5.9 | 28 | 1 | VIP_DIDMA | P39089 | didelphis m |
| 207 | 2 | 5.9 | 28 | 1 | VIP_SCYCA | P09685 | scyliorhinu |
| 208 | 2 | 5.9 | 28 | 1 | Y073_ARCFU | O30163 | archaeoglob |
| 209 | 2 | 5.9 | 28 | 1 | Y16P_BPT4 | P39248 | bacterioph |
| 210 | 2 | 5.9 | 28 | 1 | YA79_ARCFU | O29184 | archaeoglob |
| 211 | 2 | 5.9 | 29 | 1 | 12AH_CLOS4 | P21215 | clostridium |
| 212 | 2 | 5.9 | 29 | 1 | AL21_HORSE | P81216 | equus cabal |
| 213 | 2 | 5.9 | 29 | 1 | AMEL_RABIT | P12761 | oryctolagus |
| 214 | 2 | 5.9 | 29 | 1 | ATP9_PICPJ | Q06838 | pichia pijp |
| 215 | 2 | 5.9 | 29 | 1 | ATPA_BRYMA | P26965 | bryopsis ma |
| 216 | 2 | 5.9 | 29 | 1 | BR2D_RANES | P40840 | rana escule |
| 217 | 2 | 5.9 | 29 | 1 | BREE_RANES | P40841 | rana escule |
| 218 | 2 | 5.9 | 29 | 1 | CERB_CERCA | P36191 | ceratitis c |
| 219 | 2 | 5.9 | 29 | 1 | COA1_BPI22 | P15413 | bacterioph |
| 220 | 2 | 5.9 | 29 | 1 | COXJ_CANFA | Q9tr29 | canis famil |
| 221 | 2 | 5.9 | 29 | 1 | COXK_SHEEP | Q9tr28 | ovis aries |
| 222 | 2 | 5.9 | 29 | 1 | CU36_LOCFI | P11737 | locusta mig |
| 223 | 2 | 5.9 | 29 | 1 | CXD6_CONGL | Q9twm7 | conus glori |
| 224 | 2 | 5.9 | 29 | 1 | CXO7_CONGE | P05483 | conus geogr |
| 225 | 2 | 5.9 | 29 | 1 | CXOD_CONMA | Q26350 | conus magus |
| 226 | 2 | 5.9 | 29 | 1 | CXST_CONGE | P58844 | conus geogr |
| 227 | 2 | 5.9 | 29 | 1 | CYO4_VIOOD | P58436 | viola odora |
| 228 | 2 | 5.9 | 29 | 1 | DMS5_PHYSA | P80281 | phyllomedus |
| 229 | 2 | 5.9 | 29 | 1 | GLUC_ANAPL | P01276 | anas platyr |
| 230 | 2 | 5.9 | 29 | 1 | GLUC_CALMI | P13189 | callorhynch |
| 231 | 2 | 5.9 | 29 | 1 | GLUC_DIDMA | P18108 | didelphis m |
| 232 | 2 | 5.9 | 29 | 1 | GLUC_LAMFL | Q9prq9 | lampetra fl |
| 233 | 2 | 5.9 | 29 | 1 | GLUC_PLAFE | P23062 | platichthys |
| 234 | 2 | 5.9 | 29 | 1 | GLUC_RABIT | P25449 | oryctolagus |
| 235 | 2 | 5.9 | 29 | 1 | GLUC_TORMA | P09567 | torpedo mar |
| 236 | 2 | 5.9 | 29 | 1 | H2B2_ECHES | P13282 | echinus esc |
| 237 | 2 | 5.9 | 29 | 1 | HOXY_RHOOP | P22660 | rhodococcus |
| 238 | 2 | 5.9 | 29 | 1 | HRJ_BOTJA | P20416 | bothrops ja |
| 239 | 2 | 5.9 | 29 | 1 | HS98_NEUCR | P31540 | neurospora |
| 240 | 2 | 5.9 | 29 | 1 | ITH3_BOVIN | P56652 | bos taurus |
| 241 | 2 | 5.9 | 29 | 1 | ITR1_CUCMA | P01074 | cucurbita m |
| 242 | 2 | 5.9 | 29 | 1 | ITR1_LUFCY | P25849 | luffa cylin |
| 243 | 2 | 5.9 | 29 | 1 | ITR1_MOMRE | P17680 | momordica r |
| 244 | 2 | 5.9 | 29 | 1 | ITR2_BRYDI | P11968 | bryonia dio |
| 245 | 2 | 5.9 | 29 | 1 | ITR3_CYCPE | P83394 | cyclanthera |

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|-----|---|-----|----|---|-------------|--------|-------------|
| 246 | 2 | 5.9 | 29 | 1 | ITR4_CYCPE | P83395 | cyclanthera |
| 247 | 2 | 5.9 | 29 | 1 | ITR5_CYCPE | P83396 | cyclanthera |
| 248 | 2 | 5.9 | 29 | 1 | MDH_BURPS | P80536 | burkholderi |
| 249 | 2 | 5.9 | 29 | 1 | MULR_ECHML | P81798 | echis multi |
| 250 | 2 | 5.9 | 29 | 1 | PETN_ANASP | Q913p6 | anabaena sp |
| 251 | 2 | 5.9 | 29 | 1 | PETN_ARATH | P12178 | arabidopsis |
| 252 | 2 | 5.9 | 29 | 1 | PETN_CHAGL | Q8ma13 | chaetosphae |
| 253 | 2 | 5.9 | 29 | 1 | PETN_CYAPA | P48258 | cyanophora |
| 254 | 2 | 5.9 | 29 | 1 | PETN_GUIITH | O78498 | guillardia |
| 255 | 2 | 5.9 | 29 | 1 | PETN_MAIZE | Q33302 | zea mays (m |
| 256 | 2 | 5.9 | 29 | 1 | PETN_MARPO | P12177 | marchantia |
| 257 | 2 | 5.9 | 29 | 1 | PETN_MESVI | Q9mus4 | mesostigma |
| 258 | 2 | 5.9 | 29 | 1 | PETN_ODOSI | P49527 | odontella s |
| 259 | 2 | 5.9 | 29 | 1 | PETN_PINTH | P41611 | pinus thunb |
| 260 | 2 | 5.9 | 29 | 1 | PETN_PORPU | P51276 | porphyra pu |
| 261 | 2 | 5.9 | 29 | 1 | PETN_PSINU | Q8wi23 | psilotum nu |
| 262 | 2 | 5.9 | 29 | 1 | PETN_SYNEL | Q8dkn2 | synechococc |
| 263 | 2 | 5.9 | 29 | 1 | PETN_SYNY3 | P72717 | synechocyst |
| 264 | 2 | 5.9 | 29 | 1 | PK4_DICDI | P34103 | dictyosteli |
| 265 | 2 | 5.9 | 29 | 1 | PRO1_DACGL | P18689 | dactylis gl |
| 266 | 2 | 5.9 | 29 | 1 | PSAF_SYNP6 | P31083 | synechococc |
| 267 | 2 | 5.9 | 29 | 1 | PSAK_SPIOL | P14627 | spinacia ol |
| 268 | 2 | 5.9 | 29 | 1 | PSAX_SYNVU | P23320 | synechococc |
| 269 | 2 | 5.9 | 29 | 1 | PSBI_SYNVU | P12240 | synechococc |
| 270 | 2 | 5.9 | 29 | 1 | RL15_HALCU | P05971 | halobacteri |
| 271 | 2 | 5.9 | 29 | 1 | RL15_STRLI | P49975 | streptomyce |
| 272 | 2 | 5.9 | 29 | 1 | RP54_CLOKL | P38944 | clostridium |
| 273 | 2 | 5.9 | 29 | 1 | SCX1_ANDMA | P56215 | androctonus |
| 274 | 2 | 5.9 | 29 | 1 | SDHB_CLOPR | P80213 | clostridium |
| 275 | 2 | 5.9 | 29 | 1 | SLP2_LEIQH | P80670 | leiurus qui |
| 276 | 2 | 5.9 | 29 | 1 | SLP3_LEIQH | P80671 | leiurus qui |
| 277 | 2 | 5.9 | 29 | 1 | TAT_HV1Z3 | P12510 | human immun |
| 278 | 2 | 5.9 | 29 | 1 | TLP_ACTDE | P81370 | actinidia d |
| 279 | 2 | 5.9 | 29 | 1 | UN23_CLOPA | P81356 | clostridium |
| 280 | 2 | 5.9 | 29 | 1 | Y15_BPT7 | P03792 | bacterioph |
| 281 | 2 | 5.9 | 29 | 1 | Y51_BPT3 | P20326 | bacterioph |
| 282 | 2 | 5.9 | 29 | 1 | YCX4_ODOSI | P49830 | odontella s |
| 283 | 2 | 5.9 | 29 | 1 | YXCX_ODOSI | P49838 | odontella s |
| 284 | 2 | 5.9 | 30 | 1 | 2ENR_CLOTY | P11887 | clostridium |
| 285 | 2 | 5.9 | 30 | 1 | A1AT_CHIVI | P38026 | chinchilla |
| 286 | 2 | 5.9 | 30 | 1 | AATC_RABIT | P12343 | oryctolagus |
| 287 | 2 | 5.9 | 30 | 1 | AATM_RABIT | P12345 | oryctolagus |
| 288 | 2 | 5.9 | 30 | 1 | ACB1_DIGLA | P81624 | digitalis l |
| 289 | 2 | 5.9 | 30 | 1 | AMPT_BACST | P00728 | bacillus st |
| 290 | 2 | 5.9 | 30 | 1 | ANF_RANRI | P09196 | rana ridibu |
| 291 | 2 | 5.9 | 30 | 1 | CALM_LYTPI | P05935 | lytechinus |
| 292 | 2 | 5.9 | 30 | 1 | CBAL_BACST | P13722 | bacillus st |
| 293 | 2 | 5.9 | 30 | 1 | CH60_CLOPA | P81339 | clostridium |
| 294 | 2 | 5.9 | 30 | 1 | CIRA_CHAPA | P56871 | chassalia p |
| 295 | 2 | 5.9 | 30 | 1 | CLPA_PINPS | P81671 | pinus pinas |
| 296 | 2 | 5.9 | 30 | 1 | COAE_CORAM | P58101 | corynebacte |
| 297 | 2 | 5.9 | 30 | 1 | COXC_SOLTU | P80500 | solanum tub |
| 298 | 2 | 5.9 | 30 | 1 | CRG2_SCOWA | P19865 | scoliodon w |
| 299 | 2 | 5.9 | 30 | 1 | CX2A_CONBE | P58625 | conus betul |
| 300 | 2 | 5.9 | 30 | 1 | CX7A_CONTU | P58923 | conus tulip |
| 301 | 2 | 5.9 | 30 | 1 | CXEX_CONCN | P58928 | conus conso |
| 302 | 2 | 5.9 | 30 | 1 | CXK4_CONST | P58921 | conus stria |

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| 303 | 2 | 5.9 | 30 | 1 | CXOB_CONPE | P56713 | conus penna |
| 304 | 2 | 5.9 | 30 | 1 | CXVB_CONER | P58783 | conus ermin |
| 305 | 2 | 5.9 | 30 | 1 | CYO1_VIOOD | P82230 | viola odora |
| 306 | 2 | 5.9 | 30 | 1 | CYO5_VIOOD | P58437 | viola odora |
| 307 | 2 | 5.9 | 30 | 1 | CYO8_VIOOD | P58440 | viola odora |
| 308 | 2 | 5.9 | 30 | 1 | DEF2_MACMU | P82317 | macaca mula |
| 309 | 2 | 5.9 | 30 | 1 | DIDH_COMTE | P80702 | comamonas t |
| 310 | 2 | 5.9 | 30 | 1 | DIU2_HYLLI | P82015 | hyles linea |
| 311 | 2 | 5.9 | 30 | 1 | DIU2_MANSE | P24858 | manduca sex |
| 312 | 2 | 5.9 | 30 | 1 | END2_ONCKE | P01205 | oncorhynchu |
| 313 | 2 | 5.9 | 30 | 1 | FIBR_PANIN | P22775 | panulirus i |
| 314 | 2 | 5.9 | 30 | 1 | FMBB_BACNO | P17829 | bacteroides |
| 315 | 2 | 5.9 | 30 | 1 | HCY2_HOMAM | P82297 | homarus ame |
| 316 | 2 | 5.9 | 30 | 1 | HYPH_HYBPA | P58445 | hybanthus p |
| 317 | 2 | 5.9 | 30 | 1 | IHFB_RHILE | P80606 | rhizobium l |
| 318 | 2 | 5.9 | 30 | 1 | ITI1_LAGLE | P26771 | lagenaria l |
| 319 | 2 | 5.9 | 30 | 1 | ITR1_CITLA | P11969 | citrullus l |
| 320 | 2 | 5.9 | 30 | 1 | ITR1_MOMCH | P10294 | momordica c |
| 321 | 2 | 5.9 | 30 | 1 | ITR2_ECBEL | P12071 | ecballium e |
| 322 | 2 | 5.9 | 30 | 1 | ITR2_LUFCY | P25850 | luffa cylin |
| 323 | 2 | 5.9 | 30 | 1 | ITR3_CUCMC | P32041 | cucumis mel |
| 324 | 2 | 5.9 | 30 | 1 | ITR3_MOMCO | P82410 | momordica c |
| 325 | 2 | 5.9 | 30 | 1 | ITR4_CUCSA | P10292 | cucumis sat |
| 326 | 2 | 5.9 | 30 | 1 | ITR6_CYCPE | P83397 | cyclanthera |
| 327 | 2 | 5.9 | 30 | 1 | ITR7_CYCPE | P83398 | cyclanthera |
| 328 | 2 | 5.9 | 30 | 1 | KAB5_OLDAF | P58456 | oldenlandia |
| 329 | 2 | 5.9 | 30 | 1 | LAS1_PIG | P80171 | sus scrofa |
| 330 | 2 | 5.9 | 30 | 1 | LEAH_PHAVU | P81870 | phaseolus v |
| 331 | 2 | 5.9 | 30 | 1 | MDH_HELGE | P80037 | heliobacter |
| 332 | 2 | 5.9 | 30 | 1 | MMAL_DERMI | P16312 | dermatophag |
| 333 | 2 | 5.9 | 30 | 1 | NU5M_PISOC | P24999 | pisaster oc |
| 334 | 2 | 5.9 | 30 | 1 | NUO2_SOLTU | P80268 | solanum tub |
| 335 | 2 | 5.9 | 30 | 1 | P2CO_ARTSP | P37365 | arthrobacte |
| 336 | 2 | 5.9 | 30 | 1 | PCCA_MYXXA | P81185 | myxococcus |
| 337 | 2 | 5.9 | 30 | 1 | PCG1_PACGO | P82414 | pachycondyl |
| 338 | 2 | 5.9 | 30 | 1 | PCG5_PACGO | P82418 | pachycondyl |
| 339 | 2 | 5.9 | 30 | 1 | PETN_NEPOL | Q9tl01 | nephroselmi |
| 340 | 2 | 5.9 | 30 | 1 | PLF4_RABIT | P83470 | oryctolagus |
| 341 | 2 | 5.9 | 30 | 1 | PLMS_SQUAC | P82542 | squalus aca |
| 342 | 2 | 5.9 | 30 | 1 | PMGY_CANAL | P82612 | candida alb |
| 343 | 2 | 5.9 | 30 | 1 | PRT1_CLUPA | P02335 | clupea pall |
| 344 | 2 | 5.9 | 30 | 1 | PRT2_ONCMY | P02331 | oncorhynchu |
| 345 | 2 | 5.9 | 30 | 1 | PRT3_ONCMY | P02332 | oncorhynchu |
| 346 | 2 | 5.9 | 30 | 1 | PRT4_ONCMY | P02333 | oncorhynchu |
| 347 | 2 | 5.9 | 30 | 1 | PRTB_ONCMY | P12819 | oncorhynchu |
| 348 | 2 | 5.9 | 30 | 1 | PSAM_CYACA | Q9tlx5 | cyanidium c |
| 349 | 2 | 5.9 | 30 | 1 | PSAM_MESVI | Q9mus2 | mesostigma |
| 350 | 2 | 5.9 | 30 | 1 | PSAM_ODOSI | P49487 | odontella s |
| 351 | 2 | 5.9 | 30 | 1 | PSAM_PINTH | P41601 | pinus thunb |
| 352 | 2 | 5.9 | 30 | 1 | PSAM_PORPU | P51395 | porphyra pu |
| 353 | 2 | 5.9 | 30 | 1 | PYSD_METBA | P80524 | methanosarc |
| 354 | 2 | 5.9 | 30 | 1 | RIPS_MOMCO | P20655 | momordica c |
| 355 | 2 | 5.9 | 30 | 1 | RKGG_LEPKE | P21587 | lepidochely |
| 356 | 2 | 5.9 | 30 | 1 | RNP_ODOVI | P19640 | odocoileus |
| 357 | 2 | 5.9 | 30 | 1 | SCK2_TITSE | P08816 | tityus serr |
| 358 | 2 | 5.9 | 30 | 1 | SCX2_CENLI | P18927 | centruroides |
| 359 | 2 | 5.9 | 30 | 1 | SILU_RHIPU | P02885 | rhizomucor |

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| 360 | 2 | 5.9 | 30 | 1 | TAT_HV1ZH | P12512 | human immun |
| 361 | 2 | 5.9 | 30 | 1 | TL1X_SPIOL | P82537 | spinacia ol |
| 362 | 2 | 5.9 | 30 | 1 | TL29_SPIOL | P81833 | spinacia ol |
| 363 | 2 | 5.9 | 30 | 1 | TX2_HETVE | P58426 | heteropoda |
| 364 | 2 | 5.9 | 30 | 1 | UC35_MAIZE | P80641 | zea mays (m |
| 365 | 2 | 5.9 | 30 | 1 | UDDP_SULAC | P80143 | sulfolobus |
| 366 | 2 | 5.9 | 30 | 1 | URE1_ECOLI | Q03284 | escherichia |
| 367 | 2 | 5.9 | 30 | 1 | VAA1_EQUAR | Q04236 | equisetum a |
| 368 | 2 | 5.9 | 30 | 1 | VAA1_PSINU | Q04237 | psilotum nu |
| 369 | 2 | 5.9 | 30 | 1 | VAA2_PSINU | Q04239 | psilotum nu |
| 370 | 2 | 5.9 | 30 | 1 | VATN_BOVIN | P81134 | bos taurus |
| 371 | 2 | 5.9 | 30 | 1 | VG03_BPPF1 | P25137 | bacterioph |
| 372 | 2 | 5.9 | 30 | 1 | VPU_HV1SC | P05948 | human immun |
| 373 | 2 | 5.9 | 30 | 1 | VTTA_BPT3 | P20837 | bacterioph |
| 374 | 2 | 5.9 | 30 | 1 | Y161_TREPA | O83196 | treponema p |
| 375 | 2 | 5.9 | 30 | 1 | Y357_BORBU | O51332 | borrelia bu |
| 376 | 2 | 5.9 | 30 | 1 | Y425_BORBU | O51386 | borrelia bu |
| 377 | 2 | 5.9 | 30 | 1 | Y573_TREPA | O83583 | treponema p |
| 378 | 2 | 5.9 | 30 | 1 | Y932_TREPA | O83902 | treponema p |
| 379 | 2 | 5.9 | 30 | 1 | YCCB_ECOLI | P24244 | escherichia |
| 380 | 2 | 5.9 | 31 | 1 | BCAM_PIG | O19098 | sus scrofa |
| 381 | 2 | 5.9 | 31 | 1 | CIRB_CHAPA | P56879 | chassalia p |
| 382 | 2 | 5.9 | 31 | 1 | COG5_BOVIN | P83437 | bos taurus |
| 383 | 2 | 5.9 | 31 | 1 | COX4_NEUCR | P06809 | neurospora |
| 384 | 2 | 5.9 | 31 | 1 | CTRP_PENMO | P35002 | penaeus mon |
| 385 | 2 | 5.9 | 31 | 1 | CXD6_CONNI | P56710 | conus nigro |
| 386 | 2 | 5.9 | 31 | 1 | CXG6_CONTE | P58922 | conus texti |
| 387 | 2 | 5.9 | 31 | 1 | DEJP_DROME | P81160 | drosophila |
| 388 | 2 | 5.9 | 31 | 1 | EFTU_STRLU | P52390 | streptomyce |
| 389 | 2 | 5.9 | 31 | 1 | ENDE_CAMDR | P01203 | camelus dro |
| 390 | 2 | 5.9 | 31 | 1 | ER29_BOVIN | P81623 | bos taurus |
| 391 | 2 | 5.9 | 31 | 1 | ETFD_PARDE | P55932 | paracoccus |
| 392 | 2 | 5.9 | 31 | 1 | FIBB_CANFA | P02677 | canis famil |
| 393 | 2 | 5.9 | 31 | 1 | GP37_BPSP1 | O48393 | bacterioph |
| 394 | 2 | 5.9 | 31 | 1 | GT_SERMA | P22416 | serratia ma |
| 395 | 2 | 5.9 | 31 | 1 | HBA_MACEU | P81043 | macropus eu |
| 396 | 2 | 5.9 | 31 | 1 | HCY1_HOMAM | P82296 | homarus ame |
| 397 | 2 | 5.9 | 31 | 1 | HCY2_MAISQ | P82303 | maia squina |
| 398 | 2 | 5.9 | 31 | 1 | HEM2_PHAGO | P27687 | phascolopsi |
| 399 | 2 | 5.9 | 31 | 1 | LC70_LACPA | P80959 | lactobacill |
| 400 | 2 | 5.9 | 31 | 1 | LPRM_ECOLI | P10739 | escherichia |
| 401 | 2 | 5.9 | 31 | 1 | MDH_STRAR | P19982 | streptomyce |
| 402 | 2 | 5.9 | 31 | 1 | PETL_ANASP | Q8yvq2 | anabaena sp |
| 403 | 2 | 5.9 | 31 | 1 | PETL_ARATH | P56776 | arabidopsis |
| 404 | 2 | 5.9 | 31 | 1 | PETL_BETVU | P46612 | beta vulgar |
| 405 | 2 | 5.9 | 31 | 1 | PETL_CHLVU | P56306 | chlorella v |
| 406 | 2 | 5.9 | 31 | 1 | PETL_GUIITH | O78468 | guillardia |
| 407 | 2 | 5.9 | 31 | 1 | PETL_MAIZE | P19445 | zea mays (m |
| 408 | 2 | 5.9 | 31 | 1 | PETL_ODOSI | P49524 | odontella s |
| 409 | 2 | 5.9 | 31 | 1 | PETL_OENHO | Q9mtk4 | oenothera h |
| 410 | 2 | 5.9 | 31 | 1 | PETL_ORYSA | P12180 | oryza sativ |
| 411 | 2 | 5.9 | 31 | 1 | PETL_PORPU | P51221 | porphyra pu |
| 412 | 2 | 5.9 | 31 | 1 | PETL_PSINU | Q8wi03 | psilotum nu |
| 413 | 2 | 5.9 | 31 | 1 | PETL_SPIOL | Q9m310 | spinacia ol |
| 414 | 2 | 5.9 | 31 | 1 | PETL_WHEAT | P58247 | triticum ae |
| 415 | 2 | 5.9 | 31 | 1 | PETM_CYACA | Q9t1r5 | cyanidium c |
| 416 | 2 | 5.9 | 31 | 1 | PETN_CYACA | Q9t1r6 | cyanidium c |

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|-----|---|-----|----|---|------------|--------|-------------|
| 417 | 2 | 5.9 | 31 | 1 | PRT2_CLUPA | P02336 | clupea pall |
| 418 | 2 | 5.9 | 31 | 1 | PSAK_ANAVA | P23317 | anabaena va |
| 419 | 2 | 5.9 | 31 | 1 | PSAM_CYAPA | P48185 | cyanophora |
| 420 | 2 | 5.9 | 31 | 1 | PSAM_EUGGR | P31479 | euglena gra |
| 421 | 2 | 5.9 | 31 | 1 | PSBK_SYNVU | P19054 | synechococc |
| 422 | 2 | 5.9 | 31 | 1 | PSBM_MESVI | Q9muq7 | mesostigma |
| 423 | 2 | 5.9 | 31 | 1 | PSBT_CHLRE | P37256 | chlamydomon |
| 424 | 2 | 5.9 | 31 | 1 | PSBT_CHLVU | P56327 | chlorella v |
| 425 | 2 | 5.9 | 31 | 1 | PSBT_CYAPA | P48109 | cyanophora |
| 426 | 2 | 5.9 | 31 | 1 | PSBT_EUGGR | P20176 | euglena gra |
| 427 | 2 | 5.9 | 31 | 1 | PSBT_MESVI | Q9muv6 | mesostigma |
| 428 | 2 | 5.9 | 31 | 1 | PSBT_PORPU | P51323 | porphyra pu |
| 429 | 2 | 5.9 | 31 | 1 | PYSG_METBA | P80523 | methanosarc |
| 430 | 2 | 5.9 | 31 | 1 | RECX_METCL | P37865 | methylomona |
| 431 | 2 | 5.9 | 31 | 1 | RL21_STRTR | P48956 | streptococc |
| 432 | 2 | 5.9 | 31 | 1 | SARL_HUMAN | O00631 | homo sapien |
| 433 | 2 | 5.9 | 31 | 1 | SC37_MESMA | P83407 | mesobuthus |
| 434 | 2 | 5.9 | 31 | 1 | SCK5_ANDMA | P31719 | androctonus |
| 435 | 2 | 5.9 | 31 | 1 | SCKL_LEIQH | P16341 | leiurus qui |
| 436 | 2 | 5.9 | 31 | 1 | SODC_STRHE | P81163 | striga herm |
| 437 | 2 | 5.9 | 31 | 1 | TX3_HETVE | P58427 | heteropoda |
| 438 | 2 | 5.9 | 31 | 1 | TXA3_PARAC | P09949 | parasicyoni |
| 439 | 2 | 5.9 | 31 | 1 | Y191_BORBU | O51209 | borrelia bu |
| 440 | 2 | 5.9 | 31 | 1 | Y3KD_BPCHP | P19187 | bacterioph |
| 441 | 2 | 5.9 | 31 | 1 | Y603_ARCFU | O29652 | archaeoglob |
| 442 | 2 | 5.9 | 32 | 1 | A2M_PACLE | P20738 | pacifastacu |
| 443 | 2 | 5.9 | 32 | 1 | APL3_DIAGR | P81471 | diatraea gr |
| 444 | 2 | 5.9 | 32 | 1 | ATP0_PIG | P80021 | sus scrofa |
| 445 | 2 | 5.9 | 32 | 1 | ATP7_SPIOL | P80088 | spinacia ol |
| 446 | 2 | 5.9 | 32 | 1 | ATPO_SPIOL | P80087 | spinacia ol |
| 447 | 2 | 5.9 | 32 | 1 | B4G1_RAT | P80225 | r beta-1,4- |
| 448 | 2 | 5.9 | 32 | 1 | CAAP_MICEC | P21162 | micromonosp |
| 449 | 2 | 5.9 | 32 | 1 | CAL0_BOVIN | P01260 | bos taurus |
| 450 | 2 | 5.9 | 32 | 1 | CAL0_PIG | P01259 | sus scrofa |
| 451 | 2 | 5.9 | 32 | 1 | CAR1_ECHCA | Q9prp9 | echis carin |
| 452 | 2 | 5.9 | 32 | 1 | CEC_OIKKI | P83420 | oiketicus k |
| 453 | 2 | 5.9 | 32 | 1 | COA1_BPIF1 | O80295 | bacterioph |
| 454 | 2 | 5.9 | 32 | 1 | COA1_BPIKE | P03676 | bacterioph |
| 455 | 2 | 5.9 | 32 | 1 | COA2_BPFD | P03677 | bacterioph |
| 456 | 2 | 5.9 | 32 | 1 | CRP_PLEPL | P12245 | pleuronecte |
| 457 | 2 | 5.9 | 32 | 1 | CXG7_CONPE | P56711 | conus penna |
| 458 | 2 | 5.9 | 32 | 1 | CYBL_RHOGR | P32953 | rhodotorula |
| 459 | 2 | 5.9 | 32 | 1 | ER29_CHICK | P81628 | gallus gall |
| 460 | 2 | 5.9 | 32 | 1 | ER29_TRIVU | P81629 | trichosurus |
| 461 | 2 | 5.9 | 32 | 1 | ERH_PIG | P80230 | sus scrofa |
| 462 | 2 | 5.9 | 32 | 1 | FER_PORCR | P18821 | porphyridiu |
| 463 | 2 | 5.9 | 32 | 1 | FRIH_ANAPL | P80145 | anas platyr |
| 464 | 2 | 5.9 | 32 | 1 | GHR4_RAT | P33581 | rattus norv |
| 465 | 2 | 5.9 | 32 | 1 | GLB4_LAMSP | P20413 | lamellibrac |
| 466 | 2 | 5.9 | 32 | 1 | GT82_DICLA | P82608 | dicentrarch |
| 467 | 2 | 5.9 | 32 | 1 | H2AZ_ONCMY | P22647 | oncorhynch |
| 468 | 2 | 5.9 | 32 | 1 | HCYC_CHEDE | P83172 | cherax dest |
| 469 | 2 | 5.9 | 32 | 1 | IAPP_BOVIN | Q28207 | bos taurus |
| 470 | 2 | 5.9 | 32 | 1 | IAPP_PIG | Q29119 | sus scrofa |
| 471 | 2 | 5.9 | 32 | 1 | IAPP_SAGOE | Q28934 | saguinus oe |
| 472 | 2 | 5.9 | 32 | 1 | IAPP_SHEEP | Q28605 | ovis aries |
| 473 | 2 | 5.9 | 32 | 1 | ILVB_ENTAE | Q09129 | enterobacte |

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|-----|---|-----|----|---|-------------|--------|--------------|
| 474 | 2 | 5.9 | 32 | 1 | ITR2_CUCSA | P10291 | cucumis sat |
| 475 | 2 | 5.9 | 32 | 1 | LPID_ECOLI | P03060 | escherichia |
| 476 | 2 | 5.9 | 32 | 1 | LPID_EDWTA | P08140 | edwardsiell |
| 477 | 2 | 5.9 | 32 | 1 | LPIV_ECOLI | P03061 | escherichia |
| 478 | 2 | 5.9 | 32 | 1 | MDH_NITAL | P10887 | nitzschia a |
| 479 | 2 | 5.9 | 32 | 1 | MIFH_TRITR | P81748 | trichuris t |
| 480 | 2 | 5.9 | 32 | 1 | NEUB_PIG | P01297 | sus scrofa |
| 481 | 2 | 5.9 | 32 | 1 | OVOS_ANAPL | P20739 | anas platyr |
| 482 | 2 | 5.9 | 32 | 1 | P1SM_LOXIN | P83045 | loxosceles |
| 483 | 2 | 5.9 | 32 | 1 | PA22_AGKHP | P18997 | agkistrodon |
| 484 | 2 | 5.9 | 32 | 1 | PA2_RHONO | P43318 | rhophilema n |
| 485 | 2 | 5.9 | 32 | 1 | PETL_CHLRE | P50369 | chlamydomon |
| 486 | 2 | 5.9 | 32 | 1 | PETM_PORPU | P51275 | porphyra pu |
| 487 | 2 | 5.9 | 32 | 1 | PHNS_DESMU | P13062 | desulfovibr |
| 488 | 2 | 5.9 | 32 | 1 | PRI3_ONCMY | P02330 | oncorhynchu |
| 489 | 2 | 5.9 | 32 | 1 | PRT1_ONCKE | P02327 | oncorhynchu |
| 490 | 2 | 5.9 | 32 | 1 | PRT4_SCYCA | P30259 | scyliorhinu |
| 491 | 2 | 5.9 | 32 | 1 | PRT5_ONCMY | P02334 | oncorhynchu |
| 492 | 2 | 5.9 | 32 | 1 | PRT6_ONCMY | P08145 | oncorhynchu |
| 493 | 2 | 5.9 | 32 | 1 | PRT7_ONCMY | P08146 | oncorhynchu |
| 494 | 2 | 5.9 | 32 | 1 | PRT8_ONCMY | P12817 | oncorhynchu |
| 495 | 2 | 5.9 | 32 | 1 | PRT9_ONCMY | P08147 | oncorhynchu |
| 496 | 2 | 5.9 | 32 | 1 | PRTA_ONCMY | P12818 | oncorhynchu |
| 497 | 2 | 5.9 | 32 | 1 | PRTE_HALME | P28308 | halobacteri |
| 498 | 2 | 5.9 | 32 | 1 | PRT_ORYLA | Q91185 | oryzias lat |
| 499 | 2 | 5.9 | 32 | 1 | PSAM_MARPO | P31590 | marchantia |
| 500 | 2 | 5.9 | 32 | 1 | PSBT_CYACA | O19927 | cyanidium c |
| 501 | 2 | 5.9 | 32 | 1 | PSBT_GUIITH | O78512 | guillardia |
| 502 | 2 | 5.9 | 32 | 1 | PSBZ_EUGAN | Q8sl95 | euglena ana |
| 503 | 2 | 5.9 | 32 | 1 | PSBZ_EUGGA | Q8sl93 | euglena gra |
| 504 | 2 | 5.9 | 32 | 1 | PSBZ_EUGMY | Q8sl91 | euglena myx |
| 505 | 2 | 5.9 | 32 | 1 | RIP2_PHYDI | P34967 | phytolacca |
| 506 | 2 | 5.9 | 32 | 1 | RK1_RABIT | P81655 | oryctolagus |
| 507 | 2 | 5.9 | 32 | 1 | RS19_YEREN | Q56847 | yersinia en |
| 508 | 2 | 5.9 | 32 | 1 | SCK2_CENNO | P58504 | centruroide |
| 509 | 2 | 5.9 | 32 | 1 | TAT_SIVM2 | P05912 | simian immu |
| 510 | 2 | 5.9 | 32 | 1 | TRYP_PENMO | P35050 | penaeus mon |
| 511 | 2 | 5.9 | 32 | 1 | TX29_PHONI | P29426 | phoneutria |
| 512 | 2 | 5.9 | 32 | 1 | TXP7_APTSC | P49271 | aptostichus |
| 513 | 2 | 5.9 | 32 | 1 | UC09_MAIZE | P80615 | zea mays (m |
| 514 | 2 | 5.9 | 32 | 1 | Y169_TREPA | O83199 | treponema p |
| 515 | 2 | 5.9 | 32 | 1 | Y433_BORBU | O51394 | borrelia bu |
| 516 | 2 | 5.9 | 32 | 1 | YH17_HAEIN | P44295 | haemophilus |
| 517 | 2 | 5.9 | 32 | 1 | YSCA_YEREN | Q01242 | yersinia en |
| 518 | 2 | 5.9 | 32 | 1 | YTK3_ILTVT | P23985 | infectious |
| 519 | 2 | 5.9 | 33 | 1 | ACT_DICVI | Q24733 | dictyocaulu |
| 520 | 2 | 5.9 | 33 | 1 | ANP3_MYOSC | P04367 | myoxocephal |
| 521 | 2 | 5.9 | 33 | 1 | ANP5_MYOAE | P20421 | myoxocephal |
| 522 | 2 | 5.9 | 33 | 1 | ATP7_SOLTU | P80496 | solanum tub |
| 523 | 2 | 5.9 | 33 | 1 | BR2A_RANES | P40837 | rana escule |
| 524 | 2 | 5.9 | 33 | 1 | BR2B_RANES | P40838 | rana escule |
| 525 | 2 | 5.9 | 33 | 1 | BR2E_RANES | P32413 | rana escule |
| 526 | 2 | 5.9 | 33 | 1 | BR2_RANBP | P32424 | rana brevip |
| 527 | 2 | 5.9 | 33 | 1 | CECB_HELVI | P83414 | heliothis v |
| 528 | 2 | 5.9 | 33 | 1 | CECC_HELVI | P83415 | heliothis v |
| 529 | 2 | 5.9 | 33 | 1 | COA1_BPF | P03675 | bacterioph |
| 530 | 2 | 5.9 | 33 | 1 | COA2_BPI22 | P15414 | bacterioph |

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|-----|---|-----|----|---|------------|--------|-------------|
| 531 | 2 | 5.9 | 33 | 1 | COXL_ONCMY | P80330 | oncorhynchu |
| 532 | 2 | 5.9 | 33 | 1 | CU89_HUMAN | P59042 | homo sapien |
| 533 | 2 | 5.9 | 33 | 1 | CXBW_CONRA | P58804 | conus radia |
| 534 | 2 | 5.9 | 33 | 1 | CXO_CONVE | P83301 | conus ventr |
| 535 | 2 | 5.9 | 33 | 1 | DBB2_DOLAU | P83376 | dolabella a |
| 536 | 2 | 5.9 | 33 | 1 | DEF1_MESAU | P81465 | mesocricetu |
| 537 | 2 | 5.9 | 33 | 1 | DEF3_MESAU | P81467 | mesocricetu |
| 538 | 2 | 5.9 | 33 | 1 | DHE3_PIG | P42174 | sus scrofa |
| 539 | 2 | 5.9 | 33 | 1 | FER_PORAE | P18820 | porphyridiu |
| 540 | 2 | 5.9 | 33 | 1 | GAST_CAVPO | P06885 | cavia porce |
| 541 | 2 | 5.9 | 33 | 1 | GAST_CHIBR | P10034 | chinchilla |
| 542 | 2 | 5.9 | 33 | 1 | GAST_DIDMA | P33713 | didelphis m |
| 543 | 2 | 5.9 | 33 | 1 | GGN1_RANRU | P80395 | rana rugosa |
| 544 | 2 | 5.9 | 33 | 1 | GGN2_RANRU | P80396 | rana rugosa |
| 545 | 2 | 5.9 | 33 | 1 | GGN3_RANRU | P80397 | rana rugosa |
| 546 | 2 | 5.9 | 33 | 1 | HF40_MAIZE | P82865 | zea mays (m |
| 547 | 2 | 5.9 | 33 | 1 | HOXU_RHOOP | P22659 | rhodococcus |
| 548 | 2 | 5.9 | 33 | 1 | LPPY_SALTY | P08522 | salmonella |
| 549 | 2 | 5.9 | 33 | 1 | LPRH_ECOLI | P37324 | escherichia |
| 550 | 2 | 5.9 | 33 | 1 | LYC2_HORSE | P81710 | equus cabal |
| 551 | 2 | 5.9 | 33 | 1 | MBP1_MAIZE | P28794 | zea mays (m |
| 552 | 2 | 5.9 | 33 | 1 | MHAA_STRCH | P80435 | streptomyce |
| 553 | 2 | 5.9 | 33 | 1 | MYMY_MYTED | P81614 | mytilus edu |
| 554 | 2 | 5.9 | 33 | 1 | OTCC_PSEPU | P11727 | pseudomonas |
| 555 | 2 | 5.9 | 33 | 1 | PBAN_LYMDI | P43511 | lymantria d |
| 556 | 2 | 5.9 | 33 | 1 | PEN3_ADECU | P35987 | canine aden |
| 557 | 2 | 5.9 | 33 | 1 | PETM_CYAPA | P48366 | cyanophora |
| 558 | 2 | 5.9 | 33 | 1 | PETM_SYNEL | Q8dj15 | synechococc |
| 559 | 2 | 5.9 | 33 | 1 | PK1_DICDI | P34101 | dictyosteli |
| 560 | 2 | 5.9 | 33 | 1 | PK5_DICDI | P34104 | dictyosteli |
| 561 | 2 | 5.9 | 33 | 1 | PRI1_ONCMY | P02326 | oncorhynchu |
| 562 | 2 | 5.9 | 33 | 1 | PRI2_ONCMY | P02328 | oncorhynchu |
| 563 | 2 | 5.9 | 33 | 1 | PRTB_MUGCE | P08130 | mugil cepha |
| 564 | 2 | 5.9 | 33 | 1 | PRTL_ECOLI | P02338 | escherichia |
| 565 | 2 | 5.9 | 33 | 1 | PSAI_SPIOL | P17228 | spinacia ol |
| 566 | 2 | 5.9 | 33 | 1 | PSAK_CUCSA | P42051 | cucumis sat |
| 567 | 2 | 5.9 | 33 | 1 | PSBT_ARATH | P37259 | arabidopsis |
| 568 | 2 | 5.9 | 33 | 1 | PSBT_MAIZE | P37257 | zea mays (m |
| 569 | 2 | 5.9 | 33 | 1 | RL21_XENLA | P49628 | xenopus lae |
| 570 | 2 | 5.9 | 33 | 1 | RL26_XENLA | P49629 | xenopus lae |
| 571 | 2 | 5.9 | 33 | 1 | RL28_XENLA | P46780 | xenopus lae |
| 572 | 2 | 5.9 | 33 | 1 | RL4_HALCU | P05967 | halobacteri |
| 573 | 2 | 5.9 | 33 | 1 | RPOC_HETCA | P36441 | heterosigma |
| 574 | 2 | 5.9 | 33 | 1 | RRPO_BPBZ1 | P09674 | bacterioph |
| 575 | 2 | 5.9 | 33 | 1 | RS4_XENLA | P49401 | xenopus lae |
| 576 | 2 | 5.9 | 33 | 1 | RT25_BOVIN | P82669 | bos taurus |
| 577 | 2 | 5.9 | 33 | 1 | RUGA_RANRU | P80954 | rana rugosa |
| 578 | 2 | 5.9 | 33 | 1 | RUGB_RANRU | P80955 | rana rugosa |
| 579 | 2 | 5.9 | 33 | 1 | SCX9_BUTO | P04099 | buthus occi |
| 580 | 2 | 5.9 | 33 | 1 | THIO_CLOST | P81109 | clostridium |
| 581 | 2 | 5.9 | 33 | 1 | TX1_HETVE | P58425 | heteropoda |
| 582 | 2 | 5.9 | 33 | 1 | TXH1_SELHU | P56676 | selenocosmi |
| 583 | 2 | 5.9 | 33 | 1 | TXN3_SELHA | P83464 | selenocosmi |
| 584 | 2 | 5.9 | 33 | 1 | VT1B_RAT | P58200 | rattus norv |
| 585 | 2 | 5.9 | 33 | 1 | Y474_BORBU | O51430 | borrelia bu |
| 586 | 2 | 5.9 | 33 | 1 | Y50A_MYCTU | Q9cb56 | mycobacteri |
| 587 | 2 | 5.9 | 33 | 1 | Y656_TREPA | O83662 | treponema p |

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|-----|---|-----|----|---|------------|--------|-------------|
| 588 | 2 | 5.9 | 33 | 1 | Y849_BORBU | 051789 | borrelia bu |
| 589 | 2 | 5.9 | 33 | 1 | YC12_CHLRE | P50370 | chlamydomon |
| 590 | 2 | 5.9 | 33 | 1 | YC12_MARPO | P31560 | marchantia |
| 591 | 2 | 5.9 | 33 | 1 | YC12_MESVI | Q9mus3 | mesostigma |
| 592 | 2 | 5.9 | 33 | 1 | YC12_NEPOL | Q9tky6 | nephroselmi |
| 593 | 2 | 5.9 | 33 | 1 | YC12_PINTH | P41600 | pinus thunb |
| 594 | 2 | 5.9 | 33 | 1 | YL74_ARCFU | O28108 | archaeoglob |
| 595 | 2 | 5.9 | 33 | 1 | YLCH_BP82 | Q37869 | bacteriopha |
| 596 | 2 | 5.9 | 33 | 1 | YLCH_ECOLI | Q47268 | escherichia |
| 597 | 2 | 5.9 | 34 | 1 | AMP2_CHICK | P80390 | gallus gall |
| 598 | 2 | 5.9 | 34 | 1 | ASPG_PIG | P30918 | sus scrofa |
| 599 | 2 | 5.9 | 34 | 1 | BR2C_RANES | P40839 | rana escule |
| 600 | 2 | 5.9 | 34 | 1 | COL_CHICK | P11148 | gallus gall |
| 601 | 2 | 5.9 | 34 | 1 | COXA_THETH | P82543 | thermus the |
| 602 | 2 | 5.9 | 34 | 1 | COXG_THUOB | P80976 | thunnus obe |
| 603 | 2 | 5.9 | 34 | 1 | CXGS_CONGE | P15472 | conus geogr |
| 604 | 2 | 5.9 | 34 | 1 | DEF2_RABIT | P07468 | oryctolagus |
| 605 | 2 | 5.9 | 34 | 1 | DEF7_RABIT | P80223 | oryctolagus |
| 606 | 2 | 5.9 | 34 | 1 | ECAB_ECTTU | P49344 | ectatomma t |
| 607 | 2 | 5.9 | 34 | 1 | EF2_RABIT | P55823 | oryctolagus |
| 608 | 2 | 5.9 | 34 | 1 | EGGR_APLCA | P01363 | aplysia cal |
| 609 | 2 | 5.9 | 34 | 1 | H1S_STRPU | P19376 | strongyloce |
| 610 | 2 | 5.9 | 34 | 1 | HS7S_CUCMA | P31082 | cucurbita m |
| 611 | 2 | 5.9 | 34 | 1 | ITR1_MOMCO | P82408 | momordica c |
| 612 | 2 | 5.9 | 34 | 1 | ITR2_MOMCO | P82409 | momordica c |
| 613 | 2 | 5.9 | 34 | 1 | LPTN_PROVU | P28779 | proteus vul |
| 614 | 2 | 5.9 | 34 | 1 | M44E_HUMAN | Q96pgl | homo sapien |
| 615 | 2 | 5.9 | 34 | 1 | MYTA_MYTED | P81612 | mytilus edu |
| 616 | 2 | 5.9 | 34 | 1 | MYTB_MYTED | P81613 | mytilus edu |
| 617 | 2 | 5.9 | 34 | 1 | PETM_ANASP | Q9f4w2 | anabaena sp |
| 618 | 2 | 5.9 | 34 | 1 | PRT1_SAROR | P25327 | sarda orien |
| 619 | 2 | 5.9 | 34 | 1 | PRT1_SCOSC | P83264 | scomber sco |
| 620 | 2 | 5.9 | 34 | 1 | PRT1_THUTH | P02321 | thunnus thy |
| 621 | 2 | 5.9 | 34 | 1 | PRT2_SCOSC | P83265 | scomber sco |
| 622 | 2 | 5.9 | 34 | 1 | PRT2_THUTH | P02322 | thunnus thy |
| 623 | 2 | 5.9 | 34 | 1 | PRT_DICLA | Q9ps27 | dicentrarch |
| 624 | 2 | 5.9 | 34 | 1 | PRT_PERFV | P29629 | perca flave |
| 625 | 2 | 5.9 | 34 | 1 | PSAI_LOTJA | Q9bbs0 | lotus japon |
| 626 | 2 | 5.9 | 34 | 1 | PSAI_OENHO | Q9mtl2 | oenothera h |
| 627 | 2 | 5.9 | 34 | 1 | PSAI_SOYBN | P49159 | glycine max |
| 628 | 2 | 5.9 | 34 | 1 | PSBM_ARATH | P12169 | arabidopsis |
| 629 | 2 | 5.9 | 34 | 1 | PSBM_CHAGL | Q8ma15 | chaetosphae |
| 630 | 2 | 5.9 | 34 | 1 | PSBM_CHLRE | P92277 | chlamydomon |
| 631 | 2 | 5.9 | 34 | 1 | PSBM_MAIZE | P48189 | zea mays (m |
| 632 | 2 | 5.9 | 34 | 1 | PSBM_MARPO | P12168 | marchantia |
| 633 | 2 | 5.9 | 34 | 1 | PSBM_NEPOL | Q9tl37 | nephroselmi |
| 634 | 2 | 5.9 | 34 | 1 | PSBM_OENHO | Q9mtm8 | oenothera h |
| 635 | 2 | 5.9 | 34 | 1 | PSBM_PEA | P34833 | pisum sativ |
| 636 | 2 | 5.9 | 34 | 1 | PSBM_PSINU | Q8wi22 | psilotum nu |
| 637 | 2 | 5.9 | 34 | 1 | PSBM_WHEAT | Q9xps6 | triticum ae |
| 638 | 2 | 5.9 | 34 | 1 | PSBT_TOBAC | P12184 | nicotiana t |
| 639 | 2 | 5.9 | 34 | 1 | PSPC_BOVIN | P15783 | bos taurus |
| 640 | 2 | 5.9 | 34 | 1 | PSPC_CANFA | P22397 | canis famil |
| 641 | 2 | 5.9 | 34 | 1 | PTU1_PEITU | P58606 | peirates tu |
| 642 | 2 | 5.9 | 34 | 1 | PYSB_METBA | P80522 | methanosarc |
| 643 | 2 | 5.9 | 34 | 1 | RNL1_PIG | P15466 | sus scrofa |
| 644 | 2 | 5.9 | 34 | 1 | RR2_OCHNE | Q40606 | ochrosphaer |

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|-----|---|-----|----|---|------------|--------|-------------|
| 645 | 2 | 5.9 | 34 | 1 | SCXM_SCOMA | P80719 | scorpio mau |
| 646 | 2 | 5.9 | 34 | 1 | SMS_MYXGL | P19209 | myxine glut |
| 647 | 2 | 5.9 | 34 | 1 | THEM_MALSU | P13858 | malbranchea |
| 648 | 2 | 5.9 | 34 | 1 | TX33_PHONI | P81789 | phoneutria |
| 649 | 2 | 5.9 | 34 | 1 | TXP5_BRASM | P49266 | brachypelma |
| 650 | 2 | 5.9 | 34 | 1 | VLYS_BPM1 | P08229 | bacterioph |
| 651 | 2 | 5.9 | 34 | 1 | VPU_HV1W2 | P08808 | human immun |
| 652 | 2 | 5.9 | 34 | 1 | Y05J_BPT4 | P39239 | bacterioph |
| 653 | 2 | 5.9 | 34 | 1 | Y224_TREPA | O83253 | treponema p |
| 654 | 2 | 5.9 | 34 | 1 | Y848_BORBU | O51788 | borrelia bu |
| 655 | 2 | 5.9 | 34 | 1 | Y870_HAEIN | P44065 | haemophilus |
| 656 | 2 | 5.9 | 34 | 1 | Y967_HAEIN | P44086 | haemophilus |
| 657 | 2 | 5.9 | 34 | 1 | YC12_GUITH | O78460 | guillardia |
| 658 | 2 | 5.9 | 34 | 1 | YC12_ODOSI | P49529 | odontella s |
| 659 | 2 | 5.9 | 34 | 1 | YC12_PORPU | P51385 | porphyra pu |
| 660 | 2 | 5.9 | 34 | 1 | YC12_SKECO | O96797 | skeletonema |
| 661 | 2 | 5.9 | 34 | 1 | YMIA_AGRTU | P38437 | agrobacteri |
| 662 | 2 | 5.9 | 34 | 1 | Z33B_HUMAN | Q06731 | homo sapien |
| 663 | 2 | 5.9 | 35 | 1 | ADO1_AGRDO | P58608 | agriosphodr |
| 664 | 2 | 5.9 | 35 | 1 | C550_BACHA | P80091 | bacillus ha |
| 665 | 2 | 5.9 | 35 | 1 | CEC4_BOMMO | P14666 | bombyx mori |
| 666 | 2 | 5.9 | 35 | 1 | CECA_HELVI | P83413 | heliothis v |
| 667 | 2 | 5.9 | 35 | 1 | CECB_ANTPE | P01509 | antheraea p |
| 668 | 2 | 5.9 | 35 | 1 | CHI1_CASSA | P29137 | castanea sa |
| 669 | 2 | 5.9 | 35 | 1 | D3HI_RABIT | P32185 | oryctolagus |
| 670 | 2 | 5.9 | 35 | 1 | DEFB_MYTED | P81611 | mytilus edu |
| 671 | 2 | 5.9 | 35 | 1 | END4_YEREN | P42691 | yersinia en |
| 672 | 2 | 5.9 | 35 | 1 | ERFK_KLEAE | Q08599 | klebsiella |
| 673 | 2 | 5.9 | 35 | 1 | EXE2_HELSE | P04204 | heloderma s |
| 674 | 2 | 5.9 | 35 | 1 | FAS_CAPHI | P08757 | capra hircu |
| 675 | 2 | 5.9 | 35 | 1 | FLAV_NOSSM | P35707 | nostoc sp. |
| 676 | 2 | 5.9 | 35 | 1 | GBGU_MOUSE | Q61017 | mus musculu |
| 677 | 2 | 5.9 | 35 | 1 | GRDB_CLOPU | P55793 | clostridium |
| 678 | 2 | 5.9 | 35 | 1 | GUR_GYMSY | P25810 | gymnema syl |
| 679 | 2 | 5.9 | 35 | 1 | HMWC_DESGI | P38588 | desulfovibr |
| 680 | 2 | 5.9 | 35 | 1 | IAAC_HORVU | P34951 | hordeum vul |
| 681 | 2 | 5.9 | 35 | 1 | KPPR_PINPS | P81664 | pinus pinas |
| 682 | 2 | 5.9 | 35 | 1 | LCGB_LACLA | P36962 | lactococcus |
| 683 | 2 | 5.9 | 35 | 1 | NEF_HV1H3 | P05854 | human immun |
| 684 | 2 | 5.9 | 35 | 1 | PBP1_LYMDI | P34176 | lymantria d |
| 685 | 2 | 5.9 | 35 | 1 | PBP2_LYMDI | P34177 | lymantria d |
| 686 | 2 | 5.9 | 35 | 1 | PBP_HYACE | P34175 | hyalophora |
| 687 | 2 | 5.9 | 35 | 1 | PHI1_MYTCA | P35422 | mytilus cal |
| 688 | 2 | 5.9 | 35 | 1 | PSAI_CYAPA | P48116 | cyanophora |
| 689 | 2 | 5.9 | 35 | 1 | PSBM_SYNY3 | P72701 | synechocyst |
| 690 | 2 | 5.9 | 35 | 1 | PSBT_OENHO | P37258 | oenothera h |
| 691 | 2 | 5.9 | 35 | 1 | PSBT_ORYSA | P12183 | oryza sativ |
| 692 | 2 | 5.9 | 35 | 1 | PSBT_PINTH | P41625 | pinus thunb |
| 693 | 2 | 5.9 | 35 | 1 | PSPC_PIG | P15785 | sus scrofa |
| 694 | 2 | 5.9 | 35 | 1 | RL32_HALCU | P05965 | halobacteri |
| 695 | 2 | 5.9 | 35 | 1 | SCKB_PANIM | P55928 | pandinus im |
| 696 | 2 | 5.9 | 35 | 1 | SCKG_PANIM | Q10726 | pandinus im |
| 697 | 2 | 5.9 | 35 | 1 | SCX5_BUTEU | P15222 | buthus eupe |
| 698 | 2 | 5.9 | 35 | 1 | SCXP_ANDMA | P01498 | androctonus |
| 699 | 2 | 5.9 | 35 | 1 | SMS_LAMFL | Q9prro | lampetra fl |
| 700 | 2 | 5.9 | 35 | 1 | SPRC_PIG | P20112 | sus scrofa |
| 701 | 2 | 5.9 | 35 | 1 | THPA_THADA | P21381 | thaumatococ |

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| 702 | 2 | 5.9 | 35 | 1 | TXAG_AGEOP | P31328 | agelena opu |
| 703 | 2 | 5.9 | 35 | 1 | TXH4_SELHU | P83303 | selenocosmi |
| 704 | 2 | 5.9 | 35 | 1 | TXKS_STOHE | P29187 | stoichactis |
| 705 | 2 | 5.9 | 35 | 1 | TXN4_SELHA | P83471 | selenocosmi |
| 706 | 2 | 5.9 | 35 | 1 | VL3_PAPVD | P06919 | deer papill |
| 707 | 2 | 5.9 | 35 | 1 | VSPA_CERVI | P18692 | cerastes vi |
| 708 | 2 | 5.9 | 35 | 1 | WSP7_PINPS | P81086 | pinus pinas |
| 709 | 2 | 5.9 | 35 | 1 | Y320_BORBU | O51299 | borrelia bu |
| 710 | 2 | 5.9 | 35 | 1 | Y37_BPT3 | P20325 | bacteriopha |
| 711 | 2 | 5.9 | 35 | 1 | Y644_ARCFU | O29613 | archaeoglob |
| 712 | 2 | 5.9 | 35 | 1 | Y845_BORBU | O51785 | borrelia bu |
| 713 | 2 | 5.9 | 35 | 1 | Y847_BORBU | O51787 | borrelia bu |
| 714 | 2 | 5.9 | 35 | 1 | YC12_CYACA | Q9tlx0 | cyanidium c |
| 715 | 2 | 5.9 | 35 | 1 | YC69_ARCFU | O28999 | archaeoglob |
| 716 | 2 | 5.9 | 35 | 1 | YQB5_CAEEL | Q09258 | caenorhabdi |
| 717 | 2 | 5.9 | 36 | 1 | AMPL_PIG | P28839 | sus scrofa |
| 718 | 2 | 5.9 | 36 | 1 | ANFV_ANGJA | P22642 | anguilla ja |
| 719 | 2 | 5.9 | 36 | 1 | C3L1_BOVIN | P30922 | bos taurus |
| 720 | 2 | 5.9 | 36 | 1 | CBBA_NITVU | P37102 | nitrobacter |
| 721 | 2 | 5.9 | 36 | 1 | CECD_ANTPE | P01511 | antheraea p |
| 722 | 2 | 5.9 | 36 | 1 | CYC7_GEOME | P81894 | geobacter m |
| 723 | 2 | 5.9 | 36 | 1 | DESR_DESGI | P00273 | desulfovibr |
| 724 | 2 | 5.9 | 36 | 1 | F4RE_METOG | P80951 | methanogeni |
| 725 | 2 | 5.9 | 36 | 1 | GLU1_ORENI | P81026 | oreochromis |
| 726 | 2 | 5.9 | 36 | 1 | GLUC_HYDCO | P09682 | hydrolagus |
| 727 | 2 | 5.9 | 36 | 1 | H1L5_ENSMI | P27203 | ensis minor |
| 728 | 2 | 5.9 | 36 | 1 | HBB_PONPY | Q9tt34 | pongo pygma |
| 729 | 2 | 5.9 | 36 | 1 | IAA_STRAU | P04082 | streptomyce |
| 730 | 2 | 5.9 | 36 | 1 | IOB1_ISYOB | P58609 | isyndus obs |
| 731 | 2 | 5.9 | 36 | 1 | KAD_STRGR | P53398 | streptomyce |
| 732 | 2 | 5.9 | 36 | 1 | LHG_RHOVI | P04126 | rhodopseudo |
| 733 | 2 | 5.9 | 36 | 1 | LYOX_PIG | P45845 | sus scrofa |
| 734 | 2 | 5.9 | 36 | 1 | MFA1_YEAST | P34165 | saccharomyc |
| 735 | 2 | 5.9 | 36 | 1 | MPG2_DACGL | Q41183 | dactylis gl |
| 736 | 2 | 5.9 | 36 | 1 | MYPC_RAT | P56741 | rattus norv |
| 737 | 2 | 5.9 | 36 | 1 | NEUH_CARCA | P11975 | cardisoma c |
| 738 | 2 | 5.9 | 36 | 1 | NEUY_GADMO | P80167 | gadus morhu |
| 739 | 2 | 5.9 | 36 | 1 | NEUY_ONCMY | P29071 | oncorhynchu |
| 740 | 2 | 5.9 | 36 | 1 | NEUY_RABIT | P09640 | oryctolagus |
| 741 | 2 | 5.9 | 36 | 1 | NEUY_RANRI | P29949 | rana ridibu |
| 742 | 2 | 5.9 | 36 | 1 | NIFH_ENTAG | P26249 | enterobacte |
| 743 | 2 | 5.9 | 36 | 1 | NLTP_PINPI | P26912 | pinus pinea |
| 744 | 2 | 5.9 | 36 | 1 | NUCM_SOLTU | P80264 | solanum tub |
| 745 | 2 | 5.9 | 36 | 1 | OST2_CHICK | P80897 | gallus gall |
| 746 | 2 | 5.9 | 36 | 1 | PAHO_ALLMI | P06305 | alligator m |
| 747 | 2 | 5.9 | 36 | 1 | PAHO_ANSAN | P06304 | anser anser |
| 748 | 2 | 5.9 | 36 | 1 | PAHO_CERSI | P37999 | ceratotheri |
| 749 | 2 | 5.9 | 36 | 1 | PAHO_DIDMA | P18107 | didelphis m |
| 750 | 2 | 5.9 | 36 | 1 | PAHO_EQUZE | P38000 | equus zebra |
| 751 | 2 | 5.9 | 36 | 1 | PAHO_ERIEU | P41335 | erinaceus e |
| 752 | 2 | 5.9 | 36 | 1 | PAHO_LARAR | P41337 | larus argen |
| 753 | 2 | 5.9 | 36 | 1 | PAHO_MACMU | P33684 | macaca mula |
| 754 | 2 | 5.9 | 36 | 1 | PAHO_RABIT | P41336 | oryctolagus |
| 755 | 2 | 5.9 | 36 | 1 | PAHO_RANCA | P15427 | rana catesb |
| 756 | 2 | 5.9 | 36 | 1 | PAHO_RANTE | P31229 | rana tempor |
| 757 | 2 | 5.9 | 36 | 1 | PAHO_STRCA | P11967 | struthio ca |
| 758 | 2 | 5.9 | 36 | 1 | PAHO_TAPPI | P39659 | tapirus pin |

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|-----|---|-----|----|---|------------|--------|-------------|
| 759 | 2 | 5.9 | 36 | 1 | PGKH_CHLFU | P36232 | chlorella f |
| 760 | 2 | 5.9 | 36 | 1 | PSAD_PEA | P20117 | pisum sativ |
| 761 | 2 | 5.9 | 36 | 1 | PSAH_PEA | P20121 | pisum sativ |
| 762 | 2 | 5.9 | 36 | 1 | PSAI_ANGLY | P28251 | angiopteris |
| 763 | 2 | 5.9 | 36 | 1 | PSAI_BRAOL | Q31909 | brassica ol |
| 764 | 2 | 5.9 | 36 | 1 | PSAI_CARCL | Q9gdv2 | carpobrotus |
| 765 | 2 | 5.9 | 36 | 1 | PSAI_CHAGL | Q8m9x5 | chaetosphae |
| 766 | 2 | 5.9 | 36 | 1 | PSAI_CHLVU | P58214 | chlorella v |
| 767 | 2 | 5.9 | 36 | 1 | PSAI_CYACA | Q9tm24 | cyanidium c |
| 768 | 2 | 5.9 | 36 | 1 | PSAI_GUITH | O78462 | guillardia |
| 769 | 2 | 5.9 | 36 | 1 | PSAI_HORVU | P13165 | hordeum vul |
| 770 | 2 | 5.9 | 36 | 1 | PSAI_MAIZE | P30980 | zea mays (m |
| 771 | 2 | 5.9 | 36 | 1 | PSAI_MARPO | P12185 | marchantia |
| 772 | 2 | 5.9 | 36 | 1 | PSAI_MESVI | Q9muq4 | mesostigma |
| 773 | 2 | 5.9 | 36 | 1 | PSAI_NEPOL | Q9tl12 | nephroselmi |
| 774 | 2 | 5.9 | 36 | 1 | PSAI_ORYSA | P12186 | oryza sativ |
| 775 | 2 | 5.9 | 36 | 1 | PSAI_PICAB | O47040 | picea abies |
| 776 | 2 | 5.9 | 36 | 1 | PSAI_PORPU | P51387 | porphyra pu |
| 777 | 2 | 5.9 | 36 | 1 | PSAI_PSINU | Q8wi10 | psilotum nu |
| 778 | 2 | 5.9 | 36 | 1 | PSAI_SKECO | O96813 | skeletonema |
| 779 | 2 | 5.9 | 36 | 1 | PSAI_TOBAC | P12187 | nicotiana t |
| 780 | 2 | 5.9 | 36 | 1 | PSAI_WHEAT | P25410 | triticum ae |
| 781 | 2 | 5.9 | 36 | 1 | PSBI_ARATH | P09970 | arabidopsis |
| 782 | 2 | 5.9 | 36 | 1 | PSBI_HORVU | P25876 | hordeum vul |
| 783 | 2 | 5.9 | 36 | 1 | PSBI_MARPO | P09969 | marchantia |
| 784 | 2 | 5.9 | 36 | 1 | PSBI_ORYSA | P12161 | oryza sativ |
| 785 | 2 | 5.9 | 36 | 1 | PSBI_PINTH | P41599 | pinus thunb |
| 786 | 2 | 5.9 | 36 | 1 | PSBI_PSEMZ | P29796 | pseudotsuga |
| 787 | 2 | 5.9 | 36 | 1 | PSBM_CHLVU | P56325 | chlorella v |
| 788 | 2 | 5.9 | 36 | 1 | PSBM_SYNEL | Q8dha7 | synechococc |
| 789 | 2 | 5.9 | 36 | 1 | PSBY_ODOSI | P49543 | odontella s |
| 790 | 2 | 5.9 | 36 | 1 | PSBY_PORPU | P51206 | porphyra pu |
| 791 | 2 | 5.9 | 36 | 1 | PYY_AMICA | P29205 | amia calva |
| 792 | 2 | 5.9 | 36 | 1 | PYY_LEPSP | P09473 | lepisosteus |
| 793 | 2 | 5.9 | 36 | 1 | PYY_ONCKI | P09474 | oncorhynchu |
| 794 | 2 | 5.9 | 36 | 1 | PYY_PIG | P01305 | sus scrofa |
| 795 | 2 | 5.9 | 36 | 1 | PYY_RAJRH | P29206 | raja rhina |
| 796 | 2 | 5.9 | 36 | 1 | PYY_RANRI | P29204 | rana ridibu |
| 797 | 2 | 5.9 | 36 | 1 | SCK2_CENLL | P45630 | centruroide |
| 798 | 2 | 5.9 | 36 | 1 | SCK3_LEIQH | P45660 | leiurus qui |
| 799 | 2 | 5.9 | 36 | 1 | SCX1_BUTEU | P15220 | buthus eupe |
| 800 | 2 | 5.9 | 36 | 1 | SCXL_LEIQU | P45639 | leiurus qui |
| 801 | 2 | 5.9 | 36 | 1 | SPYY_PHYBI | P80952 | phyllomedus |
| 802 | 2 | 5.9 | 36 | 1 | TAEK_ACTEQ | P81897 | actinia equ |
| 803 | 2 | 5.9 | 36 | 1 | TERN_PSEUS | P82321 | pseudacanth |
| 804 | 2 | 5.9 | 36 | 1 | TLN1_CHICK | P54939 | gallus gall |
| 805 | 2 | 5.9 | 36 | 1 | TX1B_AGEAP | P15970 | agelenopsis |
| 806 | 2 | 5.9 | 36 | 1 | TX35_PHONI | P81791 | phoneutria |
| 807 | 2 | 5.9 | 36 | 1 | TXAM_METSE | P11495 | metridium s |
| 808 | 2 | 5.9 | 36 | 1 | TXD3_PARLU | P83258 | paracoelote |
| 809 | 2 | 5.9 | 36 | 1 | TXJA_HADVE | P82227 | hadronyche |
| 810 | 2 | 5.9 | 36 | 1 | TXJB_HADVE | P82226 | hadronyche |
| 811 | 2 | 5.9 | 36 | 1 | Y16L_BPT4 | P39244 | bacteriopha |
| 812 | 2 | 5.9 | 36 | 1 | Y297_ARCFU | O29945 | archaeoglob |
| 813 | 2 | 5.9 | 36 | 1 | Y4KD_BPCHP | P19188 | bacteriopha |
| 814 | 2 | 5.9 | 36 | 1 | Y609_BORBU | O51554 | borrelia bu |
| 815 | 2 | 5.9 | 36 | 1 | Y619_ARCFU | O29636 | archaeoglob |

| | | | | | | | |
|-----|---|-----|----|---|-------------|--------|-------------|
| 816 | 2 | 5.9 | 36 | 1 | Y699_TREPA | O83697 | treponema p |
| 817 | 2 | 5.9 | 36 | 1 | YC12_CYAPA | P48256 | cyanophora |
| 818 | 2 | 5.9 | 36 | 1 | YG50_HAEIN | P44281 | haemophilus |
| 819 | 2 | 5.9 | 36 | 1 | YRKG_BACSU | P54434 | bacillus su |
| 820 | 2 | 5.9 | 37 | 1 | 24KD_PLACH | P14592 | plasmodium |
| 821 | 2 | 5.9 | 37 | 1 | AFP4_MALPA | P83138 | malva parvi |
| 822 | 2 | 5.9 | 37 | 1 | ANP3_PSEAM | P02733 | pseudopleur |
| 823 | 2 | 5.9 | 37 | 1 | ATPO_SOLTU | P80504 | solanum tub |
| 824 | 2 | 5.9 | 37 | 1 | B2MG_ORENI | Q03423 | oreochromis |
| 825 | 2 | 5.9 | 37 | 1 | CAL1_PIG | P30880 | sus scrofa |
| 826 | 2 | 5.9 | 37 | 1 | CAL1_SHEEP | P30881 | ovis aries |
| 827 | 2 | 5.9 | 37 | 1 | CALR_RANRI | P31888 | rana ridibu |
| 828 | 2 | 5.9 | 37 | 1 | CEC2_MANSE | P14662 | manduca sex |
| 829 | 2 | 5.9 | 37 | 1 | CEC3_MANSE | P14663 | manduca sex |
| 830 | 2 | 5.9 | 37 | 1 | CEC4_MANSE | P14664 | manduca sex |
| 831 | 2 | 5.9 | 37 | 1 | CG2S_LUPAN | P09930 | lupinus ang |
| 832 | 2 | 5.9 | 37 | 1 | CHCD_ANTPO | P08931 | antheraea p |
| 833 | 2 | 5.9 | 37 | 1 | CS40_STAAU | P81684 | staphylococ |
| 834 | 2 | 5.9 | 37 | 1 | CUP4_SARBU | P14486 | sarcophaga |
| 835 | 2 | 5.9 | 37 | 1 | DEFA_MYTED | P81610 | mytilus edu |
| 836 | 2 | 5.9 | 37 | 1 | ECAA_ECTTU | P49343 | ectatomma t |
| 837 | 2 | 5.9 | 37 | 1 | ES2A_RANES | P40845 | rana escule |
| 838 | 2 | 5.9 | 37 | 1 | ES2B_RANES | P40846 | rana escule |
| 839 | 2 | 5.9 | 37 | 1 | F13A_BOVIN | P12260 | bos taurus |
| 840 | 2 | 5.9 | 37 | 1 | GHR3_RAT | P33580 | rattus norv |
| 841 | 2 | 5.9 | 37 | 1 | HCYB_CANPG | P83175 | cancer pagu |
| 842 | 2 | 5.9 | 37 | 1 | HOXF_RHOOP | P22658 | rhodococcus |
| 843 | 2 | 5.9 | 37 | 1 | IAPP_CRIGR | P19890 | cricetulus |
| 844 | 2 | 5.9 | 37 | 1 | LPPY_SERMA | P19937 | serratia ma |
| 845 | 2 | 5.9 | 37 | 1 | MAUR_PARVE | Q56462 | paracoccus |
| 846 | 2 | 5.9 | 37 | 1 | ME20_EUPRA | P26888 | euplotes ra |
| 847 | 2 | 5.9 | 37 | 1 | ME22_EUPRA | P58548 | euplotes ra |
| 848 | 2 | 5.9 | 37 | 1 | MIBP_PSESP | P04576 | pseudomonas |
| 849 | 2 | 5.9 | 37 | 1 | NLT3_VITSX | P80273 | vitis sp. (|
| 850 | 2 | 5.9 | 37 | 1 | NLT4_VITSX | P80274 | vitis sp. (|
| 851 | 2 | 5.9 | 37 | 1 | NUFM_SOLTU | P80266 | solanum tub |
| 852 | 2 | 5.9 | 37 | 1 | OGT1_RABIT | P81436 | oryctolagus |
| 853 | 2 | 5.9 | 37 | 1 | OP2A_OXYKI | P83248 | oxyopes kit |
| 854 | 2 | 5.9 | 37 | 1 | OP2B_OXYKI | P83249 | oxyopes kit |
| 855 | 2 | 5.9 | 37 | 1 | OP2C_OXYKI | P83250 | oxyopes kit |
| 856 | 2 | 5.9 | 37 | 1 | OP2D_OXYKI | P83251 | oxyopes kit |
| 857 | 2 | 5.9 | 37 | 1 | PETG_ANASP | P58246 | anabaena sp |
| 858 | 2 | 5.9 | 37 | 1 | PETG_ANAVA | Q913p7 | anabaena va |
| 859 | 2 | 5.9 | 37 | 1 | PETG_ARATH | P56775 | arabidopsis |
| 860 | 2 | 5.9 | 37 | 1 | PETG_CHAGL | Q8m9y4 | chaetosphae |
| 861 | 2 | 5.9 | 37 | 1 | PETG_CHLEU | P46304 | chlamydomon |
| 862 | 2 | 5.9 | 37 | 1 | PETG_CHLRE | Q08362 | chlamydomon |
| 863 | 2 | 5.9 | 37 | 1 | PETG_CHLVU | P56305 | chlorella v |
| 864 | 2 | 5.9 | 37 | 1 | PETG_CUSRE | P30398 | cuscuta ref |
| 865 | 2 | 5.9 | 37 | 1 | PETG_CYAPA | P14236 | cyanophora |
| 866 | 2 | 5.9 | 37 | 1 | PETG_EUGGR | P30396 | euglena gra |
| 867 | 2 | 5.9 | 37 | 1 | PETG_GUIITH | O78505 | guillardia |
| 868 | 2 | 5.9 | 37 | 1 | PETG_MARPO | P12120 | marchantia |
| 869 | 2 | 5.9 | 37 | 1 | PETG_MESVI | Q9mun3 | mesostigma |
| 870 | 2 | 5.9 | 37 | 1 | PETG_NEPOL | Q9tky8 | nephroselmi |
| 871 | 2 | 5.9 | 37 | 1 | PETG_ODOSI | P49470 | odontella s |
| 872 | 2 | 5.9 | 37 | 1 | PETG_ORYSA | P12121 | oryza sativ |

| | | | | | | | |
|-----|---|-----|----|---|------------|--------|-------------|
| 873 | 2 | 5.9 | 37 | 1 | PETG_PINTH | P41614 | pinus thunb |
| 874 | 2 | 5.9 | 37 | 1 | PETG_PORPU | P51318 | porphyra pu |
| 875 | 2 | 5.9 | 37 | 1 | PETG_PSINU | Q8wi02 | psilotum nu |
| 876 | 2 | 5.9 | 37 | 1 | PETG_SKECO | O96811 | skeletonema |
| 877 | 2 | 5.9 | 37 | 1 | PETG_SYNEL | Q8dki2 | synechococc |
| 878 | 2 | 5.9 | 37 | 1 | PETG_SYNP7 | Q9z3g1 | synechococc |
| 879 | 2 | 5.9 | 37 | 1 | PIIL_ACHLY | P81720 | achromobact |
| 880 | 2 | 5.9 | 37 | 1 | POLN_WEEV | P13896 | western equ |
| 881 | 2 | 5.9 | 37 | 1 | PRF1_RAT | P18889 | rattus norv |
| 882 | 2 | 5.9 | 37 | 1 | PSAI_ARATH | P56768 | arabidopsis |
| 883 | 2 | 5.9 | 37 | 1 | PSAJ_EUGGR | P30394 | euglena gra |
| 884 | 2 | 5.9 | 37 | 1 | PSBL_ARATH | P29301 | arabidopsis |
| 885 | 2 | 5.9 | 37 | 1 | PSBL_ORYSA | P12166 | oryza sativ |
| 886 | 2 | 5.9 | 37 | 1 | PSBM_PINTH | P41608 | pinus thunb |
| 887 | 2 | 5.9 | 37 | 1 | PSBY_CYACA | O19893 | cyanidium c |
| 888 | 2 | 5.9 | 37 | 1 | PSBY_GUITH | O78433 | guillardia |
| 889 | 2 | 5.9 | 37 | 1 | PYY_CHICK | P29203 | gallus gall |
| 890 | 2 | 5.9 | 37 | 1 | REV_SIVM2 | P08809 | simian immu |
| 891 | 2 | 5.9 | 37 | 1 | RK36_ARATH | P12144 | arabidopsis |
| 892 | 2 | 5.9 | 37 | 1 | RK36_ASTLO | P24355 | astasia lon |
| 893 | 2 | 5.9 | 37 | 1 | RK36_CHAGL | Q8m9v5 | chaetosphae |
| 894 | 2 | 5.9 | 37 | 1 | RK36_CHLVU | P56360 | chlorella v |
| 895 | 2 | 5.9 | 37 | 1 | RK36_CYACA | Q9tlu9 | cyanidium c |
| 896 | 2 | 5.9 | 37 | 1 | RK36_CYAPA | P48131 | cyanophora |
| 897 | 2 | 5.9 | 37 | 1 | RK36_EPIVI | P30069 | epifagus vi |
| 898 | 2 | 5.9 | 37 | 1 | RK36_EUGGR | P21532 | euglena gra |
| 899 | 2 | 5.9 | 37 | 1 | RK36_LOTJA | Q9bbq2 | lotus japon |
| 900 | 2 | 5.9 | 37 | 1 | RK36_MARPO | P12142 | marchantia |
| 901 | 2 | 5.9 | 37 | 1 | RK36_NEPOL | Q9tl26 | nephroselmi |
| 902 | 2 | 5.9 | 37 | 1 | RK36_OENHO | Q9mtj1 | oenothera h |
| 903 | 2 | 5.9 | 37 | 1 | RK36_ORYSA | P12143 | oryza sativ |
| 904 | 2 | 5.9 | 37 | 1 | RK36_PEA | P07815 | pisum sativ |
| 905 | 2 | 5.9 | 37 | 1 | RK36_PINTH | P41631 | pinus thunb |
| 906 | 2 | 5.9 | 37 | 1 | RK36_PORPU | P51296 | porphyra pu |
| 907 | 2 | 5.9 | 37 | 1 | RK36_PSINU | Q8why9 | psilotum nu |
| 908 | 2 | 5.9 | 37 | 1 | RK36_SPIOL | P12230 | spinacia ol |
| 909 | 2 | 5.9 | 37 | 1 | RL36_ANASP | Q8ypk0 | anabaena sp |
| 910 | 2 | 5.9 | 37 | 1 | RL36_AQUAE | O66487 | aquifex aeo |
| 911 | 2 | 5.9 | 37 | 1 | RL36_BACHD | O50631 | bacillus ha |
| 912 | 2 | 5.9 | 37 | 1 | RL36_BACST | P07841 | bacillus st |
| 913 | 2 | 5.9 | 37 | 1 | RL36_BORBU | O51452 | borrelia bu |
| 914 | 2 | 5.9 | 37 | 1 | RL36_CAMJE | Q9pm84 | campylobact |
| 915 | 2 | 5.9 | 37 | 1 | RL36_CLOPE | Q8xhu7 | clostridium |
| 916 | 2 | 5.9 | 37 | 1 | RL36_DEIRA | Q9rsk0 | deinococcus |
| 917 | 2 | 5.9 | 37 | 1 | RL36_HAEIN | P46361 | haemophilus |
| 918 | 2 | 5.9 | 37 | 1 | RL36_HELPJ | Q9zjt1 | helicobacte |
| 919 | 2 | 5.9 | 37 | 1 | RL36_HELPY | P56058 | helicobacte |
| 920 | 2 | 5.9 | 37 | 1 | RL36_LEPIN | Q9xd13 | leptospira |
| 921 | 2 | 5.9 | 37 | 1 | RL36_MYCGA | Q9rdv9 | mycoplasma |
| 922 | 2 | 5.9 | 37 | 1 | RL36_MYCGE | P47420 | mycoplasma |
| 923 | 2 | 5.9 | 37 | 1 | RL36_MYCLE | Q9x7a2 | mycobacteri |
| 924 | 2 | 5.9 | 37 | 1 | RL36_MYCPN | P52864 | mycoplasma |
| 925 | 2 | 5.9 | 37 | 1 | RL36_MYCPU | Q98q05 | mycoplasma |
| 926 | 2 | 5.9 | 37 | 1 | RL36_MYCSP | P38015 | mycoplasma |
| 927 | 2 | 5.9 | 37 | 1 | RL36_MYCTU | P45810 | mycobacteri |
| 928 | 2 | 5.9 | 37 | 1 | RL36_NEIMA | Q9jrb2 | neisseria m |
| 929 | 2 | 5.9 | 37 | 1 | RL36_STRCO | O86772 | streptomyce |

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|-----|---|-----|----|---|------------|--------|-------------|
| 930 | 2 | 5.9 | 37 | 1 | RL36_SYNPG | O24707 | synechococc |
| 931 | 2 | 5.9 | 37 | 1 | RL36_THETH | P80256 | thermus the |
| 932 | 2 | 5.9 | 37 | 1 | RL36_THETN | Q8r7x8 | thermoanaer |
| 933 | 2 | 5.9 | 37 | 1 | RL36_TREPA | O83239 | treponema p |
| 934 | 2 | 5.9 | 37 | 1 | RL36_UREPA | Q9pqn7 | ureaplasma |
| 935 | 2 | 5.9 | 37 | 1 | RL36_VIBCH | P78001 | vibrio chol |
| 936 | 2 | 5.9 | 37 | 1 | RL7_CLOPA | P05393 | clostridium |
| 937 | 2 | 5.9 | 37 | 1 | RS15_HELLO | P52820 | helix lucor |
| 938 | 2 | 5.9 | 37 | 1 | RUGC_RANRU | P80956 | rana rugosa |
| 939 | 2 | 5.9 | 37 | 1 | SCIT_MESTA | P81761 | mesobuthus |
| 940 | 2 | 5.9 | 37 | 1 | SCK2_LEIQH | P45628 | leiurus qui |
| 941 | 2 | 5.9 | 37 | 1 | SCK3_BUTOC | P59290 | buthus occi |
| 942 | 2 | 5.9 | 37 | 1 | SCK3_PARTR | P83112 | parabuthus |
| 943 | 2 | 5.9 | 37 | 1 | SCKA_TITSE | P46114 | tityus serr |
| 944 | 2 | 5.9 | 37 | 1 | SCKC_LEIQH | P13487 | leiurus qui |
| 945 | 2 | 5.9 | 37 | 1 | SMS_PETMA | P21779 | petromyzon |
| 946 | 2 | 5.9 | 37 | 1 | TCTP_TRYBB | P35758 | trypanosoma |
| 947 | 2 | 5.9 | 37 | 1 | THHS_HORVU | P33045 | hordeum vul |
| 948 | 2 | 5.9 | 37 | 1 | TX21_SELHU | P82959 | selenocosmi |
| 949 | 2 | 5.9 | 37 | 1 | TX22_SELHU | P82960 | selenocosmi |
| 950 | 2 | 5.9 | 37 | 1 | TXD1_PARLU | P83256 | paracoelote |
| 951 | 2 | 5.9 | 37 | 1 | TXD2_PARLU | P83257 | paracoelote |
| 952 | 2 | 5.9 | 37 | 1 | TXD4_PARLU | P83259 | paracoelote |
| 953 | 2 | 5.9 | 37 | 1 | TXJC_HADVE | P82228 | hadronyche |
| 954 | 2 | 5.9 | 37 | 1 | TXM2_AGEAP | P11058 | agelenopsis |
| 955 | 2 | 5.9 | 37 | 1 | TXM5_AGEAP | P11061 | agelenopsis |
| 956 | 2 | 5.9 | 37 | 1 | TXOF_HADVE | P81599 | hadronyche |
| 957 | 2 | 5.9 | 37 | 1 | TXP3_APTSC | P49268 | aptostichus |
| 958 | 2 | 5.9 | 37 | 1 | VA1_BPBF2 | P19347 | bacterioph |
| 959 | 2 | 5.9 | 37 | 1 | VG40_BPML5 | Q05250 | mycobacteri |
| 960 | 2 | 5.9 | 37 | 1 | VG65_BPPH2 | P16515 | bacterioph |
| 961 | 2 | 5.9 | 37 | 1 | VG65_BPPZA | P08384 | bacterioph |
| 962 | 2 | 5.9 | 37 | 1 | VP64_NPVBM | P41722 | bombyx mori |
| 963 | 2 | 5.9 | 37 | 1 | VPU_HV1Z8 | P08807 | human immun |
| 964 | 2 | 5.9 | 37 | 1 | Y268_ARCFU | O29971 | archaeoglob |
| 965 | 2 | 5.9 | 37 | 1 | Y63_BPT7 | P03799 | bacterioph |
| 966 | 2 | 5.9 | 37 | 1 | Y692_BORBU | O51635 | borrelia bu |
| 967 | 2 | 5.9 | 37 | 1 | Y700_BORBU | O51643 | borrelia bu |
| 968 | 2 | 5.9 | 37 | 1 | Y762_BORBU | O51703 | borrelia bu |
| 969 | 2 | 5.9 | 37 | 1 | Y846_BORBU | O51786 | borrelia bu |
| 970 | 2 | 5.9 | 37 | 1 | YBGT_ECOLI | P56100 | escherichia |
| 971 | 2 | 5.9 | 37 | 1 | YC12_CHLVU | P56328 | chlorella v |
| 972 | 2 | 5.9 | 37 | 1 | YDA3_SCHPO | Q10345 | schizosacch |
| 973 | 2 | 5.9 | 37 | 1 | YIM4_BPPH1 | P10428 | bacterioph |
| 974 | 2 | 5.9 | 37 | 1 | YQGE_BACCA | P28753 | bacillus ca |
| 975 | 2 | 5.9 | 37 | 1 | YRYL_CAEL | Q19177 | caenorhabdi |
| 976 | 2 | 5.9 | 38 | 1 | A2M_HOMAM | P20737 | homarus ame |
| 977 | 2 | 5.9 | 38 | 1 | AFP5_MALPA | P83139 | malva parvi |
| 978 | 2 | 5.9 | 38 | 1 | BD01_BOVIN | P46159 | bos taurus |
| 979 | 2 | 5.9 | 38 | 1 | BD08_BOVIN | P46166 | bos taurus |
| 980 | 2 | 5.9 | 38 | 1 | COA3_XANCP | Q07484 | xanthomonas |
| 981 | 2 | 5.9 | 38 | 1 | CRS3_NOTGO | P15534 | nototodarus |
| 982 | 2 | 5.9 | 38 | 1 | CU47_LACCU | P80323 | lactobacill |
| 983 | 2 | 5.9 | 38 | 1 | DCHS_MICSP | P00863 | micrococcus |
| 984 | 2 | 5.9 | 38 | 1 | DEF4_LEIQH | P41965 | leiurus qui |
| 985 | 2 | 5.9 | 38 | 1 | DEF7_SPIOL | P81573 | spinacia ol |
| 986 | 2 | 5.9 | 38 | 1 | DEFI_AESCY | P80154 | aeschna cya |

| | | | | | | |
|------|---|-----|----|---|-------------|--------------------|
| 987 | 2 | 5.9 | 38 | 1 | DEF1_MYTGA | P80571 mytilus gal |
| 988 | 2 | 5.9 | 38 | 1 | DLP3_ORNAN | P82141 ornithorhyn |
| 989 | 2 | 5.9 | 38 | 1 | DNP_DENAN | P28374 dendroaspis |
| 990 | 2 | 5.9 | 38 | 1 | DPOB_BOVIN | Q27958 bos taurus |
| 991 | 2 | 5.9 | 38 | 1 | E2F1_RAT | O09139 rattus norv |
| 992 | 2 | 5.9 | 38 | 1 | EST5_DROMO | P10095 drosophila |
| 993 | 2 | 5.9 | 38 | 1 | EXE1_HEL SU | P04203 heloderma s |
| 994 | 2 | 5.9 | 38 | 1 | FER_METPR | P81542 metallospha |
| 995 | 2 | 5.9 | 38 | 1 | GLUM_HYDCO | P23063 hydrolagus |
| 996 | 2 | 5.9 | 38 | 1 | GME1_RAT | Q9quz8 rattus norv |
| 997 | 2 | 5.9 | 38 | 1 | H5_COLLI | P02260 columba liv |
| 998 | 2 | 5.9 | 38 | 1 | HIS1_MACFA | P34084 macaca fasc |
| 999 | 2 | 5.9 | 38 | 1 | HMG2_BOVIN | P40673 bos taurus |
| 1000 | 2 | 5.9 | 38 | 1 | HOXH_RHOOP | P22661 rhodococcus |

ALIGNMENTS

RESULT 1

FABI_RHASA

ID FABI_RHASA STANDARD; PRT; 33 AA.
AC P81175;
DT 15-JUL-1998 (Rel. 36, Created)
DT 15-JUL-1998 (Rel. 36, Last sequence update)
DT 15-JUL-1998 (Rel. 36, Last annotation update)
DE Fatty acid-binding protein, intestinal (I-FABP) (FABPI) (Fragments).
OS Rhamdia sapo.
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Actinopterygii; Neopterygii; Teleostei; Ostariophysi; Siluriformes;
OC Pimelodidae; Rhamdia.
OX NCBI_TaxID=55673;
RN [1]
RP SEQUENCE.
RC TISSUE=Intestine;
RX MEDLINE=98036128; PubMed=9370361;
RA Di Pietro S.M., Dell'Angelica E.C., Veerkamp J.H., Sterin-Speziale N.,
RA Santome J.A.;
RT "Amino acid sequence, binding properties and evolutionary
RT relationships of the basic liver fatty-acid-binding protein from the
RT catfish Rhamdia sapo.";
RL Eur. J. Biochem. 249:510-517(1997).
CC -!- FUNCTION: FABP ARE THOUGHT TO PLAY A ROLE IN THE INTRACELLULAR
CC TRANSPORT OF LONG-CHAIN FATTY ACIDS AND THEIR ACYL-COA ESTERS.
CC -!- SUBCELLULAR LOCATION: Cytoplasmic.
CC -!- TISSUE SPECIFICITY: INTESTINE.
CC -!- SIMILARITY: BELONGS TO THE FABP/P2/CRBP/CRABP FAMILY OF
CC TRANSPORTERS.
DR InterPro; IPR000463; Fatty_acid_BP.
DR PROSITE; PS00214; FABP; PARTIAL.
KW Transport; Lipid-binding.
FT NON_TER 1 1
FT NON_CONS 12 13
FT NON_CONS 20 21
FT NON_CONS 28 29
FT NON_TER 33 33
SQ SEQUENCE 33 AA; 3660 MW; 5BA16CC2880B7819 CRC64;

Query Match 14.7%; Score 5; DB 1; Length 33;
Best Local Similarity 100.0%; Pred. No. 40;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 SVSEI 5
|||||
Db 13 SVSEI 17

RESULT 2

DMD_RAT

ID DMD_RAT STANDARD; PRT; 29 AA.
AC P11530;
DT 01-OCT-1989 (Rel. 12, Created)
DT 01-OCT-1989 (Rel. 12, Last sequence update)
DT 28-FEB-2003 (Rel. 41, Last annotation update)
DE Dystrophin (Fragment).
GN DMD.
OS Rattus norvegicus (Rat).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
OX NCBI_TaxID=10116;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=88122671; PubMed=3340214;
RA Nudel U., Robzyk K., Yaffe D.;
RT "Expression of the putative Duchenne muscular dystrophy gene in
RT differentiated myogenic cell cultures and in the brain.";
RL Nature 331:635-638(1988).
CC -!- FUNCTION: May play a role in anchoring the cytoskeleton to the
CC plasma membrane.
CC -!- SUBUNIT: Interacts with the syntrophins SNTA1, SNTB1, SNTB2, SNTG1
CC and SNTG2 (By similarity).
CC -----
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CC -----
DR EMBL; X07000; CAA30057.1; -.
DR PIR; S01614; S01614.
DR InterPro; IPR001589; Actbind_actnin.
DR InterPro; IPR001202; WW_Rsp5_WWP.
DR PROSITE; PS00019; ACTININ_1; PARTIAL.
DR PROSITE; PS00020; ACTININ_2; PARTIAL.
DR PROSITE; PS01159; WW_DOMAIN_1; PARTIAL.
DR PROSITE; PS50020; WW_DOMAIN_2; PARTIAL.
KW Structural protein; Actin-binding; Calcium-binding; Cytoskeleton;
KW Repeat.
FT NON_TER 1 1
FT NON_TER 29 29
SQ SEQUENCE 29 AA; 3289 MW; 8ECFB28A1A7ACAF0 CRC64;

Query Match 11.8%; Score 4; DB 1; Length 29;
Best Local Similarity 100.0%; Pred. No. 4.2e+02;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 27 KLQD 30
|||
Db 12 KLQD 15

RESULT 3

PCG3_PACGO

ID PCG3_PACGO STANDARD; PRT; 30 AA.
AC P82416;
DT 16-OCT-2001 (Rel. 40, Created)
DT 16-OCT-2001 (Rel. 40, Last sequence update)
DT 15-SEP-2003 (Rel. 42, Last annotation update)
DE Ponericin G3.
OS Pachycondyla goeldii (Ponerine ant).
OC Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
OC Neoptera; Endopterygota; Hymenoptera; Apocrita; Aculeata; Formicidae;
OC Ponerinae; Pachycondyla.
OX NCBI_TaxID=118888;
RN [1]
RP SEQUENCE, AND FUNCTION.
RC TISSUE=Venom;
RX MEDLINE=21264562; PubMed=11279030;
RA Orivel J., Redeker V., Le Caer J.-P., Krier F., Revol-Junelles A.-M.,
RA Longeon A., Chafotte A., Dejean A., Rossier J.;
RT "Ponericins, new antibacterial and insecticidal peptides from the
RT venom of the ant Pachycondyla goeldii.";
RL J. Biol. Chem. 276:17823-17829(2001).
CC -!- FUNCTION: BROAD SPECTRUM OF ACTIVITY AGAINST BOTH GRAM-POSITIVE
CC AND GRAM-NEGATIVE BACTERIA AND S.CEREVISIAE. HAS INSECTICIDAL
CC AND NON-HEMOLYTIC ACTIVITIES.
CC -!- SUBCELLULAR LOCATION: Secreted.
CC -!- MASS SPECTROMETRY: MW=3381.36; METHOD=MALDI.
KW Antibiotic; Insect immunity; Fungicide.
SQ SEQUENCE 30 AA; 3383 MW; BC0463D0AF140B53 CRC64;

Query Match 11.8%; Score 4; DB 1; Length 30;
Best Local Similarity 100.0%; Pred. No. 4.3e+02;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 10 NKGK 13
|||
Db 7 NKGK 10

RESULT 4

PSBY_SYNY3

ID PSBY_SYNY3 STANDARD; PRT; 39 AA.
AC P73676;
DT 15-DEC-1998 (Rel. 37, Created)
DT 15-DEC-1998 (Rel. 37, Last sequence update)
DT 16-OCT-2001 (Rel. 40, Last annotation update)
DE Photosystem II protein Y.
GN PSBY OR SML0007.

OS Synechocystis sp. (strain PCC 6803).
 OC Bacteria; Cyanobacteria; Chroococcales; Synechocystis.
 OX NCBI_TaxID=1148;
 RN [1]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=97061201; PubMed=8905231;
 RA Kaneko T., Sato S., Kotani H., Tanaka A., Asamizu E., Nakamura Y.,
 RA Miyajima N., Hirose M., Sugiura M., Sasamoto S., Kimura T.,
 RA Hosouchi T., Matsuno A., Muraki A., Nakazaki N., Naruo K., Okumura S.,
 RA Shimpo S., Takeuchi C., Wada T., Watanabe A., Yamada M., Yasuda M.,
 RA Tabata S.;
 RT "Sequence analysis of the genome of the unicellular cyanobacterium
 RT Synechocystis sp. strain PCC6803. II. Sequence determination of the
 RT entire genome and assignment of potential protein-coding regions.";
 RL DNA Res. 3:109-136(1996).
 CC -!- FUNCTION: MANGANESE-BINDING POLYPEPTIDE WITH L-ARGININE
 CC METABOLIZING ENZYME ACTIVITY. COMPONENT OF THE CORE OF PHOTOSYSTEM
 CC II (BY SIMILARITY).
 CC -!- SUBCELLULAR LOCATION: CELLULAR THYLAKOID MEMBRANE.
 CC -!- SIMILARITY: BELONGS TO THE PSBY FAMILY.
 CC -----
 CC This SWISS-PROT entry is copyright. It is produced through a collaboration
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 CC -----
 DR EMBL; D90908; BAA17722.1; -.
 DR PIR; S77164; S77164.
 KW Photosystem II; Transmembrane; Thylakoid; Complete proteome.
 FT TRANSMEM 5 25 POTENTIAL.
 SQ SEQUENCE 39 AA; 4202 MW; 3EA176ABAA79F6DF CRC64;

Query Match 11.8%; Score 4; DB 1; Length 39;
 Best Local Similarity 100.0%; Pred. No. 5.5e+02;
 Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 28 LQDV 31
 ||||
 Db 31 LQDV 34

RESULT 5

SR1C_SARPE

ID SR1C_SARPE STANDARD; PRT; 39 AA.
 AC P08377;
 DT 01-AUG-1988 (Rel. 08, Created)
 DT 01-AUG-1988 (Rel. 08, Last sequence update)
 DT 28-FEB-2003 (Rel. 41, Last annotation update)
 DE Sarcotoxin IC.
 OS Sarcophaga peregrina (Flesh fly) (Boettcherisca peregrina).
 OC Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
 OC Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha; Oestroidea;
 OC Sarcophagidae; Sarcophaga.
 OX NCBI_TaxID=7386;

RN [1]
 RP SEQUENCE.
 RX MEDLINE=85207747; PubMed=3888997;
 RA Okada M., Natori S.;
 RT "Primary structure of sarcotoxin I, an antibacterial protein induced
 RT in the hemolymph of *Sarcophaga peregrina* (flesh fly) larvae.";
 RL J. Biol. Chem. 260:7174-7177(1985).
 CC -!- FUNCTION: SARCOTOXINS, WHICH ARE POTENT BACTERICIDAL PROTEINS,
 CC ARE PRODUCED IN RESPONSE TO INJURY. THEY ARE CYTOTOXIC TO BOTH
 CC GRAM-POSITIVE AND GRAM-NEGATIVE BACTERIA.
 CC -!- SUBCELLULAR LOCATION: Secreted.
 CC -!- SIMILARITY: BELONGS TO THE CECROPIN FAMILY.
 DR PIR; C22625; CKFHCS.
 DR InterPro; IPR000875; Cecropin.
 DR InterPro; IPR003253; Sarctxn_cecrpn.
 DR Pfam; PF00272; cecropin; 1.
 DR ProDom; PD001670; Sarctxn_cecrpn; 1.
 DR PROSITE; PS00268; CECROPIN; 1.
 KW Insect immunity; Antibiotic; Hemolymph; Amidation; Multigene family.
 FT MOD_RES 39 39 AMIDATION.
 SQ SEQUENCE 39 AA; 4227 MW; 11E79F4F405E855A CRC64;

Query Match 11.8%; Score 4; DB 1; Length 39;
 Best Local Similarity 100.0%; Pred. No. 5.5e+02;
 Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 23 WLRK 26
 ||||
 Db 2 WLRK 5

RESULT 6

CH60_MYCSM

ID CH60_MYCSM STANDARD; PRT; 28 AA.
 AC P80673;
 DT 01-OCT-1996 (Rel. 34, Created)
 DT 01-OCT-1996 (Rel. 34, Last sequence update)
 DT 28-FEB-2003 (Rel. 41, Last annotation update)
 DE 60 kDa chaperonin (Protein Cpn60) (groEL protein) (Fragment).
 GN GROEL OR GROEL OR MOPA.
 OS *Mycobacterium smegmatis*.
 OC Bacteria; Actinobacteria; Actinobacteridae; Actinomycetales;
 OC Corynebacterineae; Mycobacteriaceae; Mycobacterium.
 OX NCBI_TaxID=1772;
 RN [1]
 RP SEQUENCE.
 RC STRAIN=ATCC 607 / mc(2)6 / NRRL B-692;
 RX MEDLINE=97387814; PubMed=9243799;
 RA Lundrigan M.D., Arceneaux J.E.L., Zhu W., Byers B.R.;
 RT "Enhanced hydrogen peroxide sensitivity and altered stress protein
 RT expression in iron-starved *Mycobacterium smegmatis*.";
 RL BioMetals 10:215-225(1997).
 CC -!- FUNCTION: Prevents misfolding and promotes the refolding and
 CC proper assembly of unfolded polypeptides generated under stress
 CC conditions.
 CC -!- SUBUNIT: Oligomer of 14 subunits composed of two stacked rings of
 CC 7 subunits (By similarity).

CC -!- SUBCELLULAR LOCATION: Cytoplasmic.
 CC -!- SIMILARITY: Belongs to the chaperonin (HSP60) family.
 DR HAMAP; MF_00600; -, 1.
 DR InterPro; IPR001844; Chaprnin_Cpn60.
 DR PROSITE; PS00296; CHAPERONINS_CPN60; PARTIAL.
 KW Chaperone; ATP-binding.
 FT NON_TER 28 28
 SQ SEQUENCE 28 AA; 3047 MW; 2F40F27B94EF8720 CRC64;

Query Match 8.8%; Score 3; DB 1; Length 28;
 Best Local Similarity 100.0%; Pred. No. 4.8e+03;
 Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 15 LNS 17
 |||
 Db 18 LNS 20

RESULT 7

COXB_SOLTU

ID COXB_SOLTU STANDARD; PRT; 28 AA.
 AC P80499;
 DT 01-FEB-1996 (Rel. 33, Created)
 DT 01-FEB-1996 (Rel. 33, Last sequence update)
 DT 15-JUL-1999 (Rel. 38, Last annotation update)
 DE Cytochrome c oxidase polypeptide Vb (EC 1.9.3.1) (Fragment).
 OS Solanum tuberosum (Potato).
 OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
 OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
 OC Asteridae; lamiids; Solanales; Solanaceae; Solanum.
 OX NCBI_TaxID=4113;
 RN [1]
 RP SEQUENCE.
 RC TISSUE=Tuber;
 RX MEDLINE=97077345; PubMed=8919912;
 RA Jansch L., Kruff V., Schmitz U.K., Braun H.P.;
 RT "New insights into the composition, molecular mass and stoichiometry
 of the protein complexes of plant mitochondria."
 RL Plant J. 9:357-368(1996).
 CC -!- CATALYTIC ACTIVITY: 4 ferrocytochrome c + O(2) = 4 ferricytochrome
 CC c + 2 H(2)O.
 CC -!- SUBCELLULAR LOCATION: Mitochondrial inner membrane.
 CC -!- SIMILARITY: BELONGS TO THE CYTOCHROME C OXIDASE VB FAMILY.
 DR InterPro; IPR002124; COX5B.
 DR PROSITE; PS00848; COX5B; PARTIAL.
 KW Oxidoreductase; Inner membrane; Mitochondrion.
 FT NON_TER 28 28
 SQ SEQUENCE 28 AA; 3101 MW; 1EAFA79E2682849C CRC64;

Query Match 8.8%; Score 3; DB 1; Length 28;
 Best Local Similarity 100.0%; Pred. No. 4.8e+03;
 Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 2 VSE 4
 |||
 Db 2 VSE 4

RESULT 8

GUN_SCHCO

ID GUN_SCHCO STANDARD; PRT; 28 AA.
 AC P81190;
 DT 15-JUL-1998 (Rel. 36, Created)
 DT 15-JUL-1998 (Rel. 36, Last sequence update)
 DT 28-FEB-2003 (Rel. 41, Last annotation update)
 DE Endoglucanase (EC 3.2.1.4) (Endo-1,4-beta-glucanase) (Cellulase)
 DE (Fragment).
 OS Schizophyllum commune (Bracket fungus).
 OC Eukaryota; Fungi; Basidiomycota; Hymenomycetes; Homobasidiomycetes;
 OC Agaricales; Schizophyllaceae; Schizophyllum.
 OX NCBI_TaxID=5334;
 RN [1]
 RP SEQUENCE.
 RX MEDLINE=97459758; PubMed=9315718;
 RA Clarke A.J., Drummelsmith J., Yaguchi M.;
 RT "Identification of the catalytic nucleophile in the cellulase from
 RT Schizophyllum commune and assignment of the enzyme to Family 5,
 RT subtype 5 of the glycosidases."
 RL FEBS Lett. 414:359-361(1997).
 CC -!- CATALYTIC ACTIVITY: Endohydrolysis of 1,4-beta-D-glucosidic
 CC linkages in cellulose, lichenin and cereal beta-D-glucans.
 CC -!- SUBCELLULAR LOCATION: Attached to the membrane by a lipid anchor
 CC (Probable).
 CC -!- SIMILARITY: BELONGS TO CELLULASE FAMILY A (FAMILY 5 OF GLYCOSYL
 CC HYDROLASES).
 DR InterPro; IPR001547; Glyco_hydro_5.
 DR PROSITE; PS00659; GLYCOSYL_HYDROL_F5; PARTIAL.
 KW Cellulose degradation; Hydrolase; Glycosidase; Zymogen; Membrane;
 KW Lipoprotein.
 FT ACT_SITE 20 20 NUCLEOPHILE.
 FT NON_TER 28 28
 SQ SEQUENCE 28 AA; 2937 MW; B3F1C0C99C9950BE CRC64;

Query Match 8.8%; Score 3; DB 1; Length 28;
 Best Local Similarity 100.0%; Pred. No. 4.8e+03;
 Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 22 EWL 24
 |||
 Db 7 EWL 9

RESULT 9

OMPA_YERPS

ID OMPA_YERPS STANDARD; PRT; 28 AA.
 AC P38399;
 DT 01-OCT-1994 (Rel. 30, Created)
 DT 01-OCT-1994 (Rel. 30, Last sequence update)
 DT 15-SEP-2003 (Rel. 42, Last annotation update)
 DE Outer membrane protein A (Outer membrane protein II) (Fragment).
 GN OMPA.
 OS Yersinia pseudotuberculosis.
 OC Bacteria; Proteobacteria; Gammaproteobacteria; Enterobacteriales;
 OC Enterobacteriaceae; Yersinia.

OX NCBI_TaxID=633;
 RN [1]
 RP SEQUENCE.
 RX MEDLINE=90038529; PubMed=2478630;
 RA Zhang J.J., Hamachi M., Hamachi T., Zhao Y.P., Yu D.T.Y.;
 RT "The bacterial outer membrane protein that reacts with anti-HLA-B27
 RT antibodies is the OmpA protein.";
 RL J. Immunol. 143:2955-2960(1989).
 CC -!- FUNCTION: REQUIRED FOR THE ACTION OF COLICINS K AND L AND FOR THE
 CC STABILIZATION OF MATING AGGREGATES IN CONJUGATION. SERVES AS A
 CC RECEPTOR FOR A NUMBER OF T-EVEN LIKE PHAGES. ALSO ACTS AS A PORIN
 CC WITH LOW PERMEABILITY THAT ALLOWS SLOW PENETRATION OF SMALL
 CC SOLUTES (BY SIMILARITY).
 CC -!- SUBUNIT: Monomer (Probable).
 CC -!- SUBCELLULAR LOCATION: Integral membrane protein. Outer membrane.
 CC -!- SIMILARITY: BELONGS TO THE OMPA FAMILY.
 DR PIR; A60752; A60752.
 DR HSSP; P02934; 1QJP.
 DR InterPro; IPR006690; OMPA_LIKE.
 DR InterPro; IPR000498; OmpA_tmem.
 DR Pfam; PF01389; OmpA_membrane; 1.
 DR PROSITE; PS01068; OMPA; PARTIAL.
 KW Conjugation; Outer membrane; Transmembrane; Phage recognition; Porin.
 FT NON_TER 28 28
 SQ SEQUENCE 28 AA; 3281 MW; E89F7526254B1E0E CRC64;

Query Match 8.8%; Score 3; DB 1; Length 28;
 Best Local Similarity 100.0%; Pred. No. 4.8e+03;
 Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 10 NKG 12
 |||
 Db 26 NKG 28

RESULT 10

PA2C_PSEPO

ID PA2C_PSEPO STANDARD; PRT; 28 AA.
 AC P20260;
 DT 01-FEB-1991 (Rel. 17, Created)
 DT 01-FEB-1991 (Rel. 17, Last sequence update)
 DT 28-FEB-2003 (Rel. 41, Last annotation update)
 DE Phospholipase A2 (EC 3.1.1.4) (Pseudexin C chain) (Phosphatidylcholine
 DE 2-acylhydrolase) (Fragment).
 OS Pseudechis porphyriacus (Red-bellied black snake).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Lepidosauria; Squamata; Scleroglossa; Serpentes; Colubroidea;
 OC Elapidae; Acanthophiinae; Pseudechis.
 OX NCBI_TaxID=8671;
 RN [1]
 RP SEQUENCE.
 RC TISSUE=Venom;
 RX MEDLINE=89388835; PubMed=2675391;
 RA Schmidt J.J., Middlebrook J.L.;
 RT "Purification, sequencing and characterization of pseudexin
 RT phospholipases A2 from Pseudechis porphyriacus (Australian
 RT red-bellied black snake).";

RL Toxicon 27:805-818(1989).
 CC -!- FUNCTION: PA2 catalyzes the calcium-dependent hydrolysis of the 2-
 CC acyl groups in 3-sn-phosphoglycerides.
 CC -!- CATALYTIC ACTIVITY: Phosphatidylcholine + H(2)O = 1-
 CC acylglycerophosphocholine + a fatty acid anion.
 CC -!- COFACTOR: Binds 1 calcium ion per subunit (By similarity).
 CC -!- SUBCELLULAR LOCATION: Secreted.
 CC -!- SIMILARITY: BELONGS TO THE PHOSPHOLIPASE A2 FAMILY. GROUP I
 CC SUBFAMILY.
 DR PIR; C32416; C32416.
 DR HSSP; P00592; 2PHI.
 DR InterPro; IPR001211; PhospholipaseA2.
 DR Pfam; PF00068; phoslip; 1.
 DR ProDom; PD000303; PhospholipaseA2; 1.
 DR PROSITE; PS00119; PA2_ASP; PARTIAL.
 DR PROSITE; PS00118; PA2_HIS; PARTIAL.
 KW Hydrolase; Lipid degradation; Calcium; Multigene family.
 FT NON_TER 28 28
 SQ SEQUENCE 28 AA; 3210 MW; 5089A7E85CAAE0D5 CRC64;

Query Match 8.8%; Score 3; DB 1; Length 28;
 Best Local Similarity 100.0%; Pred. No. 4.8e+03;
 Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 5 IQL 7
 |||
 Db 3 IQL 5

RESULT 11

SCX2_BUTSI

ID SCX2_BUTSI STANDARD; PRT; 28 AA.
 AC P15230;
 DT 01-APR-1990 (Rel. 14, Created)
 DT 01-APR-1990 (Rel. 14, Last sequence update)
 DT 28-FEB-2003 (Rel. 41, Last annotation update)
 DE Peptide II.
 OS Buthus sindicus (Scorpion).
 OC Eukaryota; Metazoa; Arthropoda; Chelicerata; Arachnida; Scorpiones;
 OC Buthoidea; Buthidae; Mesobuthus.
 OX NCBI_TaxID=42519;
 RN [1]
 RP SEQUENCE.
 RC TISSUE=Venom;
 RX MEDLINE=90060332; PubMed=2583272;
 RA Fazal A., Beg O.U., Shafqat J., Zaidi Z.H., Joernvall H.;
 RT "Characterization of two different peptides from the venom of the
 RT scorpion Buthus sindicus."
 RL FEBS Lett. 257:260-262(1989).
 CC -!- SUBCELLULAR LOCATION: Secreted.
 CC -!- TISSUE SPECIFICITY: Expressed by the venom gland.
 DR PIR; S06668; S06668.
 DR HSSP; Q9NJP7; 1DU9.
 SQ SEQUENCE 28 AA; 2968 MW; 2EA9AD78BD39A3B8 CRC64;

Query Match 8.8%; Score 3; DB 1; Length 28;
 Best Local Similarity 100.0%; Pred. No. 4.8e+03;

Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 11 KGK 13
|||
Db 11 KGK 13

RESULT 12

SLP1_LEIQH

ID SLP1_LEIQH STANDARD; PRT; 28 AA.

AC P80669;

DT 01-OCT-1996 (Rel. 34, Created)

DT 01-OCT-1996 (Rel. 34, Last sequence update)

DT 28-FEB-2003 (Rel. 41, Last annotation update)

DE Leiuropeptide I.

OS Leiurus quinquestriatus hebraeus (Yellow scorpion).

OC Eukaryota; Metazoa; Arthropoda; Chelicerata; Arachnida; Scorpiones;

OC Buthoidea; Buthidae; Leiurus.

OX NCBI_TaxID=6884;

RN [1]

RP SEQUENCE, AND STRUCTURE BY NMR.

RC TISSUE=Venom;

RX MEDLINE=97411504; PubMed=9266482;

RA Buisine E., Wieruszeski J.-M., Lippens G., Wouters D., Tartar A.,

RA Sautiere P.;

RT "Characterization of a new family of toxin-like peptides from the

RT venom of the scorpion Leiurus quinquestriatus hebraeus. 1H-NMR

RT structure of leiuropeptide II.";

RL J. Pept. Res. 49:545-555(1997).

CC -!- SUBCELLULAR LOCATION: Secreted.

CC -!- TISSUE SPECIFICITY: Expressed by the venom gland.

CC -!- SIMILARITY: BELONGS TO THE SCORPION LEIUROTOXIN FAMILY.

DR HSSP; Q9NJP7; 1DU9.

KW Toxin.

FT DISULFID 3 19

FT DISULFID 6 24

FT DISULFID 10 26

SQ SEQUENCE 28 AA; 2954 MW; 5F72AD78BD39BE1B CRC64;

Query Match 8.8%; Score 3; DB 1; Length 28;

Best Local Similarity 100.0%; Pred. No. 4.8e+03;

Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 11 KGK 13
|||
Db 11 KGK 13

RESULT 13

VIP_ALLMI

ID VIP_ALLMI STANDARD; PRT; 28 AA.

AC P48142; P01285;

DT 21-JUL-1986 (Rel. 01, Created)

DT 21-JUL-1986 (Rel. 01, Last sequence update)

DT 01-OCT-1996 (Rel. 34, Last annotation update)

DE Vasoactive intestinal peptide (VIP).

GN VIP.

OS Alligator mississippiensis (American alligator).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Archosauria; Crocodylidae; Alligatorinae; Alligator.
 OX NCBI_TaxID=8496;
 RN [1]
 RP SEQUENCE.
 RC TISSUE=Stomach;
 RX MEDLINE=93324451; PubMed=8101369;
 RA Wang Y., Conlon J.M.;
 RT "Neuroendocrine peptides (NPY, GRP, VIP, somatostatin) from the brain
 RT and stomach of the alligator.";
 RL Peptides 14:573-579(1993).
 CC -!- FUNCTION: VIP CAUSES VASODILATION, LOWERS ARTERIAL BLOOD
 CC PRESSURE, STIMULATES MYOCARDIAL CONTRACTILITY, INCREASES
 CC GLYCOGENOLYSIS AND RELAXES THE SMOOTH MUSCLE OF TRACHEA, STOMACH
 CC AND GALL BLADDER.
 CC -!- SIMILARITY: BELONGS TO THE GLUCAGON FAMILY.
 DR InterPro; IPR000532; Glucagon.
 DR Pfam; PF00123; hormone2; 1.
 DR PRINTS; PR00275; GLUCAGON.
 DR SMART; SM00070; GLUCA; 1.
 DR PROSITE; PS00260; GLUCAGON; 1.
 KW Glucagon family; Amidation; Hormone.
 FT MOD_RES 28 28 AMIDATION.
 SQ SEQUENCE 28 AA; 3320 MW; 17B42D7573FF6F37 CRC64;

Query Match 8.8%; Score 3; DB 1; Length 28;
 Best Local Similarity 100.0%; Pred. No. 4.8e+03;
 Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 15 LNS 17
 |||
 Db 23 LNS 25

RESULT 14

VIP_RANRI
 ID VIP_RANRI STANDARD; PRT; 28 AA.
 AC P81016;
 DT 01-NOV-1997 (Rel. 35, Created)
 DT 01-NOV-1997 (Rel. 35, Last sequence update)
 DT 01-NOV-1997 (Rel. 35, Last annotation update)
 DE Vasoactive intestinal peptide (VIP).
 OS Rana ridibunda (Laughing frog) (Marsh frog).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Amphibia; Batrachia; Anura; Neobatrachia; Ranoidea; Ranidae; Rana.
 OX NCBI_TaxID=8406;
 RN [1]
 RP SEQUENCE.
 RX MEDLINE=95309202; PubMed=7540547;
 RA Chartrel N., Wang Y., Fournier A., Vaudry H., Conlon J.M.;
 RT "Frog vasoactive intestinal polypeptide and galanin: primary
 RT structures and effects on pituitary adenylate cyclase.";
 RL Endocrinology 136:3079-3086(1995).
 CC -!- FUNCTION: VIP CAUSES VASODILATION, LOWERS ARTERIAL BLOOD
 CC PRESSURE, STIMULATES MYOCARDIAL CONTRACTILITY, INCREASES
 CC GLYCOGENOLYSIS AND RELAXES THE SMOOTH MUSCLE OF TRACHEA, STOMACH

CC AND GALL BLADDER.
 CC -!- SIMILARITY: BELONGS TO THE GLUCAGON FAMILY.
 DR InterPro; IPR000532; Glucagon.
 DR Pfam; PF00123; hormone2; 1.
 DR PRINTS; PR00275; GLUCAGON.
 DR PROSITE; PS00260; GLUCAGON; 1.
 KW Glucagon family; Amidation; Hormone.
 FT MOD_RES 28 28 AMIDATION.
 SQ SEQUENCE 28 AA; 3320 MW; 17B42D7573FF6F37 CRC64;

Query Match 8.8%; Score 3; DB 1; Length 28;
 Best Local Similarity 100.0%; Pred. No. 4.8e+03;
 Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 15 LNS 17
 |||
 Db 23 LNS 25

RESULT 15

VIP_SHEEP

ID VIP_SHEEP STANDARD; PRT; 28 AA.

AC P04565;

DT 13-AUG-1987 (Rel. 05, Created)

DT 13-AUG-1987 (Rel. 05, Last sequence update)

DT 01-OCT-1996 (Rel. 34, Last annotation update)

DE Vasoactive intestinal peptide (VIP).

GN VIP.

OS Ovis aries (Sheep),

OS Capra hircus (Goat), and

OS Canis familiaris (Dog).

OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

OC Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovoidea;

OC Bovidae; Caprinae; Ovis.

OX NCBI_TaxID=9940, 9925, 9615;

RN [1]

RP SEQUENCE.

RC SPECIES=Sheep; TISSUE=Brain;

RX MEDLINE=91045331; PubMed=2235680;

RA Gafvelin G.;

RT "Isolation and primary structure of VIP from sheep brain.";

RL Peptides 11:703-706(1990).

RN [2]

RP SEQUENCE.

RC SPECIES=Sheep; TISSUE=Small intestine;

RX MEDLINE=91239834; PubMed=2034821;

RA Bounjoua Y., Vandermeers A., Robberecht P., Vandermeers-Piret M.C.,

RA Christophe J.;

RT "Purification and amino acid sequence of vasoactive intestinal

RT peptide, peptide histidine isoleucinamide and secretin from the ovine

RT small intestine.";

RL Regul. Pept. 32:169-179(1991).

RN [3]

RP SEQUENCE.

RC SPECIES=C.hircus, and C.familiaris;

RX MEDLINE=86313167; PubMed=3748846;

RA Eng J., Du B.-H., Raufman J.-P., Yalow R.S.;

RT "Purification and amino acid sequences of dog, goat and guinea pig
RT VIPs.";
RL Peptides 7 Suppl. 1:17-20(1986).
CC -!- FUNCTION: VIP CAUSES VASODILATION, LOWERS ARTERIAL BLOOD
CC PRESSURE, STIMULATES MYOCARDIAL CONTRACTILITY, INCREASES
CC GLYCOGENOLYSIS AND RELAXES THE SMOOTH MUSCLE OF TRACHEA, STOMACH
CC AND GALL BLADDER.
CC -!- SIMILARITY: BELONGS TO THE GLUCAGON FAMILY.
DR PIR; A60304; A60304.
DR PIR; B60072; VRSH.
DR InterPro; IPR000532; Glucagon.
DR Pfam; PF00123; hormone2; 1.
DR PRINTS; PR00275; GLUCAGON.
DR SMART; SM00070; GLUCA; 1.
DR PROSITE; PS00260; GLUCAGON; 1.
KW Glucagon family; Amidation; Hormone.
FT MOD_RES 28 28 AMIDATION.
SQ SEQUENCE 28 AA; 3327 MW; EF313FB573FF6F3F CRC64;

Query Match 8.8%; Score 3; DB 1; Length 28;
Best Local Similarity 100.0%; Pred. No. 4.8e+03;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 15 LNS 17
|||
Db 23 LNS 25

RESULT 16

CXOC_CONMA

ID CXOC_CONMA STANDARD; PRT; 29 AA.
AC P37300;
DT 01-OCT-1994 (Rel. 30, Created)
DT 01-OCT-1994 (Rel. 30, Last sequence update)
DT 28-FEB-2003 (Rel. 41, Last annotation update)
DE Omega-conotoxin MVIIC precursor (SNX-230) (Fragment).
OS Conus magus (Magus cone).
OC Eukaryota; Metazoa; Mollusca; Gastropoda; Orthogastropoda;
OC Apogastropoda; Caenogastropoda; Sorbeoconcha; Hypsogastropoda;
OC Neogastropoda; Conoidea; Conidae; Conus.
OX NCBI_TaxID=6492;
RN [1]
RP SEQUENCE FROM N.A., AND SYNTHESIS.
RX MEDLINE=92337922; PubMed=1352986;
RA Hillyard D.R., Monje V.D., Mintz I.M., Bean B.P., Nadasdi L.,
RA Ramachandran J., Miljanich G.P., Azimi-Zoonooz A., McIntosh J.M.,
RA Cruz L.J., Imperial J.S., Olivera B.M.;
RT "A new Conus peptide ligand for mammalian presynaptic Ca2+ channels.";
RL Neuron 9:69-77(1992).
RN [2]
RP STRUCTURE BY NMR.
RX MEDLINE=95248539; PubMed=7731037;
RA Farr-Jones S., Miljanich G.P., Nadasdi L., Ramachandran J.,
RA Basus V.J.;
RT "Solution structure of omega-conotoxin MVIIC, a high affinity ligand
RT of P-type calcium channels, using 1H NMR spectroscopy and complete
RT relaxation matrix analysis.";

RL J. Mol. Biol. 248:106-124(1995).
 RN [3]
 RP STRUCTURE BY NMR.
 RX MEDLINE=99303703; PubMed=10373375;
 RA Nielsen K.J., Adams D., Thomas L., Bond T., Alewood P.F., Craik D.J.,
 RA Lewis R.J.;
 RT "Structure-activity relationships of omega-conotoxins MVIIA, MVIIC and
 RT 14 loop splice hybrids at N and P/Q-type calcium channels.";
 RL J. Mol. Biol. 289:1405-1421(1999).
 RN [4]
 RP MUTAGENESIS OF TYR-15.
 RX MEDLINE=95408251; PubMed=7677735;
 RA Kim J.I., Takahashi M., Martin-Moutot N., Seagar M.J., Ohtake A.,
 RA Sato K.;
 RT "Tyr13 is essential for the binding of omega-conotoxin MVIIC to the
 RT P/Q-type calcium channel.";
 RL Biochem. Biophys. Res. Commun. 214:305-309(1995).
 CC -!- FUNCTION: Omega-conotoxins act at presynaptic membranes, they bind
 CC and block voltage-sensitive calcium channels (VSCC). This toxin
 CC blocks N-type calcium channels as well as types of high-threshold
 CC voltage-gated calcium channels resistant to both dihydropyridines
 CC and omega-conotoxin GVIA.
 CC -!- SUBCELLULAR LOCATION: Secreted.
 CC -!- TISSUE SPECIFICITY: Expressed by the venom duct.
 CC -!- SIMILARITY: BELONGS TO THE O-SUPERFAMILY OF CONOTOXINS. OMEGA-TYPE
 CC FAMILY.
 CC -----
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 CC -----
 DR EMBL; S40826; AAB22674.1; -.
 DR PIR; JH0699; JH0699.
 DR PDB; 1OMN; 01-DEC-95.
 DR PDB; 1CNN; 31-MAY-00.
 KW Toxin; Neurotoxin; Presynaptic neurotoxin; Ionic channel inhibitor;
 KW Calcium channel inhibitor; Hydroxylation; Amidation; 3D-structure.
 FT NON_TER 1 1
 FT PROPEP <1 2
 FT PEPTIDE 3 28 OMEGA-CONOTOXIN MVIIC.
 FT BINDING 15 15 ESSENTIAL FOR CALCIUM CHANNEL BINDING.
 FT DISULFID 3 18
 FT DISULFID 10 22
 FT DISULFID 17 28
 FT MOD_RES 9 9 HYDROXYLATION (PROBABLE).
 FT MOD_RES 28 28 AMIDATION (G-29 PROVIDE AMIDE GROUP).
 FT MUTAGEN 15 15 Y->A: HIGH DECREASE IN BINDING.
 FT TURN 6 7
 FT STRAND 9 9
 FT HELIX 12 14
 FT TURN 24 25
 FT STRAND 27 27
 SQ SEQUENCE 29 AA; 3071 MW; AC7A68948474728A CRC64;

Query Match 8.8%; Score 3; DB 1; Length 29;
Best Local Similarity 100.0%; Pred. No. 4.9e+03;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 11 KGK 13
|||
Db 4 KGK 6

RESULT 17

GALA_ALLMI

ID GALA_ALLMI STANDARD; PRT; 29 AA.
AC P47215;
DT 01-FEB-1996 (Rel. 33, Created)
DT 01-FEB-1996 (Rel. 33, Last sequence update)
DT 28-FEB-2003 (Rel. 41, Last annotation update)
DE Galanin.
OS Alligator mississippiensis (American alligator).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Archosauria; Crocodylidae; Alligatorinae; Alligator.
OX NCBI_TaxID=8496;
RN [1]
RP SEQUENCE.
RC TISSUE=Stomach;
RX MEDLINE=95023390; PubMed=7524049;
RA Wang Y., Conlon J.M.;
RT "Purification and primary structure of galanin from the alligator
RT stomach.";
RL Peptides 15:603-606(1994).
CC -!- FUNCTION: CONTRACTS SMOOTH MUSCLE OF THE GASTROINTESTINAL AND
CC GENITOURINARY TRACT, REGULATES GROWTH HORMONE RELEASE, MODULATES
CC INSULIN RELEASE, AND MAY BE INVOLVED IN THE CONTROL OF ADRENAL
CC SECRETION.
CC -!- SUBCELLULAR LOCATION: Secreted.
CC -!- SIMILARITY: BELONGS TO THE GALANIN FAMILY.
DR InterPro; IPR001600; Galanin.
DR Pfam; PF01296; Galanin; 1.
DR ProDom; PD005962; Galanin; 1.
DR PROSITE; PS00861; GALANIN; 1.
KW Hormone; Neuropeptide; Amidation.
FT MOD_RES 29 29 AMIDATION.
SQ SEQUENCE 29 AA; 3216 MW; E02F019B2D3E0529 CRC64;

Query Match 8.8%; Score 3; DB 1; Length 29;
Best Local Similarity 100.0%; Pred. No. 4.9e+03;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 15 LNS 17
|||
Db 4 LNS 6

RESULT 18

GALA_AMICA

ID GALA_AMICA STANDARD; PRT; 29 AA.
AC P47214;

DT 01-FEB-1996 (Rel. 33, Created)
 DT 01-FEB-1996 (Rel. 33, Last sequence update)
 DT 28-FEB-2003 (Rel. 41, Last annotation update)
 DE Galanin.
 OS *Amia calva* (Bowfin).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Actinopterygii; Neopterygii; Amiiformes; Amiidae; *Amia*.
 OX NCBI_TaxID=7924;
 RN [1]
 RP SEQUENCE.
 RC TISSUE=Stomach;
 RX MEDLINE=95083480; PubMed=7527531;
 RA Wang Y., Conlon J.M.;
 RT "Purification and characterization of galanin from the
 RT phylogenetically ancient fish, the bowfin (*Amia calva*) and dogfish
 RT (*Scyliorhinus canicula*).";
 RL Peptides 15:981-986(1994).
 CC -!- FUNCTION: CONTRACTS SMOOTH MUSCLE OF THE GASTROINTESTINAL AND
 CC GENITOURINARY TRACT, REGULATES GROWTH HORMONE RELEASE, MODULATES
 CC INSULIN RELEASE, AND MAY BE INVOLVED IN THE CONTROL OF ADRENAL
 CC SECRETION.
 CC -!- SUBCELLULAR LOCATION: Secreted.
 CC -!- SIMILARITY: BELONGS TO THE GALANIN FAMILY.
 DR InterPro; IPR001600; Galanin.
 DR Pfam; PF01296; Galanin; 1.
 DR ProDom; PD005962; Galanin; 1.
 DR PROSITE; PS00861; GALANIN; 1.
 KW Hormone; Neuropeptide; Amidation.
 FT MOD_RES 29 29 AMIDATION.
 SQ SEQUENCE 29 AA; 3114 MW; 7518719B2D271627 CRC64;

 Query Match 8.8%; Score 3; DB 1; Length 29;
 Best Local Similarity 100.0%; Pred. No. 4.9e+03;
 Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 15 LNS 17
 |||
 Db 4 LNS 6

RESULT 19

GALA_CHICK

ID GALA_CHICK STANDARD; PRT; 29 AA.
 AC P30802;
 DT 01-JUL-1993 (Rel. 26, Created)
 DT 01-JUL-1993 (Rel. 26, Last sequence update)
 DT 28-FEB-2003 (Rel. 41, Last annotation update)
 DE Galanin.
 GN GAL OR GALN.
 OS *Gallus gallus* (Chicken).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Archosauria; Aves; Neognathae; Galliformes; Phasianidae; Phasianinae;
 OC *Gallus*.
 OX NCBI_TaxID=9031;
 RN [1]
 RP SEQUENCE.
 RC TISSUE=Intestine;

RX MEDLINE=91348254; PubMed=1715289;
 RA Norberg A., Sillard R., Carlquist M., Joernvall H., Mutt V.;
 RT "Chemical detection of natural peptides by specific structures.
 RT Isolation of chicken galanin by monitoring for its N-terminal
 RT dipeptide, and determination of the amino acid sequence.";
 RL FEBS Lett. 288:151-153(1991).
 CC -!- FUNCTION: CONTRACTS SMOOTH MUSCLE OF THE GASTROINTESTINAL AND
 CC GENITOURINARY TRACT, REGULATES GROWTH HORMONE RELEASE, MODULATES
 CC INSULIN RELEASE, AND MAY BE INVOLVED IN THE CONTROL OF ADRENAL
 CC SECRETION.
 CC -!- SUBCELLULAR LOCATION: Secreted.
 CC -!- SIMILARITY: BELONGS TO THE GALANIN FAMILY.
 DR PIR; S17147; S17147.
 DR InterPro; IPR001600; Galanin.
 DR Pfam; PF01296; Galanin; 1.
 DR PRINTS; PR00273; GALANIN.
 DR ProDom; PD005962; Galanin; 1.
 DR PROSITE; PS00861; GALANIN; 1.
 KW Hormone; Neuropeptide; Amidation.
 FT MOD_RES 29 29 AMIDATION.
 SQ SEQUENCE 29 AA; 3212 MW; EB66919B2D271629 CRC64;

Query Match 8.8%; Score 3; DB 1; Length 29;
 Best Local Similarity 100.0%; Pred. No. 4.9e+03;
 Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 15 LNS 17
 |||
 Db 4 LNS 6

RESULT 20

GALA_ONCMY

ID GALA_ONCMY STANDARD; PRT; 29 AA.
 AC P47213;
 DT 01-FEB-1996 (Rel. 33, Created)
 DT 01-FEB-1996 (Rel. 33, Last sequence update)
 DT 28-FEB-2003 (Rel. 41, Last annotation update)
 DE Galanin.
 OS Oncorhynchus mykiss (Rainbow trout) (Salmo gairdneri).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Actinopterygii; Neopterygii; Teleostei; Euteleostei;
 OC Protacanthopterygii; Salmoniformes; Salmonidae; Oncorhynchus.
 OX NCBI_TaxID=8022;
 RN [1]
 RP SEQUENCE.
 RC TISSUE=Stomach;
 RX MEDLINE=95164756; PubMed=7532194;
 RA Anglade I., Wang Y., Jensen J., Tramu G., Kah O., Conlon J.M.;
 RT "Characterization of trout galanin and its distribution in trout
 RT brain and pituitary.";
 RL J. Comp. Neurol. 350:63-74(1994).
 CC -!- FUNCTION: CONTRACTS SMOOTH MUSCLE OF THE GASTROINTESTINAL AND
 CC GENITOURINARY TRACT, REGULATES GROWTH HORMONE RELEASE, MODULATES
 CC INSULIN RELEASE, AND MAY BE INVOLVED IN THE CONTROL OF ADRENAL
 CC SECRETION.
 CC -!- SUBCELLULAR LOCATION: Secreted.

CC -!- SIMILARITY: BELONGS TO THE GALANIN FAMILY.
DR InterPro; IPR001600; Galanin.
DR Pfam; PF01296; Galanin; 1.
DR ProDom; PD005962; Galanin; 1.
DR PROSITE; PS00861; GALANIN; 1.
KW Hormone; Neuropeptide; Amidation.
FT MOD_RES 29 29 AMIDATION.
SQ SEQUENCE 29 AA; 3044 MW; 73C37190403FA349 CRC64;

Query Match 8.8%; Score 3; DB 1; Length 29;
Best Local Similarity 100.0%; Pred. No. 4.9e+03;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 15 LNS 17
|||
Db 4 LNS 6

RESULT 21

GALA_RANRI

ID GALA_RANRI STANDARD; PRT; 29 AA.
AC P47216;
DT 01-FEB-1996 (Rel. 33, Created)
DT 01-FEB-1996 (Rel. 33, Last sequence update)
DT 28-FEB-2003 (Rel. 41, Last annotation update)
DE Galanin.
OS Rana ridibunda (Laughing frog) (Marsh frog).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Amphibia; Batrachia; Anura; Neobatrachia; Ranoidea; Ranidae; Rana.
OX NCBI_TaxID=8406;
RN [1]
RP SEQUENCE.
RX MEDLINE=95309202; PubMed=7540547;
RA Chartrel N., Wang Y., Fournier A., Vaudry H., Conlon J.M.;
RT "Frog vasoactive intestinal polypeptide and galanin: primary
RT structures and effects on pituitary adenylate cyclase."
RL Endocrinology 136:3079-3086(1995).
CC -!- FUNCTION: CONTRACTS SMOOTH MUSCLE OF THE GASTROINTESTINAL AND
CC GENITOURINARY TRACT, REGULATES GROWTH HORMONE RELEASE, MODULATES
CC INSULIN RELEASE, AND MAY BE INVOLVED IN THE CONTROL OF ADRENAL
CC SECRETION.
CC -!- SUBCELLULAR LOCATION: Secreted.
CC -!- SIMILARITY: BELONGS TO THE GALANIN FAMILY.
DR InterPro; IPR001600; Galanin.
DR Pfam; PF01296; Galanin; 1.
DR ProDom; PD005962; Galanin; 1.
DR PROSITE; PS00861; GALANIN; 1.
KW Hormone; Neuropeptide; Amidation.
FT MOD_RES 29 29 AMIDATION.
SQ SEQUENCE 29 AA; 3162 MW; F718719B2D3FB529 CRC64;

Query Match 8.8%; Score 3; DB 1; Length 29;
Best Local Similarity 100.0%; Pred. No. 4.9e+03;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 15 LNS 17
|||

Db

4 LNS 6

RESULT 22

GALA_SHEEP

ID GALA_SHEEP STANDARD; PRT; 29 AA.
AC P31234;
DT 01-JUL-1993 (Rel. 26, Created)
DT 01-JUL-1993 (Rel. 26, Last sequence update)
DT 28-FEB-2003 (Rel. 41, Last annotation update)
DE Galanin.
GN GAL OR GALN OR GLNN.
OS Ovis aries (Sheep).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovoidea;
OC Bovidae; Caprinae; Ovis.
OX NCBI_TaxID=9940;
RN [1]
RP SEQUENCE.
RC TISSUE=Brain;
RX MEDLINE=92158824; PubMed=1724081;
RA Sillard R., Langel U., Joernvall H.;
RT "Isolation and characterization of galanin from sheep brain.";
RL Peptides 12:855-859(1991).
CC -!- FUNCTION: CONTRACTS SMOOTH MUSCLE OF THE GASTROINTESTINAL AND
CC GENITOURINARY TRACT, REGULATES GROWTH HORMONE RELEASE, MODULATES
CC INSULIN RELEASE, AND MAY BE INVOLVED IN THE CONTROL OF ADRENAL
CC SECRETION.
CC -!- SUBCELLULAR LOCATION: Secreted.
CC -!- SIMILARITY: BELONGS TO THE GALANIN FAMILY.
DR InterPro; IPR001600; Galanin.
DR Pfam; PF01296; Galanin; 1.
DR PRINTS; PR00273; GALANIN.
DR ProDom; PD005962; Galanin; 1.
DR PROSITE; PS00861; GALANIN; 1.
KW Hormone; Neuropeptide; Amidation.
FT MOD_RES 29 29 AMIDATION.
SQ SEQUENCE 29 AA; 3185 MW; F718719B2D3FB089 CRC64;

Query Match 8.8%; Score 3; DB 1; Length 29;
Best Local Similarity 100.0%; Pred. No. 4.9e+03;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 15 LNS 17

|||

Db 4 LNS 6

RESULT 23

GLUC_CHIBR

ID GLUC_CHIBR STANDARD; PRT; 29 AA.
AC P31297;
DT 01-JUL-1993 (Rel. 26, Created)
DT 01-JUL-1993 (Rel. 26, Last sequence update)
DT 28-FEB-2003 (Rel. 41, Last annotation update)
DE Glucagon.
GN GCG.

OS Chinchilla brevicaudata (Chinchilla).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Rodentia; Hystricognathi; Chinchillidae;
 OC Chinchilla.
 OX NCBI_TaxID=10152;
 RN [1]
 RP SEQUENCE.
 RX MEDLINE=91045327; PubMed=2235678;
 RA Eng J., Kleinman W.A., Chu L.S.;
 RT "Purification of peptide hormones from chinchilla pancreas by
 RT chemical assay.";
 RL Peptides 11:683-685(1990).
 CC -!- FUNCTION: PROMOTES HYDROLYSIS OF GLYCOGEN AND LIPIDS, AND RAISES
 CC THE BLOOD SUGAR LEVEL.
 CC -!- INDUCTION: PRODUCED IN THE A CELLS OF THE ISLETS OF LANGERHANS
 CC IN RESPONSE TO A DROP IN BLOOD SUGAR CONCENTRATION.
 CC -!- SIMILARITY: BELONGS TO THE GLUCAGON FAMILY.
 DR PIR; A60413; GCCB.
 DR HSSP; P01275; 1BH0.
 DR InterPro; IPR000532; Glucagon.
 DR Pfam; PF00123; hormone2; 1.
 DR PRINTS; PR00275; GLUCAGON.
 DR SMART; SM00070; GLUCA; 1.
 DR PROSITE; PS00260; GLUCAGON; 1.
 KW Glucagon family; Hormone.
 SQ SEQUENCE 29 AA; 3478 MW; 19ECF4DABB752B27 CRC64;

Query Match 8.8%; Score 3; DB 1; Length 29;
 Best Local Similarity 100.0%; Pred. No. 4.9e+03;
 Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 13 KHL 15
 |||
 Db 12 KHL 14

RESULT 24

IPYR_DESVH

ID IPYR_DESVH STANDARD; PRT; 29 AA.
 AC P19371;
 DT 01-NOV-1990 (Rel. 16, Created)
 DT 01-NOV-1990 (Rel. 16, Last sequence update)
 DT 28-FEB-2003 (Rel. 41, Last annotation update)
 DE Inorganic pyrophosphatase (EC 3.6.1.1) (Pyrophosphate phospho-
 DE hydrolase) (PPase) (Fragment).
 OS Desulfovibrio vulgaris (strain Hildenborough).
 OC Bacteria; Proteobacteria; Deltaproteobacteria; Desulfovibrionales;
 OC Desulfovibrionaceae; Desulfovibrio.
 OX NCBI_TaxID=882;
 RN [1]
 RP SEQUENCE.
 RX MEDLINE=90365722; PubMed=2168174;
 RA Liu M.-Y., le Gall J.;
 RT "Purification and characterization of two proteins with inorganic
 RT pyrophosphatase activity from Desulfovibrio vulgaris: rubrerythrin
 RT and a new, highly active, enzyme.";
 RL Biochem. Biophys. Res. Commun. 171:313-318(1990).

CC -!- FUNCTION: INORGANIC PYROPHOSPHATASE IS AN ESSENTIAL ENZYME FOR THE
 CC ACTIVATION OF SULFATE BY SULFATE REDUCING BACTERIA. THIS IS A HIGH
 CC ACTIVITY PYROPHOSPHATASE.
 CC -!- CATALYTIC ACTIVITY: Diphosphate + H(2)O = 2 phosphate.
 CC -!- SUBCELLULAR LOCATION: Periplasmic (Potential).
 DR PIR; A35687; A35687.
 DR HAMAP; MF_00209; -; 1.
 DR InterPro; IPR001596; Pyrophosphatase.
 DR PROSITE; PS00387; PPASE; PARTIAL.
 KW Hydrolase; Periplasmic.
 FT NON_TER 29 29
 SQ SEQUENCE 29 AA; 3201 MW; 3FC5792360F2227B CRC64;

Query Match 8.8%; Score 3; DB 1; Length 29;
 Best Local Similarity 100.0%; Pred. No. 4.9e+03;
 Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 3 SEI 5
 |||
 Db 15 SEI 17

RESULT 25

NUO1_SOLTU

ID NUO1_SOLTU STANDARD; PRT; 29 AA.
 AC P80267;
 DT 01-FEB-1994 (Rel. 28, Created)
 DT 01-FEB-1994 (Rel. 28, Last sequence update)
 DT 28-FEB-2003 (Rel. 41, Last annotation update)
 DE NADH-ubiquinone oxidoreductase 14 kDa subunit (EC 1.6.5.3)
 DE (EC 1.6.99.3) (Complex I-14KD) (CI-14KD) (Fragment).
 OS Solanum tuberosum (Potato).
 OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
 OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
 OC Asteridae; lamiids; Solanales; Solanaceae; Solanum.
 OX NCBI_TaxID=41113;
 RN [1]
 RP SEQUENCE.
 RC STRAIN=cv. Bintje; TISSUE=Tuber;
 RX MEDLINE=94124587; PubMed=8294484;
 RA Herz U., Schroeder W., Liddell A., Leaver C.J., Brennicke A.,
 RA Grohmann L.;
 RT "Purification of the NADH:ubiquinone oxidoreductase (complex I) of
 RT the respiratory chain from the inner mitochondrial membrane of
 RT Solanum tuberosum."
 RL J. Biol. Chem. 269:2263-2269(1994).
 CC -!- FUNCTION: TRANSFER OF ELECTRONS FROM NADH TO THE RESPIRATORY
 CC CHAIN. THE IMMEDIATE ELECTRON ACCEPTOR FOR THE ENZYME IS BELIEVED
 CC TO BE UBIQUINONE.
 CC -!- CATALYTIC ACTIVITY: NADH + ubiquinone = NAD(+) + ubiquinol.
 CC -!- CATALYTIC ACTIVITY: NADH + acceptor = NAD(+) + reduced acceptor.
 CC -!- SUBUNIT: COMPLEX I IS COMPOSED OF ABOUT 30 DIFFERENT SUBUNITS.
 CC -!- SUBCELLULAR LOCATION: MATRIX SIDE OF THE MITOCHONDRIAL INNER
 CC MEMBRANE.
 DR PIR; I49732; I49732.
 KW Oxidoreductase; NAD; Ubiquinone; Mitochondrion.
 FT NON_TER 29 29

SQ SEQUENCE 29 AA; 3269 MW; E2B4DFB558D423D4 CRC64;

Query Match 8.8%; Score 3; DB 1; Length 29;
Best Local Similarity 100.0%; Pred. No. 4.9e+03;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 25 RKK 27
|||
Db 2 RKK 4

RESULT 26

PCG4_PACGO

ID PCG4_PACGO STANDARD; PRT; 29 AA.
AC P82417;
DT 16-OCT-2001 (Rel. 40, Created)
DT 16-OCT-2001 (Rel. 40, Last sequence update)
DT 15-SEP-2003 (Rel. 42, Last annotation update)
DE Ponericin G4.
OS Pachycondyla goeldii (Ponerine ant).
OC Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
OC Neoptera; Endopterygota; Hymenoptera; Apocrita; Aculeata; Formicidae;
OC Ponerinae; Pachycondyla.
OX NCBI_TaxID=118888;
RN [1]
RP SEQUENCE, AND FUNCTION.
RC TISSUE=Venom;
RX MEDLINE=21264562; PubMed=11279030;
RA Orivel J., Redeker V., Le Caer J.-P., Krier F., Revol-Junelles A.-M.,
RA Longeon A., Chafotte A., Dejean A., Rossier J.;
RT "Ponericins, new antibacterial and insecticidal peptides from the
RT venom of the ant Pachycondyla goeldii."
RL J. Biol. Chem. 276:17823-17829(2001).
CC -!- FUNCTION: HAS ACTIVITY AGAINST SOME GRAM-POSITIVE BACTERIA
CC AND S.CEREVISIAE. HAS A NON-HEMOLYTIC ACTIVITY.
CC -!- SUBCELLULAR LOCATION: Secreted.
CC -!- MASS SPECTROMETRY: MW=3163.87; METHOD=MALDI.
KW Antibiotic; Insect immunity; Fungicide.
SQ SEQUENCE 29 AA; 3165 MW; 7037D0B855072AF8 CRC64;

Query Match 8.8%; Score 3; DB 1; Length 29;
Best Local Similarity 100.0%; Pred. No. 4.9e+03;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 22 EWL 24
|||
Db 11 EWL 13

RESULT 27

RS7_METTE

ID RS7_METTE STANDARD; PRT; 29 AA.
AC O93639;
DT 30-MAY-2000 (Rel. 39, Created)
DT 30-MAY-2000 (Rel. 39, Last sequence update)
DT 28-FEB-2003 (Rel. 41, Last annotation update)
DE 30S ribosomal protein S7P (Fragment).

GN RPS7P OR S7.
 OS Methanosarcina thermophila.
 OC Archaea; Euryarchaeota; Euryarchaeota orders incertae sedis;
 OC Methanosarcinales; Methanosarcinaceae; Methanosarcina.
 OX NCBI_TaxID=2210;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=DSM 1825 / TM-1;
 RX MEDLINE=99059471; PubMed=9845338;
 RA Thomas T., Cavicchioli R.;
 RT "Archaeal cold-adapted proteins: structural and evolutionary analysis
 RT of the elongation factor 2 proteins from psychrophilic, mesophilic and
 RT thermophilic methanogens.";
 RL FEBS Lett. 439:281-287(1998).
 CC -!- FUNCTION: One of the primary rRNA binding proteins, it binds
 CC directly to 16S rRNA where it nucleates assembly of the head
 CC domain of the 30S subunit. Is located at the subunit interface
 CC close to the decoding center (By similarity).
 CC -!- SUBUNIT: Part of the 30S ribosomal subunit.
 CC -!- SIMILARITY: BELONGS TO THE S7P FAMILY OF RIBOSOMAL PROTEINS.
 CC -----
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 CC -----
 DR EMBL; AF026165; AAC79199.1; -.
 DR PIR; T44245; T44245.
 DR HAMAP; MF_00480; -; 1.
 DR InterPro; IPR000235; Ribosomal_S7.
 DR PROSITE; PS00052; RIBOSOMAL_S7; PARTIAL.
 KW Ribosomal protein; RNA-binding; rRNA-binding.
 FT NON_TER 1 1
 SQ SEQUENCE 29 AA; 3217 MW; 1602B8A2E6C50C2B CRC64;

Query Match 8.8%; Score 3; DB 1; Length 29;
 Best Local Similarity 100.0%; Pred. No. 4.9e+03;
 Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 19 ERV 21
 |||
 Db 22 ERV 24

RESULT 28

SODC_OLEEU

ID SODC_OLEEU STANDARD; PRT; 29 AA.
 AC P80740;
 DT 01-NOV-1997 (Rel. 35, Created)
 DT 01-NOV-1997 (Rel. 35, Last sequence update)
 DT 15-SEP-2003 (Rel. 42, Last annotation update)
 DE Superoxide dismutase [Cu-Zn] (EC 1.15.1.1) (Allergen Ole e 5) (Ole e
 DE V) (Fragment).
 OS Olea europaea (Common olive).

OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
 OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
 OC Asteridae; lamiids; Lamiales; Oleaceae; Olea.
 OX NCBI_TaxID=4146;
 RN [1]
 RP SEQUENCE.
 RC TISSUE=Pollen;
 RX MEDLINE=98160390; PubMed=9500754;
 RA Boluda L., Alonso C., Fernandez-Caldas E.;
 RT "Purification, characterization, and partial sequencing of two new
 RT allergens of Olea europaea.";
 RL J. Allergy Clin. Immunol. 101:210-216(1998).
 CC -!- FUNCTION: Destroys radicals which are normally produced within the
 CC cells and which are toxic to biological systems (By similarity).
 CC -!- CATALYTIC ACTIVITY: 2 superoxide + 2 H(+) = O(2) + H(2)O(2).
 CC -!- COFACTOR: Binds 1 copper ion and 1 zinc ion per subunit (By
 CC similarity).
 CC -!- SIMILARITY: BELONGS TO THE CU-ZN SUPEROXIDE DISMUTASE FAMILY.
 DR InterPro; IPR001424; SOD_CU_ZN.
 DR Pfam; PF00080; sodcu; 1.
 DR PROSITE; PS00087; SOD_CU_ZN_1; PARTIAL.
 DR PROSITE; PS00332; SOD_CU_ZN_2; PARTIAL.
 KW Antioxidant; Oxidoreductase; Metal-binding; Copper; Zinc; Allergen.
 FT NON_TER 29 29
 SQ SEQUENCE 29 AA; 2973 MW; 836C7A193EDAD71E CRC64;

Query Match 8.8%; Score 3; DB 1; Length 29;
 Best Local Similarity 100.0%; Pred. No. 4.9e+03;
 Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 15 LNS 17
 |||
 Db 7 LNS 9

RESULT 29

TL16_SPIOL

ID TL16_SPIOL STANDARD; PRT; 29 AA.

AC P81834;

DT 30-MAY-2000 (Rel. 39, Created)

DT 30-MAY-2000 (Rel. 39, Last sequence update)

DT 16-OCT-2001 (Rel. 40, Last annotation update)

DE Thylakoid lumenal 16.5 kDa protein (P16.5) (Fragment).

OS Spinacia oleracea (Spinach).

OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;

OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;

OC Caryophyllidae; Caryophyllales; Chenopodiaceae; Spinacia.

OX NCBI_TaxID=3562;

RN [1]

RP SEQUENCE.

RC TISSUE=Leaf;

RX MEDLINE=98175931; PubMed=9506969;

RA Kieselbach T., Hagman A., Andersson B., Schroeder W.P.;

RT "The thylakoid lumen of chloroplasts. Isolation and
 RT characterization.";

RL J. Biol. Chem. 273:6710-6716(1998).

CC -!- SUBCELLULAR LOCATION: Chloroplast; within the thylakoid lumen.

KW Chloroplast; Thylakoid.
FT NON_TER 29 29
SQ SEQUENCE 29 AA; 3464 MW; 58B785764E2623E3 CRC64;

Query Match 8.8%; Score 3; DB 1; Length 29;
Best Local Similarity 100.0%; Pred. No. 4.9e+03;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 25 RKK 27
|||
Db 19 RKK 21

RESULT 30

CY35_DESAC

ID CY35_DESAC STANDARD; PRT; 30 AA.
AC P81079;
DT 01-NOV-1997 (Rel. 35, Created)
DT 01-NOV-1997 (Rel. 35, Last sequence update)
DT 16-OCT-2001 (Rel. 40, Last annotation update)
DE Cytochrome c3, 50 kDa (Fragment).
OS Desulfuromonas acetoxidans (Chloropseudomonas ethylica).
OC Bacteria; Proteobacteria; Deltaproteobacteria; Desulfuromonadales;
OC Desulfuromonadaceae; Desulfuromonas.
OX NCBI_TaxID=891;
RN [1]
RP SEQUENCE.
RX MEDLINE=97419123; PubMed=9271490;
RA Bruschi M., Woudstra M., Guigliarelli B., Asso M., Lojou E.,
RA Petillot Y., Abergel C.;
RT "Biochemical and spectroscopic characterization of two new
RT cytochromes isolated from Desulfuromonas acetoxidans."
RL Biochemistry 36:10601-10608(1997).
CC -!- FUNCTION: PARTICIPATES IN SULFATE RESPIRATION COUPLED WITH
CC PHOSPHORYLATION BY TRANSFERRING ELECTRONS FROM THE ENZYME
CC DEHYDROGENASE TO FERREDOXIN. THE REDOX POTENTIALS OF THIS
CC CYTOCHROME ARE -140 MV, -210 MV AND -240 MV.
CC -!- SUBUNIT: Monomer.
CC -!- SUBCELLULAR LOCATION: Periplasmic.
CC -!- PTM: BINDS 4 HEMES.
CC -!- SIMILARITY: TO OTHER C3-TYPE CYTOCHROMES.
DR InterPro; IPR000345; CytC_heme_bind.
DR PROSITE; PS00190; CYTOCHROME_C; PARTIAL.
KW Electron transport; Sulfate respiration; Heme; Periplasmic.
FT NON_TER 30 30
SQ SEQUENCE 30 AA; 3018 MW; B0D52603DD5069B8 CRC64;

Query Match 8.8%; Score 3; DB 1; Length 30;
Best Local Similarity 100.0%; Pred. No. 5.1e+03;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 11 KGK 13
|||
Db 15 KGK 17

RESULT 31

DMS3_PHYSA
 ID DMS3_PHYSA STANDARD; PRT; 30 AA.
 AC P80279;
 DT 01-FEB-1994 (Rel. 28, Created)
 DT 01-FEB-1994 (Rel. 28, Last sequence update)
 DT 15-SEP-2003 (Rel. 42, Last annotation update)
 DE Dermaseptin 3 (DS III).
 OS Phyllomedusa sauvagei (Sauvage's leaf frog).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Amphibia; Batrachia; Anura; Neobatrachia; Bufonoidea; Hylidae;
 OC Phyllomedusinae; Phyllomedusa.
 OX NCBI_TaxID=8395;
 RN [1]
 RP SEQUENCE.
 RC TISSUE=Skin secretion;
 RX MEDLINE=94139686; PubMed=8306981;
 RA Mor A., Nicolas P.;
 RT "Isolation and structure of novel defensive peptides from frog skin.";
 RL Eur. J. Biochem. 219:145-154(1994).
 CC -!- FUNCTION: POSSESSES A POTENT ANTIMICROBIAL ACTIVITY AGAINST
 CC BACTERIA FUNGI AND PROTOZOA. PROBABLY ACTS BY DISTURBING MEMBRANE
 CC FUNCTIONS WITH ITS AMPHIPATIC STRUCTURE.
 CC -!- SUBCELLULAR LOCATION: Secreted.
 CC -!- TISSUE SPECIFICITY: Skin.
 CC -!- SIMILARITY: Belongs to the frog skin active peptide (FSAP) family.
 CC Dermaseptin subfamily.
 KW Amphibian defense peptide; Antibiotic; Fungicide; Multigene family.
 SQ SEQUENCE 30 AA; 3024 MW; FD5F190C3DCBB0D7 CRC64;

Query Match 8.8%; Score 3; DB 1; Length 30;
 Best Local Similarity 100.0%; Pred. No. 5.1e+03;
 Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 26 KKL 28
 |||
 Db 23 KKL 25

RESULT 32

FTN_BACFR
 ID FTN_BACFR STANDARD; PRT; 30 AA.
 AC P28733;
 DT 01-DEC-1992 (Rel. 24, Created)
 DT 01-DEC-1992 (Rel. 24, Last sequence update)
 DT 15-SEP-2003 (Rel. 42, Last annotation update)
 DE Ferritin like protein (Fragment).
 OS Bacteroides fragilis.
 OC Bacteria; Bacteroidetes; Bacteroides (class); Bacteroidales;
 OC Bacteroidaceae; Bacteroides.
 OX NCBI_TaxID=817;
 RN [1]
 RP SEQUENCE.
 RC STRAIN=20656-2-1;
 RX MEDLINE=92406001; PubMed=1526453;
 RA Rocha E.R., Andrews S.C., Keen J.N., Brock J.H.;
 RT "Isolation of a ferritin from Bacteroides fragilis.";
 RL FEMS Microbiol. Lett. 74:207-212(1992).

CC -!- FUNCTION: MAY ALLEVIATE IRON TOXICITY IN THE PRESENCE OF
 CC OXYGEN.
 CC -!- COFACTOR: BINDS ABOUT THREE IRON ATOMS PER MOLECULE.
 CC -!- SUBUNIT: FORMS OLIGOMERS OF ABOUT 400 kDa (THE MONOMER IS ABOUT
 CC 17 kDa).
 CC -!- SIMILARITY: BELONGS TO THE FERRITIN FAMILY. PROKARYOTIC SUBFAMILY.
 CC -!- SIMILARITY: Contains 1 ferritin-like diiron domain.
 DR InterPro; IPR001519; Ferritin.
 DR Pfam; PF00210; ferritin; 1.
 DR PROSITE; PS50905; FERRITIN_LIKE; 1.
 KW Iron storage; Iron; Metal-binding.
 FT DOMAIN 1 >30 FERRITIN-LIKE DIIRON.
 FT METAL 17 17 IRON (BY SIMILARITY).
 FT NON_TER 30 30
 SQ SEQUENCE 30 AA; 3529 MW; C70505B5696EFC4F CRC64;

Query Match 8.8%; Score 3; DB 1; Length 30;
 Best Local Similarity 100.0%; Pred. No. 5.1e+03;
 Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 27 KLQ 29
 |||
 Db 5 KLQ 7

RESULT 33

GLUM_ANGAN

ID GLUM_ANGAN STANDARD; PRT; 30 AA.
 AC P41521;
 DT 01-NOV-1995 (Rel. 32, Created)
 DT 01-NOV-1995 (Rel. 32, Last sequence update)
 DT 15-SEP-2003 (Rel. 42, Last annotation update)
 DE Glucagon-like peptide (GLP).
 OS Anguilla anguilla (European freshwater eel), and
 OS Anguilla rostrata (American eel).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Actinopterygii; Neopterygii; Teleostei; Anguilliformes; Anguillidae;
 OC Anguilla.
 OX NCBI_TaxID=7936, 7938;
 RN [1]
 RP SEQUENCE.
 RC SPECIES=A.anguilla, and A.rostrata;
 RC TISSUE=Pancreas;
 RX MEDLINE=91340068; PubMed=1874385;
 RA Conlon J.M., Andrews P.C., Thim L., Moon T.W.;
 RT "The primary structure of glucagon-like peptide but not insulin has
 RT been conserved between the American eel, Anguilla rostrata and the
 RT European eel, Anguilla anguilla."
 RL Gen. Comp. Endocrinol. 82:23-32(1991).
 CC -!- SIMILARITY: BELONGS TO THE GLUCAGON FAMILY.
 DR PIR; B61125; B61125.
 DR PIR; C61125; C61125.
 DR HSSP; P01275; 1BH0.
 DR InterPro; IPR000532; Glucagon.
 DR Pfam; PF00123; hormone2; 1.
 DR SMART; SM00070; GLUCA; 1.
 DR PROSITE; PS00260; GLUCAGON; 1.

KW Glucagon family; Amidation.
FT MOD_RES 30 30 AMIDATION.
SQ SEQUENCE 30 AA; 3376 MW; 592DA5EABD6E49D0 CRC64;

Query Match 8.8%; Score 3; DB 1; Length 30;
Best Local Similarity 100.0%; Pred. No. 5.1e+03;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 28 LQD 30
|||
Db 14 LQD 16

RESULT 34

OTCC_AERPU

ID OTCC_AERPU STANDARD; PRT; 30 AA.
AC P11726;
DT 01-OCT-1989 (Rel. 12, Created)
DT 01-OCT-1989 (Rel. 12, Last sequence update)
DT 28-FEB-2003 (Rel. 41, Last annotation update)
DE Ornithine carbamoyltransferase, catabolic (EC 2.1.3.3) (OTCase)
DE (Fragment).
OS Aeromonas punctata (Aeromonas caviae).
OC Bacteria; Proteobacteria; Gammaproteobacteria; Aeromonadales;
OC Aeromonadaceae; Aeromonas.
OX NCBI_TaxID=648;
RN [1]
RP SEQUENCE.
RC STRAIN=NCIB 9232;
RX MEDLINE=85104799; PubMed=3968036;
RA Falmagne P., Portetelle D., Stalon V.;
RT "Immunological and structural relatedness of catabolic ornithine
RT carbamoyltransferases and the anabolic enzymes of enterobacteria."
RL J. Bacteriol. 161:714-719(1985).
CC -!- CATALYTIC ACTIVITY: Carbamoyl phosphate + L-ornithine = phosphate
CC + L-citrulline.
CC -!- PATHWAY: Arginine degradation via arginine deiminase; second step.
CC -!- SUBCELLULAR LOCATION: Cytoplasmic.
CC -!- SIMILARITY: BELONGS TO THE ATCASES/OTCASES FAMILY.
DR InterPro; IPR006130; Asp/Orn_Cotranf.
DR InterPro; IPR006132; OTCace_P.
DR Pfam; PF02729; OTCace_N; 1.
DR PROSITE; PS00097; CARBAMOYLTRANSFERASE; PARTIAL.
KW Transferase; Arginine metabolism.
FT NON_TER 30 30
SQ SEQUENCE 30 AA; 3654 MW; 673CB989FE72F9C1 CRC64;

Query Match 8.8%; Score 3; DB 1; Length 30;
Best Local Similarity 100.0%; Pred. No. 5.1e+03;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 4 EIQ 6
|||
Db 19 EIQ 21

RESULT 35

PCG2_PACGO

ID PCG2_PACGO STANDARD; PRT; 30 AA.
AC P82415;
DT 16-OCT-2001 (Rel. 40, Created)
DT 16-OCT-2001 (Rel. 40, Last sequence update)
DT 15-SEP-2003 (Rel. 42, Last annotation update)
DE Ponericin G2.
OS Pachycondyla goeldii (Ponerine ant).
OC Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
OC Neoptera; Endopterygota; Hymenoptera; Apocrita; Aculeata; Formicidae;
OC Ponerinae; Pachycondyla.
OX NCBI_TaxID=118888;
RN [1]
RP SEQUENCE, AND FUNCTION.
RC TISSUE=Venom;
RX MEDLINE=21264562; PubMed=11279030;
RA Orivel J., Redeker V., Le Caer J.-P., Krier F., Revol-Junelles A.-M.,
RA Longeon A., Chafotte A., Dejean A., Rossier J.;
RT "Ponericins, new antibacterial and insecticidal peptides from the
RT venom of the ant Pachycondyla goeldii.";
RL J. Biol. Chem. 276:17823-17829(2001).
CC -!- FUNCTION: BROAD SPECTRUM OF ACTIVITY AGAINST BOTH GRAM-POSITIVE
CC AND GRAM-NEGATIVE BACTERIA AND S.CEREVISIAE. HAS INSECTICIDAL
CC AND NON-HEMOLYTIC ACTIVITIES.
CC -!- SUBCELLULAR LOCATION: Secreted.
CC -!- MASS SPECTROMETRY: MW=3306.56; METHOD=MALDI.
KW Antibiotic; Insect immunity; Fungicide.
SQ SEQUENCE 30 AA; 3308 MW; A12CD4D0BAF40B5D CRC64;

Query Match 8.8%; Score 3; DB 1; Length 30;
Best Local Similarity 100.0%; Pred. No. 5.1e+03;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 11 KGK 13
|||
Db 8 KGK 10

RESULT 36

TX2_THRPR

ID TX2_THRPR STANDARD; PRT; 30 AA.
AC P83476;
DT 28-FEB-2003 (Rel. 41, Created)
DT 28-FEB-2003 (Rel. 41, Last sequence update)
DT 28-FEB-2003 (Rel. 41, Last annotation update)
DE Toxin ProTx-II.
OS Thrixopelma pruriens (Green velvet).
OC Eukaryota; Metazoa; Arthropoda; Chelicerata; Arachnida; Araneae;
OC Mygalomorphae; Theraphosidae; Thrixopelma.
OX NCBI_TaxID=213387;
RN [1]
RP SEQUENCE, FUNCTION, SUBCELLULAR LOCATION, TISSUE SPECIFICITY, MASS
RP SPECTROMETRY, AND DISULFIDE BONDS.
RC TISSUE=Venom;
RX MEDLINE=22363233; PubMed=12475222;
RA Middleton R.E., Warren V.A., Kraus R.L., Hwang J.C., Liu C.J., Dai G.,
RA Brochu R.M., Kohler M.G., Gao Y.-D., Garsky V.M., Bogusky M.J.,

RA Mehl J.T., Cohen C.J., Smith M.M.;
 RT "Two tarantula peptides inhibit activation of multiple sodium
 channels.";
 RL Biochemistry 41:14734-14747(2002).
 CC -!- FUNCTION: Inhibits voltage-gated calcium and sodium channels.
 CC Shifts the voltage-dependence of channel activation to more
 CC positive potentials.
 CC -!- SUBCELLULAR LOCATION: Secreted.
 CC -!- TISSUE SPECIFICITY: Expressed by the venom gland.
 CC -!- MASS SPECTROMETRY: MW=3827; METHOD=Electrospray.
 CC -!- MASS SPECTROMETRY: MW=3827; METHOD=MALDI.
 CC -!- SIMILARITY: BELONGS TO THE SPIDER POTASSIUM CHANNEL INHIBITORY
 CC TOXIN FAMILY.
 KW Toxin; Neurotoxin; Ionic channel inhibitor; Calcium channel inhibitor;
 KW Sodium channel inhibitor.
 FT DISULFID 2 16
 FT DISULFID 9 21
 FT DISULFID 15 25
 SQ SEQUENCE 30 AA; 3833 MW; 5B8CF4C6338C1B9B CRC64;

Query Match 8.8%; Score 3; DB 1; Length 30;
 Best Local Similarity 100.0%; Pred. No. 5.1e+03;
 Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 26 KKL 28
 |||
 Db 27 KKL 29

RESULT 37

UP61_UPEIN

ID UP61_UPEIN STANDARD; PRT; 30 AA.
 AC P82037;
 DT 30-MAY-2000 (Rel. 39, Created)
 DT 30-MAY-2000 (Rel. 39, Last sequence update)
 DT 15-SEP-2003 (Rel. 42, Last annotation update)
 DE Uperin 6.1.
 OS Uperoleia inundata (Floodplain toadlet).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Amphibia; Batrachia; Anura; Neobatrachia; Bufonoidea; Myobatrachidae;
 OC Myobatrachinae; Uperoleia.
 OX NCBI_TaxID=104953;
 RN [1]
 RP SEQUENCE, AND MASS SPECTROMETRY.
 RC TISSUE=Skin secretion;
 RA Bradford A.M., Raftery M.J., Bowie J.H., Tyler M.J., Wallace J.C.,
 RA Adams G.W., Severini C.;
 RT "Novel uperin peptides from the dorsal glands of the australian
 RT floodplain toadlet Uperoleia inundata.";
 RL Aust. J. Chem. 49:475-484(1996).
 CC -!- FUNCTION: UNKNOWN.
 CC -!- SUBCELLULAR LOCATION: Secreted.
 CC -!- TISSUE SPECIFICITY: Expressed by the skin dorsal glands.
 CC -!- MASS SPECTROMETRY: MW=3233.85; METHOD=MALDI.
 KW Amphibian defense peptide.
 SQ SEQUENCE 30 AA; 3233 MW; 4EE15B9EB110F68E CRC64;

Query Match 8.8%; Score 3; DB 1; Length 30;
Best Local Similarity 100.0%; Pred. No. 5.1e+03;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 26 KKL 28
|||
Db 24 KKL 26

RESULT 38

UP62_UPEIN

ID UP62_UPEIN STANDARD; PRT; 30 AA.
AC P82038;
DT 30-MAY-2000 (Rel. 39, Created)
DT 30-MAY-2000 (Rel. 39, Last sequence update)
DT 15-SEP-2003 (Rel. 42, Last annotation update)
DE Uperin 6.2.
OS Uperoleia inundata (Floodplain toadlet).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Amphibia; Batrachia; Anura; Neobatrachia; Bufonoidea; Myobatrachidae;
OC Myobatrachinae; Uperoleia.
OX NCBI_TaxID=104953;
RN [1]
RP SEQUENCE, AND MASS SPECTROMETRY.
RC TISSUE=Skin secretion;
RA Bradford A.M., Raftery M.J., Bowie J.H., Tyler M.J., Wallace J.C.,
RA Adams G.W., Severini C.;
RT "Novel uperin peptides from the dorsal glands of the australian
RT floodplain toadlet Uperoleia inundata.";
RL Aust. J. Chem. 49:475-484(1996).
CC -!- FUNCTION: UNKNOWN.
CC -!- SUBCELLULAR LOCATION: Secreted.
CC -!- TISSUE SPECIFICITY: Expressed by the skin dorsal glands.
CC -!- MASS SPECTROMETRY: MW=3261.85; METHOD=MALDI.
KW Amphibian defense peptide.
SQ SEQUENCE 30 AA; 3261 MW; 4EE15B9EB10841DE CRC64;

Query Match 8.8%; Score 3; DB 1; Length 30;
Best Local Similarity 100.0%; Pred. No. 5.1e+03;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 26 KKL 28
|||
Db 24 KKL 26

RESULT 39

VAA2_EQUAR

ID VAA2_EQUAR STANDARD; PRT; 30 AA.
AC Q04238;
DT 01-OCT-1996 (Rel. 34, Created)
DT 01-OCT-1996 (Rel. 34, Last sequence update)
DT 28-FEB-2003 (Rel. 41, Last annotation update)
DE Vacuolar ATP synthase catalytic subunit A, isoform 2 (EC 3.6.3.14)
DE (Fragment).
OS Equisetum arvense (Field horsetail) (Common horsetail).
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;

OC Equisetophyta; Sphenopsida; Equisetales; Equisetaceae; Equisetum.
 OX NCBI_TaxID=3258;
 RN [1]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=93138084; PubMed=8422915;
 RA Starke T., Gogarten J.P.;
 RT "A conserved intron in the V-ATPase A subunit genes of plants and
 RT algae.";
 RL FEBS Lett. 315:252-258(1993).
 CC -!- FUNCTION: CATALYTIC SUBUNIT OF THE PERIPHERAL V1 COMPLEX OF
 CC VACUOLAR ATPASE. V-ATPASE VACUOLAR ATPASE IS RESPONSIBLE FOR
 CC ACIDIFYING A VARIETY OF INTRACELLULAR COMPARTMENTS IN EUKARYOTIC
 CC CELLS.
 CC -!- CATALYTIC ACTIVITY: ATP + H(2)O + H(+) (In) = ADP + phosphate +
 CC H(+) (Out).
 CC -!- SUBUNIT: V-ATPASE IS AN HETEROMULTIMERIC ENZYME COMPOSED OF A
 CC PERIPHERAL CATALYTIC V1 COMPLEX (MAIN COMPONENTS: SUBUNITS A, B,
 CC C, D, E, AND F) ATTACHED TO AN INTEGRAL MEMBRANE V0 PROTON PORE
 CC COMPLEX (MAIN COMPONENT: THE PROTEOLIPID PROTEIN).
 CC -!- MISCELLANEOUS: TWO SEPARATE GENES ENCODE THE CATALYTIC 70 kDa
 CC V-ATPASE SUBUNIT IN PSILLOTUM AND EQUISETUM.
 CC -!- SIMILARITY: Belongs to the ATPase alpha/beta chains family.
 CC -----
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 DR EMBL; X56984; CAA40302.1; -.
 DR PIR; S21815; S21815.
 DR InterPro; IPR000194; ATPase_a/bcentre.
 DR PROSITE; PS00152; ATPASE_ALPHA_BETA; PARTIAL.
 KW ATP synthesis; Hydrogen ion transport; Hydrolase; ATP-binding;
 KW Multigene family.
 FT NON_TER 1 1
 FT NON_TER 30 30
 SQ SEQUENCE 30 AA; 3372 MW; 51CCA4A3DA9E5D84 CRC64;

Query Match 8.8%; Score 3; DB 1; Length 30;
 Best Local Similarity 100.0%; Pred. No. 5.1e+03;
 Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 18 MER 20
 |||
 Db 23 MER 25

RESULT 40
 Y523_BORBU
 ID Y523_BORBU STANDARD; PRT; 30 AA.
 AC 051473;
 DT 15-DEC-1998 (Rel. 37, Created)
 DT 15-DEC-1998 (Rel. 37, Last sequence update)
 DT 16-OCT-2001 (Rel. 40, Last annotation update)

DE Hypothetical protein BB0523.
 GN BB0523.
 OS *Borrelia burgdorferi* (Lyme disease spirochete).
 OC Bacteria; Spirochaetes; Spirochaetales; Spirochaetaceae; *Borrelia*.
 OX NCBI_TaxID=139;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=ATCC 35210 / B31;
 RX MEDLINE=98065943; PubMed=9403685;
 RA Fraser C.M., Casjens S., Huang W.M., Sutton G.G., Clayton R.A.,
 RA Lathigra R., White O., Ketchum K.A., Dodson R., Hickey E.K., Gwinn M.,
 RA Dougherty B., Tomb J.-F., Fleischmann R.D., Richardson D.,
 RA Peterson J., Kerlavage A.R., Quackenbush J., Salzberg S., Hanson M.,
 RA van Vugt R., Palmer N., Adams M.D., Gocayne J.D., Weidman J.,
 RA Utterback T., Watthey L., McDonald L., Artiach P., Bowman C.,
 RA Garland S., Fujii C., Cotton M.D., Horst K., Roberts K., Hatch B.,
 RA Smith H.O., Venter J.C.;
 RT "Genomic sequence of a Lyme disease spirochaete, *Borrelia*
 RT *burgdorferi*.";
 RL Nature 390:580-586(1997).
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 DR EMBL; AE001154; AAC66894.1; -.
 DR PIR; B70165; B70165.
 DR TIGR; BB0523; -.
 KW Hypothetical protein; Complete proteome.
 SQ SEQUENCE 30 AA; 3431 MW; DE437B15D2A48AA8 CRC64;

Query Match 8.8%; Score 3; DB 1; Length 30;
 Best Local Similarity 100.0%; Pred. No. 5.1e+03;
 Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 19 ERV 21
 |||
 Db 26 ERV 28

Search completed: January 14, 2004, 10:35:33
 Job time : 7.61371 secs